

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 08:28:56 ; Search time 1704.01 Seconds  
(without alignments)  
6154.385 Million cell updates/sec

Title: US-09-826-212-1\_COPY\_183\_959  
Perfect score: 777  
Sequence: 1 atggccggatccccaagac.....tgcttcgattgtgtgtgt

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST : \*  
1: em\_estda : \*  
2: em\_esthum : \*  
3: em\_estin : \*  
4: em\_estnu : \*  
5: em\_estov : \*  
6: em\_estpl : \*  
7: em\_estro : \*  
8: em\_hlc : \*  
9: gb\_estl : \*  
10: gb\_est2 : \*  
11: gb\_hlc : \*  
12: gb\_gss : \*  
13: em\_gss\_hum : \*  
14: em\_gss\_inv : \*  
15: em\_gss\_pln : \*  
16: em\_gss\_vrt : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	766	98.6	1034	11	BC017852 Homo sapi
2	450.4	58.0	452	9	AA861474 ak21c06.s
3	375.2	48.3	769	10	BG545631 602572889
4	368.8	47.5	923	10	BM045988 603625140
5	353	45.4	454	9	AA150541 z144b01.s
6	336.2	43.3	428	10	BF899559 PM4-MT020
7	334.4	43.0	737	10	BM046590 60362666
8	329.2	42.4	365	9	BE175577 RCS-HT058
9	315.4	40.6	538	9	AU126850 AU126850
10	307.4	39.6	826	10	BM048564 603623901
11	292.2	37.6	546	9	A1821105 nr87h08.y
12	262.8	33.8	598	9	AA150849 z144b01.t
13	260	33.5	462	9	AA150849 z144b01.t
14	236.4	30.4	484	10	BI020428 CM3-MT029
15	232.2	29.9	408	10	BI019989 CM3-MT029
16	227.2	29.2	258	9	AW372179 AW372179
17			768	10	BI753417 BI753417

18	222.2	28.6	770	10	BI825012
19	216.6	27.9	824	10	BE548028
20	213.4	27.5	821	10	BM049457
21	203.4	26.2	720	10	BG681978
22	201.8	26.0	536	9	AA453916
23	197.2	25.4	917	9	AL529460
24	193.4	24.9	1208	10	BM478250
25	186.6	24.0	787	10	BE745635
26	185.8	23.9	786	10	BI818469
27	184.6	23.8	222	10	BI025710
28	184	23.7	1156	10	BG250320
29	181.8	23.4	352	10	T71406
30	178.2	22.9	848	10	BE546076
31	175	22.5	676	10	BG436729
32	173.2	22.3	858	9	AL515088
33	172.2	22.2	209	10	BF056044
34	170.4	21.9	1073	10	BG325647
35	169.4	21.8	753	10	BE780380
36	168	21.6	492	9	AM298308
37	146.2	18.8	469	9	AA223122
38	129.8	16.7	997	10	BE563253
39	125.2	16.1	346	10	BF762329
40	125	16.1	343	9	AA031883
41	123.2	15.9	339	10	BF762292
42	120.2	15.5	790	10	BF038233
43	118.6	15.3	524	12	AO53831
44	118.6	15.3	838	12	AO748776
45	118	15.2	916	10	BM043896

#### ALIGNMENTS

RESULT 1  
LOCUS BC017852 1034 bp mRNA linear HTC 06-DEC-2001  
DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain, clone IMAGE:4700855,  
mRNA.

ACCESSION BC017852 GI:17389657  
VERSION BC017852.1  
KEYWORDS HTC.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Strausberg, R.  
TITLE 1 (bases 1 to 1034)  
JOURNAL Direct Submission  
Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LULM)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>  
Contact: (Dickson, Mark) [mdc@paxil.stanford.edu](mailto:mdc@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LULM at: <http://image.llnl.gov>  
Service: IRAL Plate: 36 Row: P Column: 3  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835042  
This clone has the following problem: frame shifted.  
Location/Qualifiers

#### FEATURES



DB	212	ATGAACACACAGCCGGGAGCTCTCCGCCAGCTGCTGAAGAGACAATGACACACAGCCCA	153
OY	562	gagactcctgcccagctgctgtaagaacaatgatcacaccacccgggagactctgccc	621
Db	152	GGGACTCTCTGCCCCAGCTGCTGTAAGAGACAATGACACACAGCCCGGGAGCTCTGCCCA	93
OY	622	gctgctgtaagaacaatgacacacacacccgggagactctgcccagctgctgtaagaaca	681
Db	92	GCTGCTGAAGAGACAATGACACACACAGCCAGGAGGACTCTGCCCGAGCTGCTGAAGAGACA	33
OY	682	atgaccaccagccgggagactctgctcttc	713
Db	32	ATGACCACCAGCCCGGGAGCTCTGCTCTTC	1
RESULT	3		
LOCUS	BG545631	769 bp	mrna
DEFINITION	602572889p1 NIH_MGC_77	Human sapiens	CDNA clone IMAGE:4700855 5',
ACCESSION	BG545631		
VERSION	BG545631.1	GI:3544296	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 769)		
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Struhsberg, Ph.D.		
	Email: <a href="mailto:cgapds-remail.nih.gov">cgapds-remail.nih.gov</a>		
	Tissue Procurement: Clontech Laboratories, Inc.		
	CDNA Library Preparation: Clontech Laboratories, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	<a href="http://Image.Lnl.gov">http://Image.Lnl.gov</a>		
	Plate: L1CMI535 row: b column: 24		
	High quality sequence stop: 617.		
FEATURES			
source	1..769		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4700855"		
	/clone_id="NIH_MGC_77"		
	/lab_host="DH10B (TI phage-resistant)"		
	/note="Organ: lung; Vector: pDMR-LIB (Clontech); Site: 1:		
	SflI (ggcgccctcgcc); Site: 2: SflI (ggccatattggcc); 5' and		
	3' adaptors were used in cloning as follows: 5' adaptor		
	sequence: 5'-CACGGCATATATGGCC-3' and 3' adaptor sequence:		
	5'-ATTCTAGAGCCGAGGAGCGCCGACACTG-dT(30)BN-3' (where B = A,		
	C, or G and N = A, C, G, or T). Average insert size 1.9		
	kb (range 0.5-4.0 kb). 12/15 colonies contained inserts		
	by PCR. This library was enriched for full-length clones		
	and was constructed by Clontech Laboratories (Palo Alto,		
	CA). Note: this is a NIH-MGC Library."		
BASE COUNT	203 a	220 g	139 t
ORIGIN			
Query Match	48.3%;	Score 375.2;	DB 10; Length 769;
Best Local Similarity	94.5%;	Pred. No. 1.6e-95;	
Matches	497; Conservative	0; Mismatches	18; Indels 11; Gaps 10;
OY	1	atgcccggatcccccaagacctaaagtctgctgctatcatcgtcgcggtcctctgcca	60
Db	199	ATGGCCCGGATCCCAAGACCTTAAGTTCGTCGTCATCGTCGCGCTCGTGCA	258
OY	61	gtccagctactctgcacacactgcccgcagggaggaattcccccagagacatgtgac	120

Db	259	GTCCAGCTTACTCTGCGCACACCTGCCGCGCAGGAGGAAGTTCCCGACGACACAGTGGCC	318
QY	121	ccacagcacagagagcacagcttcaagaaggagagagtgctccagcagagatctcatagatca	180
Db	319	CCACAGCAACAGAGGACAGCTTCAAGGGGGAGGAGTGTCCACGACGATGTCATGATCA	378
QY	181	gaacatactgagagctctgtaaccgg-tgcacagagagg-tgtgatatcaac-caagcttcc	237
Db	379	GAACATACTGGAGGCTGTGAACCCGTTGGACAGAGGGTGTGGATTACACACAGCGTTCC	438
QY	238	aacaatgacacctctctgttt-ccatgtcacagttgttaatcagatcaaaac-ataaa	295
Db	439	AACATGAACTCTTCTGCTTCCCATGTACAGTTTGTATTAATCAGATCAAAAAACGATTAAA	498
QY	296	gtctctgacacatgacccacagagacagatgtgtcagtgtaaaagagcaccttcggaaatg	355
Db	499	GTTCTGTGACCATGACACAGAGACACAGTGTGTCACTGTAAAGAAAGGCACTTCCGAGATG	558
QY	356	aaaatctcccccagagatgtgcgcggaaagtgtacaggtg-ccctatggggaaagtcgaat-	413
Db	559	GAAAATCCCCAGAGATGTGCGGAAGTGTACAGGTGACCTTATTGGGGAATCCAAATGC	618
QY	414	cagtaattgttcagctcct-aggatgatataccagatgtgttgaagaattgtgtccaatgca	472
Db	619	CAGGAATGCTAGCTACTGTGGGATGATATTCGAAGTGAAGGAAGAAATTTGGTGGCCAAATGCCA	678
QY	473	ctgttgaaacccacagctgtctgaagagacaatgaacaccacagccggg	518
Db	679	CTGTGGAAA-CCCAGATGCTGA--AGAAATGTGACACACAGCCGCGGG	721
RESULT	4		
LOCUS	BM045988	923 bp	mRNA linear EST 07-NOV-2001
DEFINITION	603625140F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5451897 5',		
ACCESSION	BM045988		
VERSION	BM045988.1	GI:16775255	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 923)		
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://Image.lnl.gov">http://Image.lnl.gov</a> Plate: LNCMI942 row: P column: 10 High quality sequence stop: 757. Location/Qualifiers 1..923 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="5451897" /clone_lib="NIH_MGC_40" /tissue_type="Carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).		
FEATURES	source		





KEYWORDS	EST
SOURCE	human
ORGANISM	Homo sapiens
REFERENCE	Eumariyola, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 428) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar. 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4*MT0201-1-031200-002-c07&t3=2000-12-03&t4=1) Seq primer: puc18 forward High quality sequence stop: 427. Location/Qualifiers 1..428 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MT0201" /dex_stage="Adult" /note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." BASE COUNT 119 a 122 c 109 g 78 t ORIGIN
Query Match	43.3%; Score 336.2; DB 10; Length 428;
Best Local Similarity	96.1%; Pred. No. 1.5e-84;
Matches 366; Conservative	0; Mismatches 13; Indels 2; Gaps 2;
QY	1 atggccgagatcccccaaacacctaaagtcgtcgtcgtcatcgtcgagtcgtctgtgcca 60
Db	46 ATGGCCCGGATGCCCAACACCTTAAAGTTTCGTCTGTCATCTGTGC-6TCTGTGGCA 104
QY	61 gtctagcttactctgtccaccactgtcccgcgacagagagaagttcccccagacagtggtc 120
Db	105 GTCTAGCTTACTCTGTGCACCACTGTGCGGAGGAGGAAGTCCCCACAGCACTGGCC 164
QY	121 ccacagcaacagagagacagcttcaaggaggagagagtgctcaagcagatctcatgatca 180
Db	165 CCACGCAACAGAGGCAAGCTTCAAGGGGGGAGAGTGTCCAGCGAGATCTCATGAGATCA 224
QY	181 gaacatactggagacctgttaaccctgacacagagagtggtgatttaacaaagcttccaac 240
Db	225 GAACATACTGGAGCGCTTTAAACCCGTGCGCAGAGGGTGTGATTTACACCAACCTTCCAAC 284
QY	241 aatgaaccttctgtctcccatgtacagttgtttaataagataccaanaacataaaagttcc 300
Db	285 AATGAACCTTCTGTCTCCCATGTACAGTTGTTAATCAGATCAAAACATTAAGTTCC 344
QY	301 tgcaccatgaccagagacacagtggtgttcaagttt-aaagaagcaccttcggaatgaa 359

Db	345	TCACCATGACACAGACAGACAGTGTGTGCTAGTATAAAGAGGACCTTCGGAATGAAAA	404
Qy	360	ctcccagagatgtgccgga	380
Db	405	CTCCCGACAGATGTCCGGAA	425
RESULT	7		
BM046590			
LOCUS	BM046590	737 bp	mRNA
DEFINITION	603626666f1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:5453129 5',		linear EST 07-NOV-2001
ACCESSION	BM046590		
VERSION	BM046590.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
TITLE	1 (bases 1 to 737)		
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@bbs.femail.nih.gov		
	Tissue Procurement: DCTD/DTF		
	CDNA Library Preparation: Ling Hong/Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: LCM1946 row: c column: 18		
FEATURES	High quality sequence stop: 737.		
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	/clone="IMAGE:5453129"		
	/clone_lib="NIH_MGC_40"		
	/tissue_type="carcinoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;		
	Site_2: EcoRI; cDNA made by oligo-dT priming.		
	Directionally cloned into EcoRI/XhoI sites using the		
	following 5' adaptor: GCGACGAG(G). Library constructed by		
	Ling Hong in the laboratory of Gerald M. Rubin (University		
	of California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: This is a NIH_MGC Library."		
BASE COUNT	182 a 209 c 196 g 150 t		
ORIGIN			
Query Match	43.0%;	Score 334.4;	DB 10; Length 737;
Best Local Similarity	83.9%;	Pred. No. 6.1e-84;	
Matches 426;	Conservative 0;	Mismatch 76;	Indels 6; Gaps 4;
Qy	6	ccgagtcgcccaagaccctaaagtcgtcgtcgtcgcgcgtcgtcgtccagtcct	65
Db	181	CCTGACGCCCAAGATCTTAAAGTTCGTGCTTCATCGTGGCGTTCGTCCGTCG	240
Qy	66	agcttactctgtccacactatgcccggcagagaggaattcccaagacaagtgtcccca	125
Db	241	GATTACCTGTGCGACCAATCCCGGCGACGACCAAGTTCCCGACGAGAGAGTGGCC	300
Qy	126	gaacaagagacacagcttcaagggagagagtgtccaagaagatctatagatcaga	185
Db	301	GCAACAGAGCGGCACACCTCAAGAGAGAGAGTGTCCACAGATCTCATATCAGAT	360
Qy	186	tacttgagcctgtlaaccctgtcagacagaggtgttgattacaaccaagcttccaatga	245
Db	361	TACTTGACCTGTTAACCCGTGTACAGAGAGGTGTGATTACACATTCCTTCAACAA	420

FEATURES	source	Location/Qualifiers
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		/db_xref="taxon:9606"
		/clone="NT2RP2000080"
		/clone_id="NT2RP2"
		/cell_type="teratocarcinoma"
		/cell_line="NT2"
		/note="Vector: pME18SFL3: mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT	136 a 154 c 141 g 100 t	
ORIGIN		others



This read is a RESEQUENCE of a previously sequenced human clone  
Original clone citation: see original entry for original citation  
Information  
This 5' resequenced clone has no previous 5' data to verify this  
new read against  
Insert length: 3185      Std Error: 0.00  
Seq primer: -40RP from c1bco  
High quality sequence stop: 408.

## 1.546

BASE COUNT	128 a	156 c	143 g	117 t	2 others
ORIGIN					

Best Local Similarity -85.5%; Pred. NO. 5.2e-72;  
Matches 32; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Db 168 CCTGACCCCAAGATCCTAAGTTCGTCGCTTCATCGTCGCGGTCTCTGCTGCCGCGTCCG 227

Db 228 GGTGACTCTGCCACCATCCCCCGGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCACA 287

Db 288 GCAACAGAGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGATTA 347

Db 348 TACTGGAGCCTGTAACCCGTGCACAGAGGTGTGATTACACCATTGCTTCCACAATT 407

Db 408 GCCTTCTTGCCCTGCTATGTACNAGTTTGTAAATCAGGTCAAACAATAAAAGTTCCTGTAC 467

Db 468 CACGACCAGACACCGTGTGTCA GTGGTGAAAGGAGCTTNCAGGATAAAACTGCC 527

Db 528 TGAGATGTGCTCGACGTGT 546

LOCUS	AA150849	398 bp	mRNA	linear	EST 19-MAY-2004
LOCUS	AA150849	398 bp	mRNA	linear	EST 19-MAY-2004

VERSION AA150849.1 GI:1722360

Mammalia; Eutheria; Primates; Catarrhini; ~~Hominini~~; Hominae; Homo.

Chissee, S., Dierlich, N., Dubucq, T., Favello, A., Gish, N., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Maris, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierly-Meg, J., Treviski, E., Underwood, K., Wohlmann, P., Watson, R., Wilson, R. and Watra, M. Generation and analysis of 260,000 human expressed sequence tags  
*Genome Res.* 6 (9), 807-828 (1996)

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: ~~test@watson.wustl.edu~~  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 1559 Std Error: 0.00  
Seq Primer: -28M13 rev2 from Amersham  
High quality sequence stop: 357.

~~/organism="Homo sapiens~~

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/dr_xref="GDB:380973"
/dr_xref="taxon:9606"
/clone="IMAGE:504745"
/clone.lib="Soares_pregnant_uterus_NBDHP"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="(Organ: uterus; Vector: pT7T3-Pac; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dN) primer [5', AACGTGAAGAAATTGCGCGCCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

```

Matches 264; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 133 ATGCCCCGATCCCCAAGACCTAAAGTTGGTCGTCGTCATCGTCGGGTCCTGCTGCCA 192

Db 193 GTCCCTAGCTTACTCTGCCACCACTGCCCGGCAAGAGGGAAGTTCGCCAGCAGACAGTGCC 252

Db 253 CCACAGCAACAGAGGCACAGCTTCAAGGGGAGGAGTGTCTCCAGCAGGATCTCATAGATCA 312

—

**DEFINITION** DKFZp6866F087\_r1 686 (synonym: h1cc3) Homo sapiens cDNA clone

ORGANISM	TITLE	JOURNAL	MEDLINE	COMMENT
Human sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 484) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAPS/PLCR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?lib=CM3&t2=CM3-MT0292- 120101-616-005&t3=2001-01-12&t4=1) Seq primer: puc 18 forward High quality sequence start: 13 High quality sequence stop: 484. Location/Qualifiers 1. .484 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MT0292" /dev_stage="Adult" /note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 , 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
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Search completed: August 13, 2002, 10:49:52  
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REFERENCE  1 (bases 1 to 408)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
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            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
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JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
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Tue Aug 13 16:24:34 2002

us-09-826-212-1\_copy\_183\_959.rst

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Page 11





GenCore version 4.5  
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Searched: 231628 seqs, 24425594 residues

Word size : 5

Total number of hits satisfying chosen parameters: 2406

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
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## SUMMARIES

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145	6	2.6	434	1	US-08-184-237-6	Sequence 6, Appl	218	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
146	6	2.6	434	1	US-08-482-920-6	Sequence 6, Appl	219	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
147	6	2.6	434	2	US-08-484-341-6	Sequence 6, Appl	220	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
148	6	2.6	434	3	US-08-483-502-6	Sequence 6, Appl	221	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
149	6	2.6	434	4	US-08-801-344-9	Sequence 9, Appl	222	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
150	6	2.6	462	4	US-09-498-599-9	Sequence 9, Appl	223	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
151	6	2.6	462	4	US-08-218-943-2	Sequence 2, Appl	224	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
152	6	2.6	487	1	US-08-999-723-2	Sequence 2, Appl	225	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
153	6	2.6	518	3	US-08-821-984-6	Sequence 2, Appl	226	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
154	6	2.6	518	4	US-08-821-984-6	Sequence 6, Appl	227	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
155	6	2.6	529	3	US-08-821-984-6	Sequence 6, Appl	228	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
156	6	2.6	529	3	US-08-821-984-6	Sequence 6, Appl	229	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
157	6	2.6	529	3	US-09-329-749-8	Sequence 8, Appl	230	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
158	6	2.6	529	4	US-09-329-749-8	Sequence 8, Appl	231	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
159	6	2.6	542	4	US-08-675-816-6	Sequence 6, Appl	232	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
160	6	2.6	547	4	US-08-930-001-2	Sequence 2, Appl	233	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
161	6	2.6	549	2	US-08-676-279-59	Sequence 59, Appl	234	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
162	6	2.6	569	2	US-08-750-723A-2	Sequence 2, Appl	235	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
163	6	2.6	569	2	US-09-191-275-2	Sequence 2, Appl	236	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
164	6	2.6	583	4	US-09-311-311C-24	Sequence 24, Appl	237	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
165	6	2.6	609	4	US-08-980-115-11	Sequence 11, Appl	238	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
166	6	2.6	609	4	US-09-232-200-69	Sequence 69, Appl	239	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
167	6	2.6	609	4	US-09-232-197-69	Sequence 69, Appl	240	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
168	6	2.6	609	4	US-09-232-201-69	Sequence 69, Appl	241	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
169	6	2.6	613	4	US-09-232-191-7	Sequence 7, Appl	242	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
170	6	2.6	613	4	US-09-232-200-7	Sequence 7, Appl	243	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
171	6	2.6	613	4	US-09-232-200-94	Sequence 94, Appl	244	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
172	6	2.6	613	4	US-09-232-197-7	Sequence 7, Appl	245	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl
173	6	2.6	613	4	US-09-232-197-94	Sequence 94, Appl	246	6	2.6	5588	4	US-08-666-473-54	Sequence 54, Appl

247	5	2.1	17	1	US-08-518-474-10	Sequence 10, Appl	320	5	2.1	30	3	US-08-433-522A-19	Sequence 19, Appl
248	5	2.1	18	1	US-08-050-319B-5	Sequence 5, Appl	321	5	2.1	30	3	US-08-801-028-82	Sequence 82, Appl
249	5	2.1	18	2	US-08-465-982-5	Sequence 5, Appl	322	5	2.1	30	3	US-09-135-166-19	Sequence 19, Appl
250	5	2.1	19	2	US-08-836-791-4	Sequence 4, Appl	323	5	2.1	30	3	US-09-340-154-82	Sequence 82, Appl
251	5	2.1	19	3	US-08-792-632A-42	Sequence 42, Appl	324	5	2.1	30	4	US-08-477-346-246	Sequence 246, Appl
252	5	2.1	20	1	US-08-103-742-30	Sequence 30, Appl	325	5	2.1	30	4	US-08-942-046-19	Sequence 19, Appl
253	5	2.1	20	2	US-08-749-852-53	Sequence 53, Appl	326	5	2.1	30	4	US-08-473-089-246	Sequence 246, Appl
254	5	2.1	20	2	US-08-749-852-55	Sequence 55, Appl	327	5	2.1	30	5	PCT-US95-09338-82	Sequence 82, Appl
255	5	2.1	21	1	US-07-969-931-2	Sequence 2, Appl	328	5	2.1	30	5	PCT-US95-09339-82	Sequence 82, Appl
256	5	2.1	21	1	US-07-855-417A-2	Sequence 2, Appl	329	5	2.1	31	1	US-08-149-839B-7	Sequence 7, Appl
257	5	2.1	21	2	US-08-997-080-4	Sequence 4, Appl	330	5	2.1	31	1	US-08-451-568-7	Sequence 7, Appl
258	5	2.1	21	2	US-08-997-080-13	Sequence 13, Appl	331	5	2.1	31	1	US-08-451-566-7	Sequence 7, Appl
259	5	2.1	21	2	US-08-997-362-4	Sequence 4, Appl	332	5	2.1	31	2	US-08-244-951A-4	Sequence 4, Appl
260	5	2.1	21	3	US-08-997-362-13	Sequence 13, Appl	333	5	2.1	31	2	US-08-777-113-7	Sequence 7, Appl
261	5	2.1	21	3	US-08-873-970-4	Sequence 4, Appl	334	5	2.1	31	4	US-09-248-588-27	Sequence 27, Appl
262	5	2.1	21	3	US-08-873-970-13	Sequence 13, Appl	335	5	2.1	32	6	5208144-16	Patent No. 5208144
263	5	2.1	21	3	US-08-478-208-14	Sequence 14, Appl	336	5	2.1	33	2	US-08-244-951A-2	Sequence 2, Appl
264	5	2.1	21	4	US-09-095-855-4	Sequence 4, Appl	337	5	2.1	33	2	US-08-389-011-2	Sequence 2, Appl
265	5	2.1	21	4	US-09-095-855-13	Sequence 13, Appl	338	5	2.1	33	3	US-08-403-917A-2	Sequence 2, Appl
266	5	2.1	21	4	US-08-705-347A-4	Sequence 4, Appl	339	5	2.1	33	4	US-09-348-952A-2	Sequence 2, Appl
267	5	2.1	21	4	US-08-705-347A-13	Sequence 13, Appl	340	5	2.1	34	2	US-08-602-264A-10	Sequence 10, Appl
268	5	2.1	21	4	US-09-324-542-4	Sequence 4, Appl	341	5	2.1	34	2	US-08-372-887-11	Sequence 11, Appl
269	5	2.1	21	4	US-09-324-542-13	Sequence 13, Appl	342	5	2.1	34	3	US-08-461-018A-10	Sequence 10, Appl
270	5	2.1	23	1	US-07-656-566-1	Sequence 1, Appl	343	5	2.1	34	4	US-09-216-958-10	Sequence 10, Appl
271	5	2.1	23	2	US-08-244-951A-3	Sequence 3, Appl	344	5	2.1	35	1	US-07-621-670-3	Sequence 3, Appl
272	5	2.1	23	4	US-09-227-357-467	Sequence 467, App	345	5	2.1	35	1	US-08-418-893D-15	Sequence 15, Appl
273	5	2.1	24	2	US-08-765-179B-22	Sequence 22, Appl	346	5	2.1	35	2	US-08-244-951A-6	Sequence 6, Appl
274	5	2.1	24	2	US-08-455-968E-23	Sequence 49, Appl	347	5	2.1	35	4	US-08-227-357-228	Sequence 228, App
275	5	2.1	24	2	US-08-455-968E-23	Sequence 23, Appl	348	5	2.1	36	4	US-08-789-333F-22	Sequence 22, Appl
276	5	2.1	26	1	US-08-484-635-94	Sequence 94, Appl	349	5	2.1	36	4	US-09-169-015-32	Sequence 32, Appl
277	5	2.1	26	2	US-08-484-631-94	Sequence 94, Appl	350	5	2.1	36	4	US-09-133-944-21	Sequence 21, Appl
278	5	2.1	26	2	US-08-139-609-12	Sequence 12, Appl	351	5	2.1	38	1	US-08-176-500-66	Sequence 66, Appl
279	5	2.1	26	2	US-08-827-570-94	Sequence 94, Appl	352	5	2.1	38	1	US-08-471-052A-66	Sequence 66, Appl
280	5	2.1	26	6	5510466-5	Patent No. 5510466	353	5	2.1	38	1	US-08-189-331-65	Sequence 65, Appl
281	5	2.1	27	2	US-08-244-951A-5	Sequence 5, Appl	354	5	2.1	38	2	US-08-471-839-66	Sequence 66, Appl
282	5	2.1	28	4	US-09-058-459-3	Sequence 3, Appl	355	5	2.1	38	2	US-08-471-800-66	Sequence 66, Appl
283	5	2.1	28	4	US-09-058-459-4	Sequence 4, Appl	356	5	2.1	38	2	US-08-471-068-66	Sequence 66, Appl
284	5	2.1	28	4	US-09-058-459-5	Sequence 5, Appl	357	5	2.1	40	3	US-09-037-524-4	Sequence 4, Appl
285	5	2.1	28	4	US-09-058-459-6	Sequence 6, Appl	358	5	2.1	40	6	5177197-36	Patent No. 5177197
286	5	2.1	28	4	US-09-058-459-7	Sequence 7, Appl	359	5	2.1	42	1	US-08-239-256-17	Sequence 17, Appl
287	5	2.1	28	4	US-09-058-459-10	Sequence 10, Appl	360	5	2.1	42	1	US-08-050-319B-42	Sequence 42, Appl
288	5	2.1	28	4	US-09-058-459-11	Sequence 11, Appl	361	5	2.1	42	2	US-08-465-982-42	Sequence 42, Appl
289	5	2.1	28	4	US-09-058-459-12	Sequence 12, Appl	362	5	2.1	43	1	US-08-050-319B-31	Sequence 31, Appl
290	5	2.1	28	4	US-09-058-459-16	Sequence 16, Appl	363	5	2.1	43	1	US-08-616-368A-33	Sequence 33, Appl
291	5	2.1	28	4	US-09-058-459-17	Sequence 17, Appl	364	5	2.1	43	2	US-08-465-982-11	Sequence 11, Appl
292	5	2.1	28	4	US-09-058-459-21	Sequence 21, Appl	365	5	2.1	43	4	US-09-054-298-33	Sequence 33, Appl
293	5	2.1	28	4	US-09-127-926-3	Sequence 3, Appl	366	5	2.1	43	4	US-08-818-655-33	Sequence 33, Appl
294	5	2.1	28	4	US-09-127-926-4	Sequence 4, Appl	367	5	2.1	44	2	US-08-559-492-13	Sequence 13, Appl
295	5	2.1	28	4	US-09-127-926-5	Sequence 5, Appl	368	5	2.1	45	4	US-08-881-450A-16	Sequence 16, Appl
296	5	2.1	28	4	US-09-127-926-6	Sequence 6, Appl	369	5	2.1	46	2	US-08-613-235-1	Sequence 1, Appl
297	5	2.1	28	4	US-09-127-926-10	Sequence 10, Appl	370	5	2.1	48	1	US-08-485-455D-65	Sequence 65, Appl
298	5	2.1	28	4	US-09-127-926-11	Sequence 11, Appl	371	5	2.1	48	2	US-08-637-759B-297	Sequence 297, App
299	5	2.1	28	4	US-09-127-926-12	Sequence 12, Appl	372	5	2.1	48	2	US-08-482-130C-65	Sequence 65, Appl
300	5	2.1	28	4	US-09-127-926-16	Sequence 16, Appl	373	5	2.1	48	2	US-08-484-211C-65	Sequence 65, Appl
301	5	2.1	28	4	US-09-127-926-17	Sequence 17, Appl	374	5	2.1	48	3	US-08-871-355A-297	Sequence 297, App
302	5	2.1	28	4	US-09-127-926-21	Sequence 21, Appl	375	5	2.1	48	3	US-08-906-769-65	Sequence 65, Appl
303	5	2.1	29	1	US-08-149-839B-5	Sequence 5, Appl	376	5	2.1	48	3	US-08-906-616-65	Sequence 65, Appl
304	5	2.1	29	1	US-08-451-568-5	Sequence 5, Appl	377	5	2.1	48	4	US-08-817-795-65	Sequence 65, Appl
305	5	2.1	29	1	US-08-451-566-5	Sequence 5, Appl	378	5	2.1	48	4	US-08-485-443B-65	Sequence 65, Appl
306	5	2.1	29	2	US-08-686-594-22	Sequence 22, Appl	379	5	2.1	48	4	US-08-639-075A-65	Sequence 65, Appl
307	5	2.1	29	2	US-08-505-486-81	Sequence 81, Appl	380	5	2.1	48	4	US-09-012-431-65	Sequence 65, Appl
308	5	2.1	29	3	US-08-777-113-5	Sequence 5, Appl	381	5	2.1	48	4	US-09-012-692-55	Sequence 55, Appl
309	5	2.1	29	3	US-08-801-028-81	Sequence 81, Appl	382	5	2.1	48	4	US-08-906-613-65	Sequence 65, Appl
310	5	2.1	29	3	US-09-340-154-81	Sequence 81, Appl	383	5	2.1	48	4	US-09-201-945-297	Sequence 297, App
311	5	2.1	29	5	PCT-US95-09338-81	Sequence 81, Appl	384	5	2.1	48	5	PCT-US95-14442A-65	Patent No. 517685-7
312	5	2.1	29	5	PCT-US95-09339-81	Sequence 81, Appl	385	5	2.1	48	6	517685-7	Patent No. 517685
313	5	2.1	30	1	US-08-149-839B-6	Sequence 6, Appl	386	5	2.1	48	6	5518916-7	Patent No. 5518916
314	5	2.1	30	1	US-08-190-802A-246	Sequence 246, App	387	5	2.1	51	2	US-08-870-518-23	Sequence 23, Appl
315	5	2.1	30	1	US-08-451-568-6	Sequence 6, Appl	388	5	2.1	51	3	US-08-974-022-44	Sequence 44, Appl
316	5	2.1	30	1	US-08-451-566-6	Sequence 6, Appl	389	5	2.1	51	4	US-08-795-445A-44	Sequence 44, Appl
317	5	2.1	30	2	US-08-372-887-12	Sequence 12, Appl	390	5	2.1	51	4	US-08-705-447A-44	Sequence 44, Appl
318	5	2.1	30	2	US-08-505-486-82	Sequence 82, Appl	391	5	2.1	51	4	US-08-974-186-44	Sequence 44, Appl
319	5	2.1	30	2	US-08-777-113-6	Sequence 6, Appl	392	5	2.1	51	4	US-08-795-446B-44	Sequence 44, Appl

393	5	2.1	52	4	US-09-330-330-10	Sequence 10, Appl	466	5	2.1	100	1	US-08-681-812-6	Sequence 6, Appl1
394	5	2.1	52	4	US-09-227-357-575	Sequence 575, App	467	5	2.1	101	2	US-08-574-959A-5	Sequence 5, Appl1
395	5	2.1	57	1	US-08-241-853-3	Sequence 3, Appl1	468	5	2.1	101	4	US-09-357-014-5	Sequence 5, Appl1
396	5	2.1	57	2	US-08-850-917-3	Sequence 3, Appl1	469	5	2.1	102	2	US-08-820-754-24	Sequence 24, Appl
397	5	2.1	58	2	US-08-465-380-60	Sequence 60, Appl	470	5	2.1	102	3	US-08-956-652-24	Sequence 24, Appl
398	5	2.1	58	2	US-08-486-397-60	Sequence 60, Appl	471	5	2.1	102	3	US-08-956-889-24	Sequence 24, Appl
399	5	2.1	58	2	US-08-486-399-60	Sequence 60, Appl	472	5	2.1	102	3	US-08-948-547-24	Sequence 24, Appl
400	5	2.1	58	2	US-08-461-965-60	Sequence 60, Appl	473	5	2.1	103	2	US-08-853-659A-55	Sequence 55, Appl
401	5	2.1	58	2	US-08-634-641-60	Sequence 60, Appl	474	5	2.1	105	3	US-08-867-381A-4	Sequence 4, Appl1
402	5	2.1	58	3	US-09-249-471-60	Sequence 60, Appl	475	5	2.1	105	4	US-09-521-144-4	Sequence 4, Appl1
403	5	2.1	58	3	US-09-249-472-60	Sequence 60, Appl	476	5	2.1	106	2	US-08-440-354-2	Sequence 2, Appl1
404	5	2.1	58	3	US-09-249-451-60	Sequence 60, Appl	477	5	2.1	106	2	US-08-463-087-2	Sequence 2, Appl1
405	5	2.1	58	3	US-08-809-455-60	Sequence 60, Appl	478	5	2.1	106	3	US-08-776-404B-1	Sequence 1, Appl1
406	5	2.1	58	3	US-09-249-461-60	Sequence 60, Appl	479	5	2.1	108	4	US-09-199-637A-227	Sequence 227, App
407	5	2.1	58	3	US-09-249-448-60	Sequence 60, Appl	480	5	2.1	108	5	PCT-US94-01840-6	Sequence 6, Appl1
408	5	2.1	58	4	US-09-227-357-297	Sequence 297, App	481	5	2.1	109	2	US-08-672-345C-3	Sequence 3, Appl1
409	5	2.1	60	2	US-08-968-542C-13	Sequence 13, Appl	482	5	2.1	109	2	US-08-672-345C-93	Sequence 93, Appl
410	5	2.1	62	1	US-07-662-005A-14	Sequence 14, Appl	483	5	2.1	109	4	US-09-214-095D-3	Sequence 3, Appl1
411	5	2.1	62	3	US-08-904-446A-17	Sequence 17, Appl	484	5	2.1	109	4	US-09-214-095D-121	Sequence 121, App
412	5	2.1	67	1	US-08-435-040-3	Sequence 3, Appl1	485	5	2.1	110	1	US-08-122-546-14	Sequence 14, Appl
413	5	2.1	67	2	US-08-244-951A-1	Sequence 1, Appl1	486	5	2.1	110	2	US-08-764-938-14	Sequence 14, Appl
414	5	2.1	67	2	US-08-389-011-1	Sequence 1, Appl1	487	5	2.1	110	3	US-09-131-052-14	Sequence 14, Appl
415	5	2.1	67	3	US-08-403-917A-1	Sequence 1, Appl1	488	5	2.1	110	4	US-09-131-053A-14	Sequence 14, Appl
416	5	2.1	67	4	US-09-020-216-3	Sequence 3, Appl1	489	5	2.1	111	1	US-09-091-725-39	Sequence 39, Appl
417	5	2.1	67	4	US-09-348-952A-1	Sequence 1, Appl1	490	5	2.1	112	1	US-07-754-918A-12	Sequence 12, Appl
418	5	2.1	68	4	US-08-936-165A-434	Sequence 434, App	491	5	2.1	112	3	US-08-666-360-1	Sequence 6, Appl1
419	5	2.1	71	1	US-07-704-288C-15	Sequence 15, Appl	492	5	2.1	112	4	US-09-157-370-6	Sequence 6, Appl1
420	5	2.1	71	1	US-08-379-259-15	Sequence 15, Appl	493	5	2.1	113	4	US-09-056-556-230	Sequence 230, App
421	5	2.1	72	4	US-09-188-930-182	Sequence 182, App	494	5	2.1	114	4	US-09-055-113-3	Sequence 3, Appl1
422	5	2.1	74	4	US-08-866-545-1	Sequence 1, Appl1	495	5	2.1	115	2	US-08-580-988A-25	Sequence 25, Appl
423	5	2.1	75	3	US-09-042-012-8	Sequence 8, Appl1	496	5	2.1	115	4	US-09-374-135-3	Sequence 3, Appl1
424	5	2.1	75	4	US-09-305-086-2	Sequence 2, Appl1	497	5	2.1	115	6	US-09-374-135-3	Sequence 3, Appl1
425	5	2.1	75	4	US-09-457-324-8	Sequence 8, Appl1	498	5	2.1	116	1	US-08-542-363-23	Sequence 23, Appl
426	5	2.1	76	2	US-08-465-380-29	Sequence 29, Appl	499	5	2.1	116	3	US-08-621-018B-4	Sequence 23, Appl1
427	5	2.1	76	2	US-08-480-478-58	Sequence 58, Appl	500	5	2.1	116	4	US-09-100-089-23	Sequence 23, Appl
428	5	2.1	76	2	US-08-486-397-29	Sequence 29, Appl	501	5	2.1	118	1	US-08-300-386A-64	Sequence 64, Appl
429	5	2.1	76	2	US-08-486-399-29	Sequence 29, Appl	502	5	2.1	118	3	US-08-931-645-64	Sequence 64, Appl
430	5	2.1	76	2	US-08-461-965-29	Sequence 29, Appl	503	5	2.1	118	5	US-08-881-771A-1	Sequence 1, Appl1
431	5	2.1	76	2	US-08-326-110A-58	Sequence 58, Appl	504	5	2.1	118	3	PCT-US95-11235-64	Sequence 64, Appl
432	5	2.1	76	2	US-08-634-641-29	Sequence 29, Appl	505	5	2.1	119	1	US-08-497-025-6	Sequence 6, Appl1
433	5	2.1	76	3	US-09-249-471-29	Sequence 29, Appl	506	5	2.1	119	1	US-08-256-077-6	Sequence 4, Appl1
434	5	2.1	76	3	US-09-249-472-29	Sequence 29, Appl	507	5	2.1	119	1	US-08-466-127-4	Sequence 4, Appl1
435	5	2.1	76	3	US-09-249-451-29	Sequence 29, Appl	508	5	2.1	120	1	US-08-047-033-2	Sequence 2, Appl1
436	5	2.1	76	3	US-08-809-455-29	Sequence 29, Appl	509	5	2.1	120	2	US-08-869-733-3	Sequence 3, Appl1
437	5	2.1	76	3	US-09-249-461-29	Sequence 29, Appl	510	5	2.1	121	1	US-08-047-033-1	Sequence 1, Appl1
438	5	2.1	77	3	US-09-249-448-29	Sequence 29, Appl	511	5	2.1	124	1	US-08-050-319B-4	Sequence 4, Appl1
439	5	2.1	77	4	US-09-025-151-20	Sequence 20, Appl	512	5	2.1	124	2	US-08-465-982-4	Sequence 4, Appl1
440	5	2.1	80	4	US-09-040-285A-3	Sequence 3, Appl1	513	5	2.1	128	4	US-08-348-548-2	Sequence 2, Appl1
441	5	2.1	81	2	US-08-332-362A-86	Sequence 86, Appl	514	5	2.1	128	5	PCT-US95-15716-2	Sequence 2, Appl1
442	5	2.1	84	2	US-08-332-562A-89	Sequence 14, Appl	515	5	2.1	129	4	US-09-476-482-8	Sequence 8, Appl1
443	5	2.1	86	1	US-08-149-839B-14	Sequence 14, Appl	516	5	2.1	129	6	US-09-476-482-8	Sequence 8, Appl1
444	5	2.1	86	1	US-08-451-568-14	Sequence 14, Appl	517	5	2.1	134	1	US-08-246-242-5	Sequence 5, Appl1
445	5	2.1	86	1	US-08-451-568-14	Sequence 14, Appl	518	5	2.1	134	2	US-08-684-101-2	Sequence 2, Appl1
446	5	2.1	86	2	US-08-451-568-14	Sequence 14, Appl	519	5	2.1	138	2	US-08-684-101-2	Sequence 2, Appl1
447	5	2.1	89	1	US-08-777-113-14	Sequence 14, Appl	520	5	2.1	138	2	US-08-771-602D-45	Sequence 45, Appl
448	5	2.1	89	2	US-08-241-853-32	Sequence 32, Appl	521	5	2.1	138	4	US-09-205-814-2	Sequence 2, Appl1
449	5	2.1	89	1	US-08-850-917-32	Sequence 32, Appl	522	5	2.1	146	1	US-07-998-003A-91	Sequence 91, Appl
450	5	2.1	91	2	US-08-633-682-5	Sequence 5, Appl1	523	5	2.1	146	1	US-08-453-274B-91	Sequence 91, Appl
451	5	2.1	91	3	US-08-936-772-5	Sequence 5, Appl1	524	5	2.1	146	1	US-08-453-695A-91	Sequence 91, Appl
452	5	2.1	91	6	US-09-395-918-5	Sequence 5, Appl1	525	5	2.1	146	1	US-08-268-161A-91	Sequence 91, Appl
453	5	2.1	92	1	US-08-725-531-3	Sequence 3, Appl1	526	5	2.1	146	4	US-08-453-702A-91	Sequence 91, Appl
454	5	2.1	92	2	US-08-738-127-1	Sequence 1, Appl1	527	5	2.1	146	5	US-09-099-639-91	Sequence 91, Appl
455	5	2.1	92	2	US-08-738-127-3	Sequence 3, Appl1	528	5	2.1	146	5	PCT-US93-12588-91	Sequence 91, Appl
456	5	2.1	92	2	US-09-213-392-3	Sequence 3, Appl1	529	5	2.1	148	1	US-08-256-077-2	Sequence 2, Appl1
457	5	2.1	92	2	US-09-083-661-3	Sequence 3, Appl1	530	5	2.1	148	1	US-08-466-127-2	Sequence 2, Appl1
458	5	2.1	92	4	US-09-247-155-120	Sequence 120, App	531	5	2.1	148	3	US-08-466-127-2	Sequence 3, Appl1
459	5	2.1	94	2	US-08-717-169-8	Sequence 8, Appl1	532	5	2.1	149	2	US-08-329-799-35	Sequence 35, Appl
460	5	2.1	96	1	US-08-565-386-23	Sequence 23, Appl1	533	5	2.1	152	1	US-08-815-175-3	Sequence 3, Appl1
461	5	2.1	97	4	US-09-227-357-465	Sequence 465, App	534	5	2.1	152	1	US-08-602-100A-16	Sequence 16, Appl
462	5	2.1	98	1	US-08-308-086-4	Sequence 4, Appl1	535	5	2.1	152	4	US-08-680-726A-16	Sequence 16, Appl
463	5	2.1	98	2	US-08-479-078-5	Sequence 5, Appl1	536	5	2.1	153	2	US-09-092-609-16	Sequence 16, Appl
464	5	2.1	98	4	US-08-975-040-22	Sequence 22, Appl	537	5	2.1	153	4	US-08-219-237B-4	Sequence 4, Appl1
465	5	2.1	99	1	US-08-202-389-38	Sequence 38, Appl	538	5	2.1	153	4	US-08-476-862-3	Sequence 12, Appl

539	5	2.1	153	4	US-08-468-560C-4	Sequence 4, Appl	612	5	2.1	150	3	US-09-312-934-12	Sequence 12, Appl
540	5	2.1	154	2	US-08-232-087A-10	Sequence 10, Appl	613	5	2.1	150	4	US-08-858-207A-505	Sequence 505, App
541	5	2.1	156	1	US-08-074-121-5	Sequence 5, Appl	614	5	2.1	191	4	US-09-011-961-1	Sequence 1, Appl
542	5	2.1	156	2	US-08-162-402B-20	Sequence 20, Appl	615	5	2.1	192	2	US-08-469-537A-37	Sequence 37, Appl
543	5	2.1	156	5	PCT-US94-06447-5	Sequence 5, Appl	616	5	2.1	193	1	US-08-616-368A-8	Sequence 1, Appl
544	5	2.1	157	1	US-08-050-319B-50	Sequence 50, Appl	617	5	2.1	193	1	US-08-616-368A-8	Sequence 8, Appl
545	5	2.1	157	2	US-08-465-982-50	Sequence 50, Appl	618	5	2.1	193	1	US-08-616-368A-13	Sequence 13, Appl
546	5	2.1	158	1	US-08-050-319B-54	Sequence 54, Appl	619	5	2.1	193	2	US-08-739-485A-13	Sequence 1, Appl
547	5	2.1	158	2	US-08-465-982-54	Sequence 54, Appl	620	5	2.1	193	2	US-08-739-485-9	Sequence 9, Appl
548	5	2.1	159	2	US-08-232-087A-11	Sequence 11, Appl	621	5	2.1	193	2	US-08-861-549-4	Sequence 4, Appl
549	5	2.1	159	2	US-08-219-237B-6	Sequence 6, Appl	622	5	2.1	193	2	US-08-765-536-1	Sequence 1, Appl
550	5	2.1	159	4	US-08-477-347-15	Sequence 15, Appl	623	5	2.1	193	3	US-08-842-976-3	Sequence 3, Appl
551	5	2.1	159	4	US-08-476-862-6	Sequence 6, Appl	624	5	2.1	193	3	US-08-842-976-4	Sequence 4, Appl
552	5	2.1	159	4	US-08-468-560C-6	Sequence 6, Appl	625	5	2.1	193	3	US-09-213-397-3	Sequence 3, Appl
553	5	2.1	161	4	US-09-336-394-2	Sequence 2, Appl	626	5	2.1	193	3	US-09-213-397-4	Sequence 4, Appl
554	5	2.1	163	1	US-08-475-213-5	Sequence 5, Appl	627	5	2.1	193	3	US-09-416-489-3	Sequence 3, Appl
555	5	2.1	163	5	PCT-US93-11703-1	Sequence 1, Appl	628	5	2.1	193	3	US-09-416-489-4	Sequence 4, Appl
556	5	2.1	165	2	US-08-935-138-8	Sequence 8, Appl	629	5	2.1	193	4	US-09-054-298-1	Sequence 1, Appl
557	5	2.1	167	1	US-08-050-319B-2	Sequence 2, Appl	630	5	2.1	193	4	US-09-054-298-8	Sequence 8, Appl
558	5	2.1	167	1	US-08-050-319B-57	Sequence 57, Appl	631	5	2.1	193	4	US-09-054-298-13	Sequence 13, Appl
559	5	2.1	167	2	US-08-465-982-57	Sequence 2, Appl	632	5	2.1	193	4	US-08-818-655-1	Sequence 1, Appl
560	5	2.1	167	4	US-09-062-440-9	Sequence 57, Appl	633	5	2.1	193	4	US-08-818-655-8	Sequence 8, Appl
561	5	2.1	168	4	US-09-052-830B-2	Sequence 9, Appl	634	5	2.1	193	4	US-08-818-655-13	Sequence 13, Appl
562	5	2.1	168	3	PCT-US95-04910-12	Sequence 2, Appl	635	5	2.1	193	5	PCT-US95-08401-1	Sequence 1, Appl
563	5	2.1	171	5	US-08-812-645-1	Sequence 12, Appl	636	5	2.1	194	1	US-08-117-083-21	Sequence 21, Appl
564	5	2.1	172	2	US-08-756-387B-13	Sequence 13, Appl	637	5	2.1	194	4	US-09-364-083-2	Sequence 2, Appl
565	5	2.1	172	2	US-08-756-387B-13	Sequence 13, Appl	638	5	2.1	195	4	US-09-011-961-2	Sequence 2, Appl
566	5	2.1	174	4	US-09-285-873-13	Sequence 13, Appl	639	5	2.1	196	2	US-08-484-126-7	Sequence 7, Appl
567	5	2.1	174	4	US-09-011-961-3	Sequence 3, Appl	640	5	2.1	197	2	US-07-914-284A-8	Sequence 8, Appl
568	5	2.1	174	4	US-09-011-961-5	Sequence 5, Appl	641	5	2.1	197	2	US-08-505-606-1	Sequence 1, Appl
569	5	2.1	174	4	US-08-858-207A-424	Sequence 424, App	642	5	2.1	197	2	US-08-756-387B-11	Sequence 11, Appl
570	5	2.1	175	1	US-07-783-705A-6	Sequence 6, Appl	643	5	2.1	197	3	US-08-756-387B-11	Sequence 2, Appl
571	5	2.1	175	1	US-08-078-683A-34	Sequence 34, Appl	644	5	2.1	197	4	US-08-788-954-2	Sequence 2, Appl
572	5	2.1	175	1	US-08-624-125-7	Sequence 7, Appl	645	5	2.1	197	4	US-09-285-873-11	Sequence 11, Appl
573	5	2.1	178	3	US-08-791-522-1	Sequence 1, Appl	646	5	2.1	198	4	US-08-842-976-2	Sequence 2, Appl
574	5	2.1	178	3	US-08-314-777-1	Sequence 1, Appl	647	5	2.1	199	1	US-08-838-673B-2	Sequence 2, Appl
575	5	2.1	179	1	US-08-193-977-6	Sequence 6, Appl	648	5	2.1	199	2	US-08-050-319B-48	Sequence 48, Appl
576	5	2.1	179	2	US-08-469-537A-84	Sequence 84, Appl	649	5	2.1	199	2	US-08-465-982-48	Sequence 48, Appl
577	5	2.1	179	2	US-08-993-328-33	Sequence 33, Appl	650	5	2.1	200	6	US-08-948-616-11	Sequence 11, Appl
578	5	2.1	179	3	US-08-867-381A-52	Sequence 52, Appl	651	5	2.1	202	2	US-09-193-510-11	Sequence 11, Appl
579	5	2.1	179	4	US-09-521-144-52	Sequence 52, Appl	652	5	2.1	202	2	US-09-193-510-11	Sequence 11, Appl
580	5	2.1	180	2	US-08-624-650-1	Sequence 1, Appl	653	5	2.1	202	4	US-08-247-946A-4	Sequence 4, Appl
581	5	2.1	181	1	US-08-185-432-6	Sequence 6, Appl	654	5	2.1	204	1	US-08-516-801-3	Sequence 3, Appl
582	5	2.1	181	2	US-08-353-476-74	Sequence 74, Appl	655	5	2.1	204	2	US-09-078-917-14	Sequence 14, Appl
583	5	2.1	181	4	US-09-087-465-16	Sequence 16, Appl	656	5	2.1	204	4	US-08-248-355-3	Sequence 3, Appl
584	5	2.1	181	4	US-09-011-961-4	Sequence 4, Appl	657	5	2.1	204	5	PCT-US95-06420-4	Sequence 4, Appl
585	5	2.1	182	1	US-08-308-883-2	Sequence 2, Appl	658	5	2.1	204	5	PCT-US95-06683-3	Sequence 3, Appl
586	5	2.1	182	1	US-08-730-163-2	Sequence 2, Appl	659	5	2.1	205	2	US-08-861-549-1	Sequence 1, Appl
587	5	2.1	182	2	US-08-333-476-93	Sequence 93, Appl	660	5	2.1	205	2	US-08-861-549-3	Sequence 3, Appl
588	5	2.1	182	4	US-08-256-799-2	Sequence 2, Appl	661	5	2.1	205	4	US-09-396-357-2	Sequence 2, Appl
589	5	2.1	182	4	US-08-462-437-2	Sequence 2, Appl	662	5	2.1	207	1	US-07-656-566-2	Sequence 2, Appl
590	5	2.1	182	4	US-08-462-437-31	Sequence 31, Appl	663	5	2.1	207	3	US-08-957-302A-10	Sequence 10, Appl
591	5	2.1	185	1	US-08-278-091-14	Sequence 14, Appl	664	5	2.1	207	4	US-09-542-403-10	Sequence 10, Appl
592	5	2.1	185	1	US-08-483-859-14	Sequence 14, Appl	665	5	2.1	207	4	US-09-415-522-2	Sequence 2, Appl
593	5	2.1	185	1	US-08-472-173-14	Sequence 14, Appl	666	5	2.1	208	4	US-08-934-627B-2	Sequence 2, Appl
594	5	2.1	185	1	US-08-487-167-14	Sequence 14, Appl	667	5	2.1	209	3	US-09-040-285A-4	Sequence 8, Appl
595	5	2.1	185	2	US-08-482-816-14	Sequence 14, Appl	668	5	2.1	210	4	US-08-849-764C-4	Sequence 4, Appl
596	5	2.1	185	2	US-08-296-149-14	Sequence 14, Appl	669	5	2.1	210	4	US-09-171-461-14	Sequence 34, Appl
597	5	2.1	185	2	US-08-801-499-14	Sequence 14, Appl	670	5	2.1	211	1	US-08-588-163-4	Sequence 4, Appl
598	5	2.1	185	2	US-08-615-271-14	Sequence 14, Appl	671	5	2.1	211	1	US-09-111-070-4	Sequence 4, Appl
599	5	2.1	185	3	US-09-074-660-14	Sequence 14, Appl	672	5	2.1	214	2	US-08-846-790A-1	Sequence 1, Appl
600	5	2.1	185	3	US-09-074-659-14	Sequence 14, Appl	673	5	2.1	214	3	US-08-935-333-1	Sequence 1, Appl
601	5	2.1	185	3	US-09-106-468-14	Sequence 14, Appl	674	5	2.1	215	4	US-09-198-723A-46	Sequence 46, Appl
602	5	2.1	185	4	US-09-106-466A-14	Sequence 14, Appl	675	5	2.1	215	4	US-09-198-723A-5	Sequence 50, Appl
603	5	2.1	185	4	US-09-106-467-14	Sequence 14, Appl	676	5	2.1	215	4	US-09-198-723A-53	Sequence 53, Appl
604	5	2.1	185	6	5514590-10	Patent No. 5514590	677	5	2.1	215	4	US-09-198-723A-57	Sequence 57, Appl
605	5	2.1	188	2	US-08-160-524A-5	Sequence 5, Appl	678	5	2.1	216	4	US-09-198-723A-1	Sequence 1, Appl
606	5	2.1	188	3	US-08-722-126A-5	Sequence 5, Appl	679	5	2.1	216	4	US-09-198-723A-2	Sequence 2, Appl
607	5	2.1	188	3	US-09-332-934-2	Sequence 2, Appl	680	5	2.1	216	4	US-09-198-723A-3	Sequence 3, Appl
608	5	2.1	188	5	PCT-US95-04258-5	Sequence 5, Appl	681	5	2.1	216	4	US-09-198-723A-4	Sequence 4, Appl
609	5	2.1	189	6	5171685-2	Patent No. 5171685	682	5	2.1	216	4	US-09-198-723A-5	Sequence 5, Appl
610	5	2.1	189	6	5518916-2	Patent No. 5518916	683	5	2.1	216	4	US-09-198-723A-6	Sequence 6, Appl
611	5	2.1	190	3	US-09-332-934-11	Sequence 11, Appl	684	5	2.1	216	4	US-09-198-723A-7	Sequence 7, Appl

685	5	2.1	216	4	US-09-198-723A-8	Sequence 8, Appli	758	5	2.1	238	6	5405943-2	Patent No. 5405943
686	5	2.1	216	4	US-09-198-723A-9	Sequence 9, Appli	759	5	2.1	240	1	US-08-261-822A-82	Sequence 82, Appl
687	5	2.1	216	4	US-09-198-723A-10	Sequence 10, Appl	760	5	2.1	240	5	PCT-US95-07744A-82	Sequence 82, Appl
688	5	2.1	218	1	US-07-816-679A-3	Sequence 3, Appli	761	5	2.1	245	2	US-08-874-138-2	Sequence 2, Appli
689	5	2.1	218	1	US-08-247-946A-3	Sequence 3, Appli	762	5	2.1	245	4	US-08-879-941-4	Sequence 4, Appli
690	5	2.1	218	5	PCT-US92-11270-3	Sequence 3, Appli	763	5	2.1	245	4	US-09-747-116-4	Sequence 4, Appli
691	5	2.1	218	5	PCT-US95-06420-3	Sequence 3, Appli	764	5	2.1	246	3	US-08-906-769-127	Sequence 127, App
692	5	2.1	219	2	US-08-625-377-2	Sequence 2, Appli	765	5	2.1	246	3	US-08-906-616-127	Sequence 127, App
693	5	2.1	219	2	US-08-479-733A-23	Sequence 23, Appli	766	5	2.1	246	4	US-08-639-075A-127	Sequence 127, App
694	5	2.1	219	3	US-08-487-427-23	Sequence 23, Appli	767	5	2.1	246	4	US-09-012-431-127	Sequence 127, App
695	5	2.1	219	3	US-08-479-727A-23	Sequence 23, Appli	768	5	2.1	246	4	US-09-012-692-127	Sequence 127, App
696	5	2.1	219	3	US-08-482-369A-23	Sequence 23, Appli	769	5	2.1	246	4	US-08-906-613-127	Sequence 127, App
697	5	2.1	219	4	US-09-009-217-8	Sequence 8, Appli	770	5	2.1	246	4	US-09-336-093-5	Sequence 5, Appli
698	5	2.1	219	4	US-09-009-217-9	Sequence 9, Appli	771	5	2.1	247	1	US-08-465-980-3	Sequence 3, Appli
699	5	2.1	219	4	US-09-009-656-8	Sequence 8, Appli	772	5	2.1	247	2	US-09-053-303-3	Sequence 3, Appli
700	5	2.1	219	4	US-09-009-656-9	Sequence 9, Appli	773	5	2.1	247	3	US-09-129-888-2	Sequence 2, Appli
701	5	2.1	219	4	US-09-204-841-2	Sequence 2, Appli	774	5	2.1	247	5	PCT-US95-07093-3	Sequence 3, Appli
702	5	2.1	219	5	PCT-US95-07439-23	Sequence 23, Appli	775	5	2.1	248	2	US-08-755-559-1	Sequence 1, Appli
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704	5	2.1	220	4	US-09-009-217-4	Sequence 4, Appli	777	5	2.1	248	3	US-09-539-774-1	Sequence 1, Appli
705	5	2.1	220	4	US-09-009-217-5	Sequence 5, Appli	778	5	2.1	248	6	5169835-15	Patent No. 5169835
706	5	2.1	220	4	US-09-009-656-1	Sequence 1, Appli	779	5	2.1	249	1	US-08-597-236-5	Sequence 5, Appli
707	5	2.1	220	4	US-09-009-656-4	Sequence 4, Appli	780	5	2.1	249	1	US-08-746-682A-5	Sequence 5, Appli
708	5	2.1	220	4	US-09-009-656-5	Sequence 5, Appli	781	5	2.1	249	2	US-08-685-982-28	Sequence 28, Appli
709	5	2.1	220	4	US-09-052-089A-4	Sequence 4, Appli	782	5	2.1	249	2	US-09-144-925-28	Sequence 28, Appli
710	5	2.1	222	1	US-07-969-931-9	Sequence 9, Appli	783	5	2.1	249	3	US-09-189-760-6	Sequence 6, Appli
711	5	2.1	222	1	US-07-855-417A-9	Sequence 9, Appli	784	5	2.1	249	3	US-09-188-811-6	Sequence 6, Appli
712	5	2.1	222	2	US-08-491-204A-18	Sequence 18, Appli	785	5	2.1	249	4	US-09-514-422-6	Sequence 6, Appli
713	5	2.1	223	2	US-08-121-436A-2	Sequence 2, Appli	786	5	2.1	251	1	US-07-882-202A-2	Sequence 2, Appli
714	5	2.1	223	4	US-09-254-733-7	Sequence 7, Appli	787	5	2.1	251	1	US-07-683-682B-4	Sequence 4, Appli
715	5	2.1	224	1	US-08-707-793A-6	Sequence 6, Appli	788	5	2.1	251	1	US-08-021-615A-2	Sequence 2, Appli
716	5	2.1	224	1	US-08-707-792A-6	Sequence 6, Appli	789	5	2.1	251	1	US-08-321-777-2	Sequence 2, Appli
717	5	2.1	224	3	US-08-974-022-50	Sequence 50, Appli	790	5	2.1	251	1	US-08-463-931-6	Sequence 6, Appli
718	5	2.1	224	4	US-08-795-445A-50	Sequence 50, Appli	791	5	2.1	251	1	US-08-464-237A-6	Sequence 4, Appli
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720	5	2.1	224	4	US-08-974-186-50	Sequence 50, Appli	793	5	2.1	251	5	PCT-US93-04933-2	Sequence 4, Appli
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## ALIGNMENTS

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Sequence 2, Appli  
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Sequence 13, Appli  
Sequence 39, Appli  
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Sequence 7, Appli  
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RESULT 1  
US-09-006-353A-2  
Sequence 2, Application US/09006353A  
Patent No. 6261801

GENERAL INFORMATION:  
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APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
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INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 259 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-006-353A-2

Query Match 100.0%; Score 233; DB 4; Length 259;

Best Local Similarity 100.0%; Pred. No. 9,5e-235;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 27 TTARQEEVPOQTVAPOQQRHSFKEGPCAGSHRSEHTGACNCTEGVDYTNASNNPSCF 86  
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PCTVCKSDQKHSSCTMTRDYVCOCKEGFRFRENSEPMCKRCSRPSGEVOVSNCTSMDD 146  
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## RESULT 2

US-09-153-927-3  
Sequence 3, Application US/09153927A  
Patent No. 6297022

GENERAL INFORMATION:  
APPLICANT: McDonnell, Peter C.  
APPLICANT: Young, Peter R.  
APPLICANT: Zou, Jun  
TITLE OF INVENTION: A Method of Identifying Agonists and  
TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3  
FILE REFERENCE: GH50031  
CURRENT APPLICATION NUMBER: US/09/153,927A  
CURRENT FILING DATE: 1998-09-16  
EARLIER APPLICATION NUMBER: 60/061,334  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Human  
US-09-153-927-3

Query Match 100.0%; Score 233; DB 4; Length 299;  
Best Local Similarity 100.0%; Pred. No. 1,1e-234;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTARQEEVPOQTVAPOQQRHSFKEGPCAGSHRSEHTGACNCTEGVDYTNASNNPSCF 60  
|||||  
Db 67 TTARQEEVPOQTVAPOQQRHSFKEGPCAGSHRSEHTGACNCTEGVDYTNASNNPSCF 126  
QY 61 PCTVCKSDQKHSSCTMTRDYVCOCKEGFRFRENSEPMCKRCSRPSGEVOVSNCTSMDD 120  
PCTVCKSDQKHSSCTMTRDYVCOCKEGFRFRENSEPMCKRCSRPSGEVOVSNCTSMDD 186  
Db 127 PCTVCKSDQKHSSCTMTRDYVCOCKEGFRFRENSEPMCKRCSRPSGEVOVSNCTSMDD 186  
QY 121 IOCVEFGANATVETPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPA 180  
|||||  
Db 187 IOCVEFGANATVETPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPA 246  
QY 181 PAEETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIVLVLLIVFV 233  
|||||  
Db 247 PAEETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIVLVLLIVFV 299

## RESULT 3

US-09-086-483A-2  
Sequence 2, Application US/09086483A  
Patent No. 6214580

GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10



```

; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF399
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 386 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-086-483A-2

Query Match      6.08; Score 14; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGACNPGTEGYDT 50
   |||||
Db 93 TGACNPGTEGYDT 106

RESULT 4
; Sequence 4, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRONEH, ALEMSSEED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 303
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-333-593A-4

Query Match      3.48; Score 8; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 SPEMCRKC 102
   |||||
Db 41 SPEMCRKC 48

RESULT 5
; Sequence 2, Application US/09329633A
; Patent No. 6252050
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chundharapal, Anan
; APPLICANT: Kim, K. Jin
; TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
; FILE REFERENCE: P14681 (REVISED)
; CURRENT APPLICATION NUMBER: US/09/329,633A
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/089,253
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: xaa
; LOCATION: 410
; OTHER INFORMATION: xaa = leu or met
; US-09-329-633A-2

Query Match      3.48; Score 8; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 SPEMCRKC 102
   |||||
Db 149 SPEMCRKC 156

RESULT 6
; Sequence 1, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chundharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
```

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genetech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-09-079-029-1
```

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Query Match 3.4%; Score 8; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 95 SPEMCRKC 102
|11111111
Db 149 SPEMCRKC 156
```

```
RESULT 7
US-09-333-593A-2
; Sequence 2, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 412
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
;
; US-09-333-593A-2
```

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Query Match 3.4%; Score 8; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 95 SPEMCRKC 102
|11111111
Db 149 SPEMCRKC 156
```

```
RESULT 8
US-09-333-593A-8
```

```
;
; Sequence 8, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 424
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
;
; US-09-333-593A-8
```

```
Query Match 3.4%; Score 8; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 95 SPEMCRKC 102
|11111111
Db 149 SPEMCRKC 156
```

```
RESULT 9
US-08-883-036A-2
; Sequence 2, Application US/08883036A
; Patent No. 6072047
; GENERAL INFORMATION:
; APPLICANT: Rauch, Charles
; APPLICANT: Walczak, Henning
; TITLE OF INVENTION: Receptor That Binds TRAIL
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle,
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Macintosh 7.6
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,036A
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US --to be assigned--
; FILING DATE: 04-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/829,536
; FILING DATE: 28-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/815,255
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/799,861  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2625-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-883-036A-2

Query Match 3.4%; Score 8; DB 3; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRKC 102  
|||  
Db 149 SPEMCRKC 156

RESULT 10  
US-08-465-380-61  
Sequence 61, Application US/08465380  
Patent No. 5863894  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,380  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 213/268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-08-465-380-61

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCQCKEG 88  
|||  
Db 37 VCQCKEG 43

RESULT 11  
US-08-486-397-61  
Sequence 61, Application US/08486397  
Patent No. 5865542  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 357  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,397  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 213/269  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-08-486-397-61

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|111111|  
Db 37 VCCKEG 43

## RESULT 12

US-08-486-399-61  
; Sequence 61, Application US/08486399  
; Patent No. 5865543

## GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,399

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 213/270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Necator americanus

Query Match 3.0%; Score 7; DB 2; Length 61;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|111111|  
Db 37 VCCKEG 43

## RESULT 13

US-08-461-965-61

; Sequence 61, Application US/08461965

; Patent No. 5872098

; GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,965

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 210/243

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Necator americanus

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|111111|  
Db 37 VCCKEG 43

## RESULT 14

US-08-634-641-61

; Sequence 61, Application US/08634641

; Patent No. 5955294

; GENERAL INFORMATION:

APPLICANT: Vlasuk, George P. Vlasuk

APPLICANT: Stanssens, Patric Eric Hugo

APPLICANT: Mensens, Joris Hilda Lieven

APPLICANT: Lauwereys, Marc Josef

APPLICANT: Jespers, Yves Rene

APPLICANT: Ganssemans, Yannick Stephane

APPLICANT: Moyle, Matthew

APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,641  
FILING DATE: April 19, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 219/136  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-08-634-641-61

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

RESULT 15  
US-09-249-471-61  
Sequence 61, Application US/09249471  
Patent No. 6040441  
GENERAL INFORMATION:  
APPLICANT: Vlausk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,471  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-09-249-471-61

Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

RESULT 16  
US-09-249-472-61  
Sequence 61, Application US/09249472  
Patent No. 6046318  
GENERAL INFORMATION:  
APPLICANT: Vlausk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef

APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssems, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Bergum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,472  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-09-249-472-61  
Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

RESULT 17  
US-09-249-451-61  
; Sequence 61, Application US/09249451  
; Patent No. 6087487

GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Llieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssems, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Bergum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,451  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-09-249-451-61  
Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

RESULT 18  
US-08-809-455-61  
Sequence 61, Application US/08809455  
Patent No. 6090916  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/809,455  
FILING DATE: April 17, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-08-809-455-61

Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VCCCKEG 88

Db 37 VCCCKEG 43

RESULT 19  
US-09-249-461-61  
Sequence 61, Application US/09249461  
Patent No. 6096877  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,461  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-09-249-461-61

Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VCCKEG 88  
DB 37 VCCKEG 43

RESULT 20  
US-09-249-448-61

; Sequence 61, Application US/09249448

; Patent No. 6121435

; GENERAL INFORMATION:

; APPLICANT: Vlasuk, George Phillip

; APPLICANT: Stanssens, Patrick Eric Hugo

; APPLICANT: Messens, Joris Hilda Llieven

; APPLICANT: Lauwereys, Marc Josef

; APPLICANT: Laroche, Yves Rene

; APPLICANT: Jespers, Laurent Stephane

; APPLICANT: Ganssems, Yannick Georges Jozef

; APPLICANT: Moyle, Matthew

; APPLICANT: Bergum, Peter W.

; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT

; NUMBER OF SEQUENCES: 356

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: Storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/249,448

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/809,455

; FILING DATE: April 17, 1997

; APPLICATION NUMBER: PCT/US95/13231

; FILING DATE: October 17, 1995

; APPLICATION NUMBER: 08/486,399

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/486,397

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/465,380

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/461,965

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/326,110

; FILING DATE: October 18, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BIGGS, SUZANNE L.

; REGISTRATION NUMBER: 30,158

; REFERENCE/DOCKET NUMBER: 216/270

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELETYPE: 67-3510

; INFORMATION FOR SEQ ID NO: 61:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 61 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; ORIGINAL SOURCE:  
; ORGANISM: Necator americanus  
; US-09-249-448-61

Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VCCKEG 88  
DB 37 VCCKEG 43

RESULT 21

US-08-118-270-335

; Sequence 335, Application US/08118270

; Patent No. 5508384

; GENERAL INFORMATION:

; APPLICANT: Murphy, Randall B.

; APPLICANT: Schuster, David I.

; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

; NUMBER OF SEQUENCES: 348

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/118,270

; FILING DATE: 09-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/943,236

; FILING DATE: 10-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Townsend, Kevin G.

; REGISTRATION NUMBER: 34,033

; REFERENCE/DOCKET NUMBER: MURPHY-2A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELETYPE: 248633

; INFORMATION FOR SEQ ID NO: 335:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 93 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-118-270-335

Query Match 3.0%; Score 7; DB 1; Length 93;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
DB 9 LIVLLIV 15

RESULT 22

PCT-US93-08528-335

; Sequence 335, Application PC/TUS9308528

; GENERAL INFORMATION:



APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
CLASSIFICATION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 335:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-335

Query Match 3.0%; Score 7; DB 5; Length 93;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLLIV 231  
|||||||  
DB 9 LIVLLIV 15

RESULT 23  
US-08-928-213B-60  
Sequence 60, Application US/08928213B  
Patent No. 6238905  
GENERAL INFORMATION:  
APPLICANT: McHenry, Charles S.  
Seville, Mark  
Cull, Millard G.  
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III  
NUMBER OF SEQUENCES: 195  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,213B  
FILING DATE: 12-Sep-1997  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: ENZYCO-02550  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-705-8410  
TELEFAX: 415-397-8338  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 60:  
US-08-928-213B-60

Query Match 3.0%; Score 7; DB 4; Length 219;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 CPSEGEVQ 111  
|||||||  
DB 165 CPSEGEVQ 171

RESULT 24  
US-08-818-112-142  
Sequence 142, Application US/08818112  
Patent No. 6290969  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Dillon, Davin C.  
APPLICANT: Campos-Neto, Antonio  
APPLICANT: Houghton, Raymond  
APPLICANT: Vedyick, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,112  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.411C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 142:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-818-112-142

Query Match 3.0%; Score 7; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QQTVAPO 16  
|||||  
Db 236 QQTVAPO 242

RESULT 25  
US-08-818-111-137  
; Sequence 137, Application US/08818111  
; Patent No. 6338852  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Dillon, David C.  
; APPLICANT: Campos-Neto, Antonia  
; APPLICANT: Houghton, Raymond  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Twardzik, Daniel R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818, 111  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.417C6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 137:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-818-111-137

Query Match 3.0%; Score 7; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QQTVAPO 16  
|||||  
Db 236 QQTVAPO 242

RESULT 26  
US-09-056-556-142  
; Sequence 142, Application US/09056556

Patent No. 6350456  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND  
; NUMBER OF SEQUENCES: 241  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056, 556  
; FILING DATE: 07-APR-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.457  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 142:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-056-556-142

Query Match 3.0%; Score 7; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QQTVAPO 16  
|||||  
Db 236 QQTVAPO 242

RESULT 27  
US-08-467-559B-9  
; Sequence 9, Application US/08467559B  
; Patent No. 5928890  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; TITLE OF INVENTION: HUMAN AMINE RECEPTOR  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467, 559B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0840000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-467-559B-9

Query Match 3.0%; Score 7; DB 2; Length 365;  
Best local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
|||||  
DB 38 LIVLLIV 44

RESULT 28  
US-08-118-270-14  
Sequence 14, Application US/08118270  
Patent No. 5508384  
GENERAL INFORMATION:  
APPLICANT: Murphy, Randall B.  
APPLICANT: Schuster, David I.  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 377 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-14

Query Match 3.0%; Score 7; DB 1; Length 377;

Best local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
|||||  
DB 9 LIVLLIV 15

RESULT 29  
PCT-US93-08528-14  
Sequence 14, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 377 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-14

Query Match 3.0%; Score 7; DB 5; Length 377;  
Best local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
|||||  
DB 9 LIVLLIV 15

RESULT 30  
PCT-US96-09848-31  
Sequence 31, Application PC/TUS9609848  
GENERAL INFORMATION:  
APPLICANT: Tripp, Cynthia A.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: NOVEL FILARIN NEMATODE CYSTEINE  
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09848  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,036  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-33-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-09848-31

Query Match 3.0%; Score 7; DB 5; Length 401;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 226 IVLIVF 232  
Db 5 IVLIVF 11

RESULT 31  
PCT-US96-09848-15  
Sequence 15, Application PC/TUS9609848  
GENERAL INFORMATION:  
APPLICANT: Tripp, Cynthia A.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE  
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
City: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09848  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,036  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-33-PCT

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 407 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-09848-15

Query Match 3.0%; Score 7; DB 5; Length 407;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 226 IVLIVF 232  
Db 11 IVLIVF 17

RESULT 32  
US-09-086-483A-6  
Sequence 6, Application US/09086483A  
Patent No. 6214580  
GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/086,483A  
FILING DATE: May-29-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,936  
FILING DATE: May-30-97  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,112  
FILING DATE: Dec-9-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF379  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-086-483A-6

Query Match 3.0%; Score 7; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 YTNASN 55  
Db 154 YTNASN 160

## RESULT 33

US-08-390-000A-7  
Sequence 7, Application US/08390000A  
Patent No. 5985583  
GENERAL INFORMATION:  
APPLICANT: Sealion, Stuart C.  
TITLE OF INVENTION: Cloning and Expression of  
TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,000A  
FILING DATE: 17-FEB-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6923-052  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 468 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-390-000A-7

Query Match 3.0%; Score 7; DB 2; Length 468;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLLIV 231  
Db 58 LIVLLIV 64

## RESULT 34

US-09-013-895A-2  
Sequence 2, Application US/09013895A  
Patent No. 6342363  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Rosen, Craig A.  
APPLICANT: Pan, James G.  
APPLICANT: Gentz, Reiner L.  
APPLICANT: Dixit, Vishva M.  
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death  
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor  
TITLE OF INVENTION: Superfamily and Binding to Trall (AP02-L)  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/013,895A  
FILING DATE: 27-JAN-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1300002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 468 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-013-895A-2

Query Match 3.0%; Score 7; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 YTNASN 55  
Db 154 YTNASN 160

## RESULT 35

US-08-194-338-6  
Sequence 6, Application US/08194338  
Patent No. 5474898  
GENERAL INFORMATION:  
APPLICANT: Venter, John C.  
APPLICANT: Fraser, Claire M.  
APPLICANT: McCombie, William R.  
TITLE OF INVENTION: OCTOPAMINE RECEPTOR  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive, Sixteenth Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/194,338  
FILING DATE: 08-FEB-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,174  
FILING DATE: 28-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelson, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH101.001DV1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 472 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-194-338-6

Query Match 3.0%; Score 7; DB 1; Length 472;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
|||||  
Db 67 LIVLLIV 73

RESULT 36  
US-08-087-772A-16  
Sequence 16, Application US/08087772A  
Patent No. 5691155  
GENERAL INFORMATION:  
APPLICANT: Nahmlas, Clara  
APPLICANT: Emorine, Jean L.  
APPLICANT: Strosberg, Donny A.  
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine  
TITLE OF INVENTION: Beta3-Adrenergic Receptor and their Applications  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5691155th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,772A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Linker, Raymond O.  
REGISTRATION NUMBER: 26,419  
REFERENCE/DOCKET NUMBER: 3339-195  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-087-772A-16

Query Match 3.0%; Score 7; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 225 LIVLLIV 231

Db 67 LIVLLIV 73  
|||||

RESULT 37  
US-09-404-650-5  
Sequence 5, Application US/09404650  
Patent No. 6309858  
GENERAL INFORMATION:  
APPLICANT: Dietrich, Paul S.  
APPLICANT: McGivern, Joseph G.  
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
TITLE OF INVENTION: AND USES  
FILE REFERENCE: R0043B-REG sequence listing  
CURRENT APPLICATION NUMBER: US/09/404,650  
CURRENT FILING DATE: 1999-09-23  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 1835  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-09-404-650-5

Query Match 3.0%; Score 7; DB 4; Length 1835;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 PGTAPA 152  
|||||  
Db 467 PGTAPA 473

RESULT 38  
US-09-320-878-2  
Sequence 2, Application US/09320878A  
Patent No. 6117659  
GENERAL INFORMATION:  
APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
FILE REFERENCE: 300622002120  
CURRENT APPLICATION NUMBER: US/09/320,878A  
CURRENT FILING DATE: 1999-05-27  
EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
EARLIER FILING DATE: 1998-08-28  
EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
EARLIER FILING DATE: 1998-05-06  
EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
EARLIER FILING DATE: 1997-04-30  
EARLIER APPLICATION NUMBER: 60/119,139  
EARLIER FILING DATE: 1999-02-08  
EARLIER APPLICATION NUMBER: 60/100,880  
EARLIER FILING DATE: 1998-09-22  
EARLIER APPLICATION NUMBER: 60/087,080  
EARLIER FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 3739  
TYPE: PRT  
ORGANISM: Streptomyces venezuelae  
US-09-320-878-2

Query Match 3.0%; Score 7; DB 3; Length 3739;  
Best Local Similarity 100.0%; Pred. No. 1,9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEET 156  
|111111|  
Db 464 APAEET 470

RESULT 39  
US-09-105-537-33  
; Sequence 33, Application US/09105537A  
; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600 438US1  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 3739  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-33

Query Match 3.0%; Score 7; DB 4; Length 3739;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEET 156  
|111111|  
Db 464 APAEET 470

RESULT 40  
US-09-105-537-6  
; Sequence 6, Application US/09105537A  
; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600 438US1  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 11877  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-6

Query Match 3.0%; Score 7; DB 4; Length 11877;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEET 156  
|111111|  
Db 5413 APAEET 5419

RESULT 41  
US-08-630-916A-89  
; Sequence 89, Application US/08630916A  
; Patent No. 6011137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozki, Gregorio

APPLICANT: Kay, Brian K.  
APPLICANT: Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennile & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-89

Query Match 2.6%; Score 6; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 PGRPAP 151  
|111111|  
Db 1 PGRPAP 6

RESULT 42  
US-08-630-915A-145  
; Sequence 145, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennile & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/630,915A  
;; FILING DATE: 03-APR-1996  
;; CLASSIFICATION: 536  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-174  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-8864/9741  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 145:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-08-630-915A-145

Query Match 2.6%; Score 6; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 PGRPAP 151  
|||||  
Db 1 PGRPAP 6

RESULT 43  
US-08-792-832A-39  
; Sequence 39, Application US/08/92832A  
; Patent No. 6017734  
; GENERAL INFORMATION:  
; APPLICANT: Summers Dr., Max D.  
; APPLICANT: Braunagel Dr., Sharon C.  
; APPLICANT: Hong Dr., Tao  
; TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID  
; TITLE OF INVENTION: SEQUENCE AND USES THEREOF  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/792,832A  
; FILING DATE: 30-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,955  
; FILING DATE: 07-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/678,435  
; FILING DATE: 03-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hibler, David W.  
; REGISTRATION NUMBER: 41,071  
; REFERENCE/DOCKET NUMBER: TAMK:190  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/474-7577  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
US-08-792-832A-39

Query Match 2.6%; Score 6; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 IVLLIV 231  
|||||  
Db 4 IVLLIV 9

RESULT 44  
US-08-792-832A-33  
; Sequence 33, Application US/08/92832A  
; Patent No. 6017734  
; GENERAL INFORMATION:  
; APPLICANT: Summers Dr., Max D.  
; APPLICANT: Braunagel Dr., Sharon C.  
; APPLICANT: Hong Dr., Tao  
; TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID  
; TITLE OF INVENTION: SEQUENCE AND USES THEREOF  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/792,832A  
; FILING DATE: 30-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,955  
; FILING DATE: 07-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/678,435  
; FILING DATE: 03-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hibler, David W.  
; REGISTRATION NUMBER: 41,071  
; REFERENCE/DOCKET NUMBER: TAMK:190  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/474-7577  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-792-832A-33

Query Match 2.6%; Score 6; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 IVLLIV 231  
|||||  
Db 4 IVLLIV 9



RESULT 45  
US-09-023-339-5  
Sequence 5, Application US/09023339  
Patent No. 6127145  
GENERAL INFORMATION:  
APPLICANT: Sutliff, Thomas D.  
APPLICANT: Rodriguez, Raymond L.  
TITLE OF INVENTION: Production of '1-Antitrypsin  
TITLE OF INVENTION: In Plants  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: P.O. Box 60850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,339  
FILING DATE: 13-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/037,991  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Petithory, Joanne R.  
REGISTRATION NUMBER: P42,995  
REFERENCE/DOCKET NUMBER: 0665-0003.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: Ramyla signal peptide  
US-09-023-339-5

Query Match 2.6%; Score 6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLIYVL 229  
Db 11 VLIYVL 16

RESULT 46  
US-08-477-877B-56  
Sequence 56, Application US/08477877B  
Patent No. 5730979  
GENERAL INFORMATION:  
APPLICANT: Bazin, Herv  
APPLICANT: Latine, Dominique  
TITLE OF INVENTION: LO-CD2a Antibody and Uses thereof for Inhibiting T-cell Active  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,877B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993  
APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-146  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
US-08-477-877B-56

Query Match 2.6%; Score 6; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 TMTTDT 81  
Db 3 TMTTDT 8

RESULT 47  
US-08-472-281A-56  
Sequence 56, Application US/08472281A  
Patent No. 5817311  
GENERAL INFORMATION:  
APPLICANT: Bazin, Herv  
APPLICANT: Latine, Dominique  
TITLE OF INVENTION: LO-CD2a Antibody and Uses thereof for Inhibiting T-cell Act  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,281A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993

APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
US-08-472-281A-56

Query Match 2.6%; Score 6; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 TMTTDT 81  
Db 3 TMTTDT 8

RESULT 48  
US-08-477-989B-56  
Sequence 56, Application US/08477989B  
Patent No. 5951983  
GENERAL INFORMATION:  
APPLICANT: Bazin, Herv  
APPLICANT: Latune, Dominique  
APPLICANT: Kaplan, Ruth  
APPLICANT: Kleber, Emmons, Thomas  
APPLICANT: Postema, Christina E.  
APPLICANT: White-Scharf, Mary  
TITLE OF INVENTION: LO-CD2a Antibody and Uses  
TITLE OF INVENTION: Thereof for Inhibiting  
TITLE OF INVENTION: T-Cell Activation and  
TITLE OF INVENTION: Proliferation  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gillfillan,  
ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,989B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993  
APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-147  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
US-08-477-989B-56

Query Match 2.6%; Score 6; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 TMTTDT 81  
Db 3 TMTTDT 8

RESULT 49  
US-08-792-832A-56  
Sequence 56, Application US/08792832A  
Patent No. 6017734  
GENERAL INFORMATION:  
APPLICANT: Summers Dr., Max D.  
APPLICANT: Braungel Dr., Sharon C.  
APPLICANT: Hong Dr., Tao  
TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID  
TITLE OF INVENTION: SEQUENCE AND USES THEREOF  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,832A  
FILING DATE: 30-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,955  
FILING DATE: 07-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/678,435  
FILING DATE: 03-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hibler, David W.  
REGISTRATION NUMBER: 41,071  
REFERENCE/DOCKET NUMBER: TAMK.190  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-792-832A-56

Query Match 2.6%; Score 6; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLLIV 231  
|||||  
Db 4 IVLLIV 9

RESULT 50  
US-08-050-319B-30  
; Sequence 30, Application US/08050319B  
; Patent No. 5633145  
; GENERAL INFORMATION:  
; APPLICANT: M.Feldmann, P.W. Gray,  
; APPLICANT: M.J.C. Turner, F.M. Brennan  
; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robbins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,319B  
; FILING DATE: 10-May-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robbins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 5150-0030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 617-8999  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-050-319B-30

Query Match 2.6%; Score 6; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 78 TRDTVC 83  
|||||  
Db 30 TRDTVC 35

Search completed: August 13, 2002, 08:38:18  
Job time: 192 sec



16:24:31 2002

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
August 13, 2002, 08:57:31 ; Search time 1842.34 seconds  
(without alignments)  
8825.688 Million cell updates/sec

US-09-826-212-1\_COPY\_183\_959  
Title: 1 atggccgcgatacccaagac.....tgcttcgattgtgttgc 777  
Sequence: 1 atggccgcgatacccaagac.....tgcttcgattgtgttgc 777  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
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2: gb\_in:\*  
3: gb\_ov:\*  
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5: gb\_ov:\*  
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8: gb\_ov:\*  
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10: gb\_ov:\*  
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31: gb\_ov:\*  
32: gb\_ov:\*  
33: gb\_ov:\*

us-09-826-212-1\_copy\_183\_959.rge

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2	777	100.0	900	6	AF020502	AF020502 Homo sapi
3	777	100.0	1102	6	AX077019	AX077019 Sequence
4	777	100.0	1180	6	AF012536	AF012536 Homo sapi
5	777	100.0	1365	9	AF014794	AF014794 Homo sapi
6	777	100.0	1377	9	AF013854	AF013854 Homo sapi
7	777	100.0	1410	6	AF030333	AF030333 Homo sapi
8	777	100.0	1388	6	AF016267	AF016267 Homo sapi
9	740	95.2	1111	6	AX088363	AX088363 Sequence
10	683	87.9	947	6	AX088365	AX088365 Sequence
11	381.4	49.1	1158	9	AF021232	AF021232 Homo sapi
12	381.4	49.1	11726	9	AF021233	AF021233 Homo sapi
13	381.4	49.1	11726	9	AF021233	AF021233 Homo sapi
14	379.8	48.9	1333	9	BC012866	BC012866 Homo sapi
15	379.8	48.9	1407	9	HSU90875	HSU90875 Homo sapi
16	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
17	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
18	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
19	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
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23	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
24	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
25	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
26	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
27	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
28	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
29	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
30	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
31	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
32	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
33	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
34	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
35	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
36	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
37	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
38	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
39	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
40	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
41	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
42	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
43	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
44	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi
45	379.8	48.9	1407	9	AF016658	AF016658 Homo sapi

ALIGNMENTS

RESULT 1  
LOCUS AF012629  
DEFINITION Homo sapiens antagonist decoy receptor for TRAIL/Apo-2L (TRID)  
ACCESSION AF012629  
VERSION AF012629  
KEYWORDS mRNA, complete cds.  
SOURCE AF012629.1 GI:2338430  
ORGANISM human.  
REFERENCE  
AUTHORS Pan, G., Ni, J., Wei, Y., Yu, G., Gentz, R. and Dixit, V.M.  
TITLE Antagonist decoy receptor and a death domain-containing receptor  
JOURNAL Science 277 (5327), 815-818 (1997)  
MEDLINE 97390508  
REFERENCE 2 (bases 1 to 780)  
AUTHORS Pan, G., Ni, J., Wei, Y., Yu, G., Gentz, R. and Dixit, V.M.  
TITLE Direct Substitution  
JOURNAL Submitted (06-JUL-1997) Pathology, University of Michigan, 1301 Catherine Road, Room 7518, Ann Arbor, MI 48109, USA

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Location/Qualifiers
1..780
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/db_xref="taxon:9606"
1..780
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QY 181 gaacatactgagcctgttaaccggtgcacagagggtgtgatatcaaccacgcttccaac 240  
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Db 301 GAACATATCGAGCCTGTAAACCGGTGCACAGAGGGTGTGGATTACACCAAGCTTCCAAAC 360  
QY 241 aatgaaccttctgtccctccatgtacagttgttaaatcagaatacaaaaataaagtcc 300  
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Db 361 AATGAACCTTCTGTCTTCCATGTACAGTTGTAAATCAGATCAAAAACATAAAGTTCC 420  
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RESULT 3  
AX077019 1102 bp DNA Linear PAT 22-FEB-2001  
LOCUS AX077019  
DEFINITION Sequence 7 from Patent WO0105972.  
ACCESSION AX077019  
VERSION AX077019.1 GI:13121655  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1102)  
AUTHORS Ashkenazi,A.J., Baker,K.P., Fong,S., Goddard,A., Godowski,P.J.,  
Gurney,A.L., Hillan,K.J., Mark,M.R., Marsters,S.A., Pitti,R.M.,  
Tuma,D., Watanabe,C.K. and Wood,W.I.  
Tumors, D., Marsters, S.A., and Wood, W.I.  
Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0105972-A 7 25-JAN-2001;  
Genentech, Inc. (US)  
FEATURES  
source 1..1102  
location/Qualifiers  
BASF COUNT 269 a 319 c 297 g 217 t  
ORIGIN  
Query Match 100.0%; Score 777; DB 6; Length 1102;  
Best Local Similarity 100.0%; Pred. No.1.4e-210;  
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 gtctagcttactctgtccacactgtcccgagagagaagtccccaagacagttgac 120  
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Db 313 CCACAGCAACAGAGCACAGCTTCAAGGGGAGAGGTGTCCAGCAGATCTCATATGATCA 372  
QY 181 gaacatactgagcctgttaaccggtgcacagagggtgtgatatcaaccacgcttccaac 240  
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Db 373 GAACATATCGAGCCTGTAAACCGGTGCACAGAGGGTGTGGATTACACCAAGCTTCCAAAC 432  
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Db 493 TGCACATGACACAGACAGACAGTGTGTAAAGAGGACCTTCCGGAATGAAAAAC 552  
QY 361 tccccagagatgtgcggaaggtgacaggtgccttaagtggggaagtcacagtcagta 420  
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Db 553 TCCCCAGAGATGTGCCGAAGTGTAGCAGTGTCCCTAGTGGGAAAGTCCAAAGTCAAT 612  
QY 421 tttacgtctcgtgagatgatatccagttgttgaagaattgtgtccaatgtccactgtgaa 480  
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Db 733 GAGACAAATGAACACAGCCAGCGGAGCTCTGCCAGTGTGTGAAGACATGACACAC 792  
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Db 913 CTCATCATGACACATGATGATGATTTGTGTGTGTGTGTGTGTGTGTGT 969  
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LOCUS AF012536  
DEFINITION Homo sapiens decoy receptor 1 (DcR1) mRNA, complete cds.  
ACCESSION AF012536  
VERSION AF012536.1 GI:2338421  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1180)  
AUTHORS Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Skubatch,M.,  
Baldwin,D., Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I.,  
Goddard,A.D., Godowski,P. and Ashkenazi,A.  
Control of TRAIL-induced apoptosis by a family of signaling and  
decoy receptors  
JOURNAL Science 277 (5327), 818-821 (1997)  
MEDLINE 97390509  
REFERENCE 2 (bases 1 to 1180)

**AUTHORS** Sheridan, J.P., Marsters, S.A., Pitti, R.M., Gurney, A., Baldwin, D., Ramakrishnan, L., Gray, C.L., Baker, K., Wood, W.I., Goddard, A.D., Godowski, P., and Ashkenazi, A.

**JOURNAL** Submitted (06-JUL-1997) Molecular Oncology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA

**FEATURES** Location/Qualifiers

**source**

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**organism**="Homo sapiens"

**/db\_xref**="taxon:9606"

1..1180

**/gene**="DcR1"

193..972

**/gene**="DcR1"

**/note**="tumor necrosis factor receptor family member; inhibits apoptosis induction by TRAIL/Apo2L"

**/product**="decoy receptor 1"

**/protein\_id**="BAB67104.1"

**/db\_xref**="GI:2338422"

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**BASE COUNT** 338 a 326 c 298 g 218 t

**ORIGIN**

Query Match 100.0%; Score 777; DB 9; Length 1180;  
Best Local Similarity 100.0%; Pred. No. 1.4e-210;  
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggccggagatccccaagaacctaaagtgtcgtcgtcatcgatcgagtcgtcgtcgtcga 60  
Db 193 ATGCGCCGGATCCCAAGACCCCTAAAGTTGCTGCTCATCGTGGCGTCTGCTGCCA 252

QY 61 gtccatgactactctgcccacactgcccggcagagagaagttccccaagacagtgagcc 120  
Db 253 GTCTAGCTTACTCTGCCACCATCTCCGCGAGAGAAAGTTCCCAAGACAGTGGCC 312

QY 121 ccaagacagaagagagacaggttcaaggaggagagtgctcagacagatcatatagatca 180  
Db 313 CCACGACACAGAGGACACAGCTTCAAGGGGAGAGGTGTCCAGCAGATCTCATATAGATCA 372

QY 181 gaacatactgagacctgtcaaccgctgacacagaggtgtgtgattacacacagcttccac 240  
Db 373 GAACATACTGAGCGCTGTAAACCCGTGCACAGAGGGTGTGATTTACCAACGCTTCCAA 432

QY 241 aatgaaccttctgtcttccatgtacagttgttaaatcaaatcaaaaacataaaagtcc 300  
Db 433 AATGAACCTTCTTCTTCCATGTACAGTTGTAAATCAGATCAAAAACATTAAGTTCC 492

QY 301 tgcacatgacacagagacaggtgtgtatgttaagaagacaccttcggaatgaacac 360  
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QY 361 tccccaagatgtgccggaagtgtatagcagtgccctagtggggaagtcacaaagtcagta 420  
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QY 421 tgtatgctctggtgatatatccagtgtgtgaagaattgtgccaatgacactgtgaa 480  
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QY 481 acccagctgtctgaagagacatgaacacacgcccggagatctctgcccagctgtcga 540  
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Db 853 GCCCAGCTGTCTGAAGAGACATGACACACACCCGGGAGCTCTGCTCTCATATAC 912

QY 721 ctctcatgacacatgtagatgataatgtcaattgtgctctgattgtgtgt 777  
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**RESULT** 5

**AF014794** 1365 bp mRNA linear PRI 12-MAR-1998

**LOCUS** Homo sapiens TNF related TRAIL receptor (TRAIL-R3) mRNA, complete

**DEFINITION** Homo sapiens TNF related TRAIL receptor (TRAIL-R3) mRNA, complete

**ACCESSION** AF014794

**VERSION** AF014794.1 GI:2957263

**KEYWORDS** cds.

**SOURCE** human.

**ORGANISM** Homo sapiens

**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

**AUTHORS** Degli-Esposti, M.A., Smolak, P.J., Malczak, H., Waugh, J., Huang, C.P., Dubose, R.F., Goodwin, R.G., and Smith, C.A.

**TITLE** Cloning and characterization of TRAIL-R3, a novel member of the emerging TRAIL receptor family

**JOURNAL** J. Exp. Med. 186 (7), 1165-1170 (1997)

**REFERENCE** 2 (bases 1 to 1365)

**AUTHORS** Degli-Esposti, M.A.

**TITLE** Direct Submission

**JOURNAL** Submitted (15-JUL-1997) Biochemistry, Immunex, 51 University Street, Seattle, WA 98101, USA

**FEATURES** Location/Qualifiers

**source**

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**/organism**="Homo sapiens"

**/db\_xref**="taxon:9606"

**/chromosome**="8"

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**/gene**="TRAIL-R3"

**/product**="TNF related TRAIL receptor"

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**BASE COUNT** 332 a 403 c 363 g 267 t

**ORIGIN**

Query Match 100.0%; Score 777; DB 9; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 1.4e-210;  
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggccggagatccccaagaacctaaagtgtcgtcgtcatcgatcgagtcgtcgtcgtcga 60  
Db 150 ATGCGCCGGATCCCAAGACCCCTAAAGTTGCTGCTCATCGTGGCGTCTGCTGCCA 209

QY 61 gtccatgactactctgcccacactgcccggcagagagaagttccccaagacagtgagcc 120  
Db 210 GTCTAGCTTACTCTGCCACCATCTCCGCGAGAGAAAGTTCCCAAGACAGTGGCC 269





QY	721	ctctatgacacatgtaggagatcagttctcaattggtctctatggtttt	777
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RESULT	7		
LOCUS	E63033	1410 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Tumor necrosis factor receptor-associated protein TR5.		
ACCESSION	E63033		
VERSION	E63033.1	GI:18625351	
KEYWORDS	JP 2000078995-A/1.		
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 1410)		
AUTHORS	Young, P.R., Tan, K.B., Renox, A.R. and Lyn, S.D.P.		
TITLE	Tumor necrosis factor receptor-associated protein TR5		
JOURNAL	Patent: JP 2000078995-A 1 21-MAR-2000;		
COMMENT	SMITHKLINE BEECHAM CORP		
	OS Unidentified		
	PN JP 2000078995-A/1		
	PD 21-MAR-2000		
	PF 01-SEP-1999 JP 1999247636		
	PR 05-FEB-1997 US 08/795910, 28-JUL-1997 US 08/901469		
	PETER R YOUNG, KONG B TAN, ANA RISA RENOX,		
	PI SALLY DOREN PATRICIA LYNN		
	PC 612N5/09, A61K31/7052, A61K38/00, A61K45/00, A61K48/00, A61P31/04,		
	PC A61P31/12		
	PC A61P35/00, A61P37/02, C07K14/705, C07K16/28, C12N1/15, C12N1/19, PC		
	C12N1/21,		
	PC C12N5/10, C12P21/02//C12P21/08, C12N15/00, A61K37/02, C12N5/00 CC		
	Strandedness: Single;		
	CC Topology: Linear;		
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		Location/Qualifiers	
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ORIGIN			
Query Match	100.0%; Score 777; DB 6; Length 1410;		
Best Local Similarity	100.0%; Pred. No. 1.4e-210;		
Matches	777: Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	189	atggcccgccgattcccaagacccttaaaagttcgctgctcatcgtctcgagtcctctgcc	248
QY	61	gtccagcttactctgccaacacgtcccgagcagagaggaagttccccagcagacagtggcc	120
Db	249	gttcctagcttactctgccaacacgtcccgagcagagaggaagttccccagcagacagtggcc	308
QY	121	ccacagcaacagagacagagcttcaaggaggagagtgctccagcagagatctcatagatca	180
Db	309	ccacagcaacagagacagagcttcaaggaggagagtgctccagcagagatctcatagatca	368
QY	181	gaactactgagacctgttaaccctgagcagagaggtgtgagatatacaacaagctccaac	240
Db	369	gaactactgagacctgtgttaaccctgagcagagaggtgtgagatatacaacaagctccaac	428
QY	241	aatgacactctctgttcccatgtacagtgtttaaatacagatcaaaaacatgaaagtcc	300
Db	429	aatgacactctctgttcccatgtacagtgtttaaatacagatcaaaaacatgaaagtcc	488
QY	301	tgcacatgacacagacagacagtgctgacagtgttaaagagagacaccttcggaaatgaaac	360
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OY	421	tgtacgtccctggaatgatalatccagtgtcttgaagaatttgytgcacatgtccactgttgaa	480
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OY	481	accccagctgtctgaagaagacaaltgaacacccagcccgggagctctctgtcccagctgtctgaa	540
Db	669	accccagctgtctgaagaagacaaltgaacaccccgggagctctgtcccagctgtctgaa	728
OY	541	gagacaatgaaacaccagcccgaggagctctctgtcccagctgtctgaagaagacaaltgacaccc	600
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Db	789	agcccgaggagctctgtcccagctgtctgaagaagacaaltgaacacccagcccgaggagctct	848
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Db	849	gcccagcagctgtgaagaagacaaltgaacaccccgaggagctctgtcctcttcatatc	908
OY	721	ctctcatgacacatctgtaggatcatatgttcatatgtgtctctgtatgtgtttgt	777
Db	909	ctctcatgacacatctgtaggatctatgttcttaattgtcttcatatgtgtgtttgt	965

RESULT	8				
LOCUS	AF016267	1388 bp	mRNA	linear	PRI 04-MAR-1999
DEFINITION	Homo sapiens TRAIL receptor 3 mRNA, complete cds.				
ACCESSION	AF016267				
VERSION	AF016267.1				
KEYWORDS	GI:2529564				
SOURCE	.				
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1388) Schneider,P., Bodmer,J.-L., Thome,M., Hofmann,K., Holler,N. and Tschoep,J. Characterization of two receptors for TRAIL FEBS Lett. 416 (3), 329-334 (1997)				
TITLE	JOURNAL MEDLINE REFERENCE AUTHORS				
TITLE	2 (bases 1 to 1388) Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and Tschoep,J. Direct Submission Submitted (28-JUL-1997) Institute of Biochemistry, University of Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066, Switzerland				
JOURNAL					
FEATURES					
SOURCE	Location/Qualifiers 1..1388 /organism="Homo sapiens" /db_xref="taxon:9606" /tissue-type="liver and spleen" /dev_stage="fetal" 188..967 /function="binds cytotoxic ligand TRAIL" /note="DR4 homolog; contains no intracellular domain"				
CDS	/codon_start=1 /product="TRAIL receptor 3" /protein_id="AAB1181.1" /db_xref="gi:2529565" /translation="MARPKLKFFVYIVAVLLPVLAYSATTARQEEYPQOTVAPOOC RHSKGECPAGSHSEHTGACNCFETGVDTNNSNNPSCFCTVCSDCKHKSSCT MTRTVCOCKEGTFRNNNSPEMKCRKCSRGEGVOYSCTSMDDIQCYEEFGANATVE TPAAEETNTSPGTAPAPAETNTMTSTPTAPAAETWTTSPTGTPAAPAEETMTTSPT TPAAAEETMTSTGTPASPSHYLTCTTGVIIVLVLLIVEY"				
BASE COUNT	331 a 415 c 368 g 274 t				
ORIGIN					



LOCUS	AX088365	947 bp	DNA	Linear	PAT 17-MAR-2001
DEFINITION	Sequence 4 from Patent W00114542.				
ACCESSION	AX088365				
VERSION	AX088365.1	GI:13397238			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct. artificial sequence.				
REFERENCE	1 (bases 1 to 947)				
AUTHORS	Denome,S.A., Swain,P.M. and Tzellas,N.				
TITLE	A transmembrane trap for isolating membrane bound proteins				
JOURNAL	Patent: WO 0114542-A 4 01-MAR-2001; Genome Therapeutics Corporation (US)				
FEATURES	Location/Qualifiers				
source	1..947 /organism="synthetic construct" /db_xref="taxon:32630" /note="CDNA clone"				
BASE COUNT	246 a	271 c	256 g	174 t	
ORIGIN					
Query Match	87.9%;	Score 683;	DB 6;	Length 947;	
Best Local Similarity	96.4%;	Pred. No. 8.7e-184;			
Matches	720;	Conservative	0;	Mismatches	0; Indels 27; Gaps 1;
OY	1	atggcccgagatccccaagacccctaaagtcgtcgtcgtcatcgtcgtcgagtcctgtgcca	60		
Db	182	ATGGCCCGGAGTCCCAAGACCTTAAAGTTCGTGTCATGTCGTGGCTCTGTCGCCA	241		
OY	61	gtccctagcttactctgccc-----accatggccggcag	93		
Db	242	GTCTTAGCTTACTCTGTGCCGATTACAAGCATGACGATTAAGCTTACCACTGCGCGCAG	301		
OY	94	gaggaagttccccaagacagatgtgcccacacagacagagcacagcttcaagggag	153		
Db	302	GAGGAAGTTCCCAAGACAGAGTGGCCCCACACGACAGACAGACAGCTTCAAGGGGAG	361		
OY	154	gagtgtcacagcagatctcatagatcagaacaactatgtagcctgtaacccgtgcacag	213		
Db	362	GAGTGTCCACGCGAGTCTCATGATCAACAACACTACTGAGCCTGTAAACCCGTGCACAG	421		
OY	214	gtgtgagttaccacaagcttccacaatgaaccttctgttccatgtacagtttgt	273		
Db	422	GGTGTGATTATACCAACGCTTCCACACATGAACTTGTGCTTCCATGTACAGTTTGT	481		
OY	274	aaatcagatcaaaaaataaaagtcttcctgcacatgcagacagacagatgtgtcagtt	333		
Db	482	AAATCAGATCAAAAAATRAAAGTTCCTGTCACATGACCAGACAGACAGTGTGATGCT	541		
OY	334	aaagaagcaccttccggaatgaaaactccccaagatgtccggaaagtgttagcaggtgc	393		
Db	542	AAAGAAAGCACACTTCCGGAATGAAACATCTCCACAGAGTGTGCGGGAAGTGAAGCAGTGC	601		
OY	394	cctagtggagagttccaagtcatgtatgttactgttcctggatgatatccagtgtgttaa	453		
Db	602	CTTACTGGGGAAGTCCAAAGTCAGTAATTGTACGTCTGGGAGATATCCAGTGTTTGAA	661		
OY	454	gaattgtgtccaatgcacatgtggaaaaccacagctgtcttgaagagagacaatgaaccagc	513		
Db	662	GAATTGTGTGCCAATGCGCACATCTGTGAAACCCACAGTCTGTGAAGAGACATGACCCAGC	721		
OY	514	ccggggactcctgcccacagctgtctgaagagacaatgaaacacacagcccgaggactcctgc	573		
Db	722	CCGGGAGACTCTCGCCCCAGCTGCTGAAGAAGACAAATGAACACACGCCCGAGGAGCTCTGCC	781		
OY	574	ccaagtgtctgaagagacaatgacccaagcccgaggactcctgtcccacagctgtctgaag	633		
Db	782	CCAGCTGCTGAAGACATGACCAACCCAGCCCGGGAATCTCTGCCCCAGCTGTGAAGAG	841		
OY	634	acaatgaccacacagccggggagactcctgtcccagctgttgaagagacaatgaaccaaccgc	693		
Db	842	ACAATGACCACACGCCCGGGAGCTCTCCCCAGCTGTGAAGAGACATGACCAACCCAGC	901		

[illegible]

[illegible]



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Db 355 TACTGAGCCTGTAAACCGTGACAGAGGGTGTGGATTACACATTGCTTCAACAATT 414
Oy 246 accctctgtctccatgtacagtttgttaataatagatcaataaataaagttccgtcac 305
Db 415 GCGTTCTGCTGCTGTATGTACAGTTTGTAAATAGGTCAACAAATTAAGTTCCTGTAC 474
Oy 306 catgaccagagagacagtggtcagtgtaagaagacacccctccgaatgaataactccc 365
Db 475 CACGACACAGAGACACCGTGTGTAGTGTGAAGAAAGAAAGTCCAGAGTAAGAACTCCCC 534
Oy 366 agagatgtgcgggaagtgtgca---ggtgcctagtgtgggaagtcacgaatgtaattg 422
Db 535 TGAGATGTGCGGACGCTGTGAACAGGGTCTCCAGAGGATGTCTAAGGTCAAGTAAATTG 594
Oy 423 taagtctgtgagatataccagtggtgtgaagaattgtgtccaatgccaatgctgtgaac 482
Db 595 TAGGCCCCGAGTGTACATCAAGTGCAGAAATGATATCAGTGTCCAGTTCGAGGAAAC 654
Oy 483 cccagctgtcgaagacatgaacacacccagcccgaggaactcctgcccaagctgtgaaga 542
Db 655 CCCAGAGCGGAGAGACATGACACACCATCTGTGGGATGCTTGCCTTCCTATACACTA 714
Oy 543 gacaatgaaca 553
Db 715 CCTATCATCA 725

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## RESULT 15

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LOCUS BC012866 1723 bp mRNA linear PRI 22-AUG-2001
DEFINITION Homo sapiens, similar to tumor necrosis factor receptor
             superfamily, member 10a, clone MGC:9365 IMAGE:3857315, mRNA,
             complete cds.
ACCESSION BC012866
VERSION BC012866.1 GI:15277526
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
          Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1723)
AUTHORS Strausberg, R.
          Direct Submission
          Submitted (20-AUG-2001) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
          USA
JOURNAL

```

REMARK  
COMMENT  
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [villalobcm.tmc.edu](mailto:villalobcm.tmc.edu)  
Villalon, D.K., Luna, R.A., Hale, S.M., Huliy, S., Lu, X., Garcia,  
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
Muzny, D.M., Gibbs, R.A.

## FEATURES

source  
1. 1723  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="MGC:9365 IMAGE:3857315"

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Series: IRAX Plate: 21 Row: b Column: 21  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Genomescan gene  
prediction, similarity but not identity to protein.  
Location/Qualifiers  
1. 1723

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/issue_type="Ovary, adenocarcinoma"
/clone_lib="NIH_MGC_66"
/lab_host="DH10B"
/notes="Vector: pCMV-Sport6"
66.1472
/codon_start=1
/product="Similar to tumor necrosis factor receptor
superfamily, member 10a"
/protein_id="AAH12866.1"
/db_xref="GI:15277527"
/translation="MAPPPARVHLGAFIAVTENPGSASGTEAATAATPSKWSGSAGR
IEPRGGRGALPTSMGQHGPSAARAGRAPGPAPAEASPRLRVHRTKFEVYVGLLO
VWPSAATIKLHDOSIGTQWHSPLGELCPSPSHRSEHPGACNRCDEGVYNSNN
LFACLPCTACKSDSEERSPCTTIRNACOCPTPFNDNSAEMCRKSCSGPGAWKY
KOCPTPMSDIECVKHSNGNHNILVYLIVYLLIYAVLYVCCCTIGSGGPGPKMD
RYCFPRFLGIRRGAGADNHNELNSADLSITPSYQWESQWESQEPALDTEYVQSEEA
OCILGFAEAGSQRRLVLPANGADPTETLMDFDFANIVPDSMDOLRQDLTKN
EIDVVRAGTAGPDALYAMLKMWNVNIGRNASIHITLIDLALERMERHAKETIDLLVD
SGFYLEEDGTGSVAVSLE"

```

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BASE COUNT 426 a 413 c 502 g 382 t
ORIGIN

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Query Match 29.8%; Score 231.4; DB 9; Length 1723;  
Best Local Similarity 73.4%; Pred. No. 6e-55;  
Matches 343; Conservative 0; Mismatches 106; Indels 18; Gaps 3;

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Oy 6 ccgagatccccaagaacctaaagtgtcgtcgtatcgtgtcgtcgtcgtcgtcgtcgtc 65
Db 323 CCGGCTCCACAAAGACCTTCAAGTTGTG-----TGTGCGGGTCTGTGTCAGGTCT 376
Oy 66 agcttactctgccaccactgcccgagaggaagtccccaagaagtcagtgccccaca 125
Db 377 ACCTAGCTCAGCTGCAACATC-----AAACTTCATGATCAATCAATTTGGCACA 427
Oy 126 gcaacagaagacacagcttcaaggaggagtggttcacagagatcctaatagaaca 185
Db 428 GCAATGGGAACATPAGCCCTTGGGAGAGTGTGTCCACACAGGATCTATGATCAGAA 487
Oy 186 tactgagacctgtacaccggtgacagagaggtgtgtatcaaccaagctccaacatga 245
Db 488 TCTTGGAGCCTGTACCGGTCACAGAGGGTGTGTACCAATCTTCCAAACAATTT 547
Oy 246 accctctgtctccatgtacagtttgttaataatagatcaataaataaagttccgtcac 305
Db 548 GTTTGCTTGCCTCCATGTACAGTGTAAATGATGATGAAGAAGAGAGTCCCTGCAC 607
Oy 306 catgaccagagacagtggtcagtgtaagaagacaccttccgaatgaataactccc 365
Db 608 CACGACACAGAGACACACACATGTCTAGTCACCAACGAACTTCCGGAATGACAAATTCTGC 667
Oy 366 agagatgtgcgggaagtgtgca---ggtgcctagtgtgggaagtcacgaatgtaattg 422
Db 668 TGAGATGTGCGGAGAGTGAAGTGTGAGGGTGTGTCAGAGGATGTGTCAGAGATTG 727
Oy 423 taagtctgtgagatataccagtggtgtgaagaattgtgtggtccaatg 469
Db 728 TAGCCCTGTGAGTGTACATCAAGTGTGTCCAAAGAAATCAGGCAATG 774

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Search completed: August 13, 2002, 11:21:04  
Job time: 8613 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 09:01:41 ; Search time 210.69 Seconds

(without alignments)  
6331.779 Million cell updates/sec

Title: US-09-826-212-1\_COPY\_183\_959

Perfect score: . 777  
Sequence: 1 atgcccgcgatccccaagac.....tgcttcgatgtgtgtgt 777

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq\_032802:\*

- 1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
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- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	777	100.0	900	20	AAV27280
2	777	100.0	1102	22	AAV27280
3	777	100.0	1102	22	AAV27280
4	777	100.0	1102	22	AAV27280
5	777	100.0	1180	20	AAV84347
6	777	100.0	1347	20	AAV16692
7	777	100.0	1392	19	AAV51348
8	777	100.0	1392	22	AAV90774
9	777	100.0	1410	19	AAV56990

10	775.4	99.8	1121	20	AAV21096
11	775.4	99.8	1365	20	AAV23412
12	773.8	99.6	1361	20	AAV25349
13	740	95.2	1111	22	AAH19325
14	683	87.9	947	22	AAH19326
15	381.4	49.1	1431	21	AAV50893
16	381.4	49.1	1552	20	AAV18926
17	381.4	49.1	2082	20	AAV25093
18	381.4	49.1	3552	22	AAV21413
19	381.4	49.1	3552	22	AAV21413
20	381.4	49.1	3552	22	AAV21413
21	381.4	49.1	3552	22	AAV21413
22	379.8	48.9	1296	20	AAV18927
23	379.8	48.9	3559	20	AAV19957
24	262.8	33.8	398	20	AAV72110
25	262.8	33.8	398	22	AAV91417
26	229.8	29.6	1407	20	AAV23411
27	229.8	29.6	1407	21	AAV64326
28	229.8	29.6	2152	19	AAV49527
29	229.8	29.6	2152	21	AAV02214
30	229.4	29.5	1053	20	AAV27281
31	229.4	29.5	3518	20	AAV25348
32	227.8	29.3	1921	24	AAV94860
33	227.8	29.3	4051	19	AAV62672
34	226.2	29.1	1323	19	AAV46372
35	220.2	28.3	1407	20	AAV08960
36	220.2	28.3	1407	22	AAV91010
37	196.6	25.3	1236	20	AAV27279
38	196.6	25.3	1236	20	AAV23410
39	195	25.1	1236	20	AAV23721
40	195	25.1	1600	19	AAV61469
41	195	25.1	1600	21	AAV81544
42	195	25.1	1799	20	AAV84352
43	195	25.1	1799	20	AAV72526
44	195	25.1	1799	21	AAV39630
45	195	25.1	1799	22	AAV07626

#### ALIGNMENTS

RESULT	1
ID	AAV27280 standard; DNA; 900 BP.
XX	AAV27280:
XX	02-JUN-1999 (first entry)
XX	Human TRAIL-R3 coding sequence.
XX	Human, DR5, DR5s, TRAIL-R3; apoptosis related condition; cancer; therapy;
XX	autoimmune disease; viral infection; degenerative disorder;
XX	amyotrophic lateral sclerosis; retinitis pigmentosa; ischemic injury;
XX	cerebellar degeneration; myelodysplastic syndrome; ss.
XX	Homo sapiens.
XX	WO9909165-A1.
XX	25-FEB-1999.
XX	14-AUG-1998; 98MO-US16945.
XX	15-AUG-1997; 97US-0055906.
XX	(IDUN-) IDUN PHARM INC.
XX	Alnemur ES;
XX	WPI; 1999-181035/15.
XX	P-PDB; AAV00933.

Human secreted pro  
Human hsp90 DNA.  
Tumour necrosis fa  
Coding sequence fo  
Coding sequence fo  
Human receptor-ass  
Human TRAIL recept  
Inhibitor of Apo-2  
Human CDNA sequenc  
Nucleotide sequenc  
Human TNF receptor  
Human TNF recepto  
Human TR10 recept  
Human TRAIL recept  
Human TANGO-74 enc  
Human TNF receptor  
Human CDNA clone A  
Human APOB DNA.  
DNA encoding a hum  
Human DR4 genomic  
Human Death Domain  
Human DR5 coding  
Tumour necrosis fa  
Human DNA sequence  
Tumour necrosis fa  
Human TRAIL recept  
Human death recept  
Human DR4 DNA. Ho  
Human DR5 coding s  
Human hsp90 DNA.  
Human killer adria  
Human death domain  
Human death domain  
Human Apo-2 ligand  
Human Apo-2 CDNA.  
Human Apo-2 polype  
Human CDNA encodin

PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
 PT protein - useful in for screening for (ant)agonists that modulate  
 the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
 XX  
 PS Claim 7; Page 62-63; 71pp: English.  
 XX  
 CC This sequence encodes the human TRAIL receptor TRAIL-R3 of the invention.  
 CC An antibody against the TRAIL receptors is useful for detecting mammalian  
 CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
 CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
 CC (Ant)agonists identified by the assay are useful for modulating the  
 CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
 CC related conditions which are treated in this way, include cancer  
 CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
 CC erythematosus and immune-mediated glomerulonephritis), viral infections  
 CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
 CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
 CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
 CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial  
 CC infarction and stroke). The polynucleotides can also be used to treat  
 CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
 CC used to form a composition that is useful for inhibiting expression of a  
 CC human DR5 or TRAIL-R3 protein.  
 CC  
 SQ Sequence 900 BP; 228 A; 262 C; 240 G; 170 T; 0 other;

Query Match 100.0%; Score 777; DB 20; Length 900;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-224;  
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atggccggatccccaagcctaagctgctgcgtcatcgtgcgctcgtcgtgca 60  
 DB 121 atggccggatccccaagcctaagctgctgcgtcatcgtgcgctcgtcgtgca 180  
 OY 61 gtctagcttactctgctgacacacacgctgcgagaggaattcccgacagatggcc 120  
 DB 181 gtctagcttactctgctgacacacacgctgcgagaggaattcccgacagatggcc 240  
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 DB 241 ccacagcaacagagcagcagcttcaaggggagagagtcacagagatcctatagatca 300  
 OY 181 gaacatactgagcgttcaaccgctgcacagaggggtgtgattacacaaagcttccac 240  
 DB 301 gaacatactgagcgttcaaccgctgcacagaggggtgtgattacacaaagcttccac 360  
 OY 241 aatgaacctctgctcccatgtacagttgttaatacacaataaacaataaagttcc 300  
 DB 361 aatgaacctctgctcccatgtacagttgttaatacacaataaacaataaagttcc 420  
 OY 301 tgcacatgacagagacagatgtgtcagtgtaaaagaagcacttcggaatgaaac 360  
 DB 421 tgcacatgacagagacagatgtgtcagtgtaaaagaagcacttcggaatgaaac 480  
 OY 361 tcccacagagatgtgcggaagtgtcaggtgcacctagtgggaagtccaagtcaaat 420  
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 DB 661 gagacaatgaacaacagcccgaggactctgtcccgacgtcgtaagagacaatgacacc 720  
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DB 721 agcccgaggactctgtcccgacgtcgtaagagacaatgacaccagcccgaggactct 780  
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 DB 781 gcccacgtctgtgaagagaaatgacacacagcccgaggactctgtcttccattac 840  
 OY 721 ctctcagcaccatcagtagatcatagttcaattgtcttcgtgattgttgc 777  
 DB 841 ctctcagcaccatcagtagatcatagttcaattgtcttcgtgattgttgc 897  
 RESULT 2  
 AAS21393  
 ID AAS21393 standard; cDNA; 1102 BP.  
 XX  
 AC AAS21393;  
 XX  
 DT 24-OCT-2001 (first entry)  
 DE  
 XX Human cDNA sequence encoding for PRO366 polypeptide.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumor necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 PD  
 XX 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000MO-US32678.  
 XX  
 PR 01-DEC-1999; 99MO-US28301.  
 PR 01-DEC-1999; 99MO-US28634.  
 PR 02-DEC-1999; 99MO-US28551.  
 PR 02-DEC-1999; 99MO-US28564.  
 PR 02-DEC-1999; 99MO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 20-DEC-1999; 99MO-US30999.  
 PR 30-DEC-1999; 99MO-US31243.  
 PR 06-JAN-2000; 2000MO-US00277.  
 PR 06-JAN-2000; 2000MO-US00376.  
 PR 11-FEB-2000; 2000MO-US03565.  
 PR 18-FEB-2000; 2000MO-US04341.  
 PR 18-FEB-2000; 2000MO-US04342.  
 PR 22-FEB-2000; 2000MO-US04414.  
 PR 24-FEB-2000; 2000MO-US04914.  
 PR 24-FEB-2000; 2000MO-US05004.  
 PR 01-MAR-2000; 2000MO-US05601.  
 PR 20-MAR-2000; 2000MO-US07377.  
 PR 21-MAR-2000; 2000MO-US07352.  
 PR 30-MAR-2000; 2000MO-US08439.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 10-NOV-2000; 2000MO-US30873.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 DR WPI; 2001-408281/43.  
 XX P-PADB; AAU12321.  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 other PRO polypeptides, link bioactive molecules to cells expressing







CC vector incorporating human breast carcinoma cDNA; isolation of  
CC yeast clones secreting amylase; PCR amplification (see AAW84349-50)  
CC of the insert directly from the yeast colony and purification of  
CC DNA for sequencing; use of an isolated sequence (DNA11705) as a  
CC probe to screen a human foetal lung library; and isolation of the  
CC full-length clone, which is deposited as ATCC 209087. An  
CC alternative translational initiation site encodes amino acid  
CC residues -40 to 259 of Apo-2DcR (see AAW84409). The invention  
CC provides vectors and host cells for recombinant production of  
CC Apo-2DcR polypeptides, antibodies, and transgenic and knockout  
CC animals (useful e.g. for screening and developing drugs that protect  
CC against excessive apoptosis). Apo-2DcR, or chimeras comprising  
CC Apo-2DcR or its extracellular domain fused to a heterologous  
CC polypeptide are used to modulate apoptosis of mammalian cells  
CC (claimed) and/or NF-kappaB activation by Apo-2 ligand, and may be  
CC expressed in vivo or ex vivo for gene therapy. They can be used in  
CC methods for the modulation and diagnosis of apoptosis e.g. in cases  
CC of neurodegeneration, autoimmune diseases and inflammation. Most  
CC human tumour cells do not express Apo-2DcR transcripts, but normal  
CC tissues do, suggesting that Apo-2DcR may permit selective killing  
CC of cancer cells by Apo-2 ligand, possibly by protecting normal, but  
CC not cancerous, cells.

XX Sequence 1180 BP; 338 A; 326 C; 298 G; 218 T; 0 other;

Query Match 100.0%; Score 777; DB 20; Length 1180;

Best Local Similarity 100.0%; Pred. No. 4.5e-224; Mismatches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggccggatccccaagaacctaaagtctgctgcatcgtcggctctgtccca 60  
DB 193 atggccggatccccaagaacctaaagtctgctgcatcgtcggctctgtccca 252  
QY 61 gtcttagcttcttgcacacatgcccggcaggaggagagttccccaacacagtgcc 120  
DB 253 gtccatgcttcttgcacacatgcccggcaggaggagagttccccaacacagtgcc 312  
QY 121 ccacagcacacagagcacagcttcaaggaggagagtgctccagcagatcccatagaca 180  
DB 313 ccacagcacacagagcacagcttcaaggaggagagtgctccagcagatcccatagaca 372  
QY 181 gaacatctgagcctgtaacccgtgacagagggtgtgattacacacagcttccaac 240  
DB 373 gaacatctgagcctgtaacccgtgacagagggtgtgattacacacagcttccaac 432  
QY 241 aatgaaccttcttcccatgtacagtgtgttaatacagttcaaaaagaattccc 300  
DB 433 aatgaaccttcttcccatgtacagtgtgttaatacagttcaaaaagaattccc 492  
QY 301 tgcaccatgacagacagacagtgctgacgttaaaagagcaccttcggatgtaaac 360  
DB 493 tgcaccatgacagacagacagtgctgacgttaaaagagcaccttcggatgtaaac 552  
QY 361 tccccaagatgctccggaagtgtacagcgtgcccctagtggggaagttcaagtaac 420  
DB 553 tccccaagatgctccggaagtgtacagcgtgcccctagtggggaagttcaagtaac 612  
QY 421 tttatgctccttgatgataccagtgctgttaagaatttggtgcaatgacacgtgtgaa 480  
DB 613 tttatgctccttgatgataccagtgctgttaagaatttggtgcaatgacacgtgtgaa 672  
QY 481 acccaacgtgtgaagaacatgaacacccagccgggagatctctgcccacgtgttaa 540  
DB 673 acccaacgtgtgaagaacatgaacacccagccgggagatctctgcccacgtgttaa 732  
QY 541 gagacaatgaacacccagccaggtactctgcccacgtgtgaagaacatgaacaccc 600  
DB 733 gagacaatgaacacccagccaggtactctgcccacgtgtgaagaacatgaacaccc 792  
QY 601 agcccgaggagatctctgcccacgtgtgaagaacatgaacacccagccgggagatctct 660  
DB 793 agcccgaggagatctctgcccacgtgtgaagaacatgaacacccagccgggagatctct 852

QY 661 gccacagctgtgaagaacatgacacacccagccgggagatctctgcttccatrac 720  
DB 853 gccacagctgtgaagaacatgacacacccagccgggagatctctgcttccatrac 912  
QY 721 ctctcatgacacatcgttaggagatcatagttctaattgcttctcgtatgttgtt 777  
DB 913 ctctcatgacacatcgttaggagatcatagttctaattgcttctcgtatgttgtt 969

# RESULT 6

AAK16692 standard; CDNA: 1347 BP.

AAK16692;

04-MAY-1999 (first entry)

Human TNF-related apoptosis-inducing ligand binding protein cDNA.

Human: TNF-related apoptosis-inducing ligand binding protein; clotting;

thrombotic microangiopathy; thrombotic thrombocytopenic purpura;

haemolytic-uraemic syndrome; systemic lupus erythematosus; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 24..923

FT tag a

MO9900423-A1.

07-JAN-1999.

25-JUN-1998; 98MO-US13491.

26-JUN-1997; 97US-0883529.

(IMMUNEX CORP.

Smith CA, Walczak H;

WPI: 1999-095685/08.

P-PSDB: AAW94671.

New isolated TRAIL binding protein - which binds to a tumour

necrosis factor-related apoptosis inducing ligand, used in the

diagnosis and treatment of TRAIL-mediated disorders

Claim 1; Fig 1; 47pp; English.

The present sequence encodes human tumour necrosis factor (TNF)-related

apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be

used for inhibiting the biological activities of TRAIL or for purifying

TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated

disorder such as T cell death in HIV-infected patients. They can be used

for treating thrombotic microangiopathies such as thrombotic

thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small

blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic

acids can also be used for gene therapy. They can also be used as

carriers for delivering attached agents to cells bearing TRAIL.

Sequence 1347 BP; 326 A; 401 C; 361 G; 259 T; 0 other;

Query Match 100.0%; Score 777; DB 20; Length 1347;

Best Local Similarity 100.0%; Pred. No. 4.8e-224; Mismatches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggccggatccccaagaacctaaagtctgctgcatcgtcggctctgtccca 60  
DB 144 atggccggatccccaagaacctaaagtctgctgcatcgtcggctctgtccca 203

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QY 61 gtccatgcttctgccaacactgcccggcaggaggaagtccccaagcagatggcc 120
D 204 gtcttagcttctctgtccacacactgcccggcaggaggaagtccccaagcagatggcc 263
QY 121 ccacagaacaagagagcagatcctcaaggggaggagtgctccagcagatcctcatagatca 180
D 264 ccacagaacaagagagcagatcctcaaggggaggagtgctccagcagatcctcatagatca 323
QY 181 gaacatctgagagctgttaaccgtgacacagagtgctgtgttaccacaaagcttccaaac 240
D 324 gaacatctgagagctgttaaccgtgacacagagtgctgtgttaccacaaagcttccaaac 383
QY 241 aatgaacctcttcttcccaatgagctgttaacatcagaatcaaaaacataaagtcc 300
D 384 aatgaacctcttcttcccaatgagctgttaacatcagaatcaaaaacataaagtcc 443
QY 301 tgcacatgacacagacagatgctgacagtgtaaaagagcacttccggatgtaaaac 360
D 444 tgcacatgacacagacagatgctgacagtgtaaaagagcacttccggatgtaaaac 503
QY 361 tccccaagatgtgcccgaagtgtgacagtgccctagtggggagagtcacagtaaat 420
D 504 tccccaagatgtgcccgaagtgtgacagtgccctagtggggagagtcacagtaaat 563
QY 421 tgtacgctccgagtgatcctcaatgctgttgaagaattgtgtgccaatgccaactgtgaa 480
D 564 tgtacgctccgagtgatcctcaatgctgttgaagaattgtgtgccaatgccaactgtgaa 623
QY 481 acccagctctgtaagaacaatgaacacagcccgggactcttgcacagctgtgaa 540
D 624 acccagctctgtaagaacaatgaacacagcccgggactcttgcacagctgtgaa 683
QY 541 gagacatgtaacacacacagggactcctgcccagctgtgtgaagaacatgacacac 600
D 684 gagacatgtaacacacacagggactcctgcccagctgtgtgaagaacatgacacac 743
QY 601 agcccgaggactcctgcccagctgtgtgaagaacatgacacacagcccgggactcct 660
D 744 agcccgaggactcctgcccagctgtgtgaagaacatgacacacagcccgggactcct 803
QY 661 gcccaagctctgtaagaacaatgaacacagcccgggactcctgcttctcaatcac 720
D 804 gcccaagctctgtaagaacaatgaacacagcccgggactcctgcttctcaatcac 863
QY 721 ctccacagcaccatcgtgagagatcatagttctaatgtgtctctgattgtgtgt 777
D 864 ctccacagcaccatcgtgagagatcatagttctaatgtgtctctgattgtgtgt 920

RESULT 7
AAVS1348
ID AAVS1348 standard; DNA: 1392 BP.
XX
AC AAVS1348;
XX
DT 23-OCT-1998 (first entry)
XX
DE Human TR1D genomic DNA.
XX
KW TRAIL receptor without intracellular domain; TR1D; TNFR-5; human;
KW tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;
KW haematopoietic tissue; immune system; ligand; apoptosis; treatment; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 183..962
FT sig_peptide 183..260
FT mat_peptide 261..959
FT /*tag= c

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FT /*product= "TR1D"
FT /note= "TRAIL receptor without intracellular domain"
XX
PN W09830693-A2.
XX
PD 16-JUL-1998.
XX
PE 13-JAN-1998; 98WC-US00152.
XX
PR 07-AUG-1997; 97US-0054885.
PR 14-JAN-1997; 97US-0035496.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Edner R, Feng P, Gentz RL, Ni J, Ruben SM, Wei Y;
PI Yu G;
DR WPI: 1998-399141/34.
DR P-PSDB: AAW64668.
XX
PT Human TRAIL receptor without an intracellular domain polypeptide -
PT used in the diagnosis of immune system-related disorder(s)
XX
PS Claim 2; Fig 1; 90pp; English.
XX
CC This sequence encodes a human TR1D (TRAIL (TNF-related apoptosis-inducing
CC ligand) receptor without an intracellular domain). TR1D is a member of
CC the tumour necrosis factor receptor (TNFR) family also known as TNFR-5.
CC TR1D is expressed in haematopoietic tissues and other normal human
CC tissues. For a number of immune system-related disorders, substantially
CC altered (whether increased or decreased) levels of TR1D gene expression
CC can be detected, therefore the TR1D polypeptides, nucleic acids and
CC antibodies are useful in the diagnosis of such immune system related
CC disorders. Mutations of the TR1D gene can also be detected. TR1D can also
CC be used to identify ligands which may be useful in the treatment of
CC apoptosis related disorders. TR1D is administered to humans at a
CC perenteral dose of 0.01 to 1 mg/kg/day.
XX
SQ Sequence 1392 BP; 329 A; 418 C; 368 G; 277 T; 0 other;

Query Match 100.0%; Score 777; DB 19; Length 1392;
Best Local Similarity 100.0%; Pred. No. 4,8e-224;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggccggatcccccaagacctaaagtgtgtgtcgtacatgctcggtctctgca 60
D 183 atggccggatcccccaagacctaaagtgtgtgtcgtacatgctcggtctctgca 242
QY 61 gtccatgcttctgccaacactgcccggcaggaggaagtccccaagcagatggcc 120
D 243 gtccatgcttctctgtccacacactgcccggcaggaggaagtccccaagcagatggcc 302
QY 121 ccacagaacaagagagcagatcctcaaggggaggagtgctccagcagatcctcatagatca 180
D 303 ccacagaacaagagagcagatcctcaaggggaggagtgctccagcagatcctcatagatca 362
QY 181 gaacatctgagagctgttaaccgtgacacagagtgctgtgttaccacaaagcttccaaac 240
D 363 gaacatctgagagctgttaaccgtgacacagagtgctgtgttaccacaaagcttccaaac 422
QY 241 aatgaaccttcttcccaatgagctgttaacatcagaatcaaaaacataaagtcc 300
D 423 aatgaaccttcttcccaatgagctgttaacatcagaatcaaaaacataaagtcc 482
QY 301 tgcacatgacacagacagatgctgacagtgtaaaagagcacttccggatgtaaaac 360
D 483 tgcacatgacacagacagatgctgacagtgtaaaagagcacttccggatgtaaaac 542
QY 361 tccccaagatgtgcccgaagtgtgacagtgccctagtggggagagtcacagtaaat 420
D 543 tccccaagatgtgcccgaagtgtgacagtgccctagtggggagagtcacagtaaat 602

```





Db 843 gccccagctgtgagagacaatgaccacagccgggactcctgctctcattac 902  
 Oy 721 ctccacgaccacatcagagatcatatgtcttctgctgattgttgc 777  
 Db 903 ctccacgacacatcagagatcatatgtcttctgctgattgttgc 959  
 RESULT 9  
 ID AAV56990 standard; cDNA: 1410 BP.  
 XX AAV56990;  
 AC AAV56990;  
 XX 11-JAN-1999 (first entry)  
 DE Human tumour necrosis related receptor TR5 cDNA.  
 KW Tumour necrosis related receptor; TR5; human; inflammation;  
 KW arthritis; septicemia; transplant rejection; autoimmune disease;  
 KW inflammatory bowel disease; graft versus host disease; infection;  
 KW stroke; ischaemia; acute respiratory disease syndrome; psoriasis;  
 KW atherosclerosis; brain injury; AIDS; bone disease; cancer;  
 KW atherosclerosis; Alzheimer's disease; therapy; diagnosis; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 69..968  
 FT sig\_peptide /\*tag= a  
 FT 69..263 /\*tag= b  
 FT 264..965 /\*tag= b  
 FT mat\_peptide  
 XX EP867509-A2.  
 XX 30-SEP-1998.  
 XX 04-FEB-1998; 98EP-0300827.  
 XX 28-JUL-1997; 97US-0901469.  
 PR 05-FEB-1997; 97US-0795910.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA LYN SDP, Tan KB, Truneh A, Young PR;  
 XX WPI, 1998-497862/43.  
 DR P-PSDB; AAW76331.  
 XX New polynucleotide encoding TR5 polypeptide - used to diagnose,  
 PT prevent and treat e.g. inflammation, arthritis, septicemia,  
 PT autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis,  
 PT restenosis; brain injury, AIDS and bone diseases  
 PT Claim 4; Fig 1; 22pp; English.  
 PS This nucleotide sequence codes for human tumour necrosis related  
 CC receptor, TR5 (see AAW76331). An expressed sequence tag (EST 213397)  
 CC derived from a cDNA library made from human prostate was found to  
 CC have sequence similarity to the human tumour necrosis factor (TNF)  
 CC receptor. A search through several overlapping ESTs indicated that  
 CC this represented the 5' most EST of the assemble and so it was  
 CC completely sequenced. Analysis of the 1410 cDNA sequence indicated  
 CC that it encoded a complete open reading frame for a novel member of  
 CC the TNF receptor superfamily. A polynucleotide encoding TR5 can  
 CC be obtained from a cDNA library derived from mRNA in cells of  
 CC prostate, endothelial cells, interleukin-1 beta-treated smooth  
 CC muscle cells, foetal liver spleen cells, and pregnant uterus using  
 CC expressed sequence tag analysis. Treatment of a subject in need of  
 CC enhanced TR5 polypeptide activity comprises administering an agonist  
 CC to the polypeptide and/or providing TR5 polynucleotide in a form so  
 CC as to effect production of the polypeptide activity in vivo.

CC Treatment of a subject with the need to inhibit TR5 polypeptide  
 CC activity comprises administering an antagonist to the polypeptide,  
 CC administering a nucleic acid that inhibits the expression of the  
 CC nucleotide sequence encoding the polypeptide and/or administering a  
 CC polypeptide that competes with the polypeptide for its ligand.  
 CC substrate or receptor. Diagnosing a disease or a susceptibility  
 CC to a disease related to expression or activity of TR5 polypeptide,  
 CC comprises determining the presence or absence of mutation in the  
 CC nucleotide sequence encoding the TR5 polypeptide in the genome of  
 CC the subject and/or analysing for the presence or amount of TR5  
 CC polypeptide expression in a sample. Identification of compounds  
 CC which bind to TR5 comprises contacting host cells with a candidate  
 CC compound and assessing the ability of it to bind to the cells. The  
 CC active agents can be used for the treatment of chronic and acute  
 CC inflammation, arthritis, septicemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis), transplant rejection,  
 CC graft vs host disease, infection, stroke, ischaemia, acute  
 CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone  
 CC diseases, cancer (e.g. lymphoproliferative disorders),  
 CC atherosclerosis and Alzheimer's disease.  
 XX Sequence 1410 BP; 342 A; 420 C; 371 G; 277 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 777; DB 19; Length 1410;  
 Best Local Similarity 100.0%; Pred. No. 4,9e-224;  
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 atggccggatccccaagaccctaagtctgctgcatcgtcgcgctctcga 60  
 Db 189 atggccggatccccaagaccctaagtctgctgcatcgtcgcgctctcga 248  
 Oy 61 gtcttaactactctgcacacacgtcccgagaggaagtccccaagacgtgccc 120  
 Db 249 gtcttaactactctgcacacacgtcccgagaggaagtccccaagacgtgccc 308  
 Oy 121 ccacagcaacagagagcagcttcaagggagagagtgctccagagatcctataga 180  
 Db 309 ccacagcaacagagagcagcttcaagggagagagtgctccagagatcctataga 368  
 Oy 181 gaacatctgagcctgtaaccgctgcacagagggtgtgattacacaacgtctcaac 240  
 Db 369 gaacatctgagcctgtaaccgctgcacagagggtgtgattacacaacgtctcaac 428  
 Oy 241 aatgaactcttcttcccatgacagtggttgaatcaagatacaaaaataaagtcc 300  
 Db 429 aatgaactcttcttcccatgacagtggttgaatcaagatacaaaaataaagtcc 488  
 Oy 301 tgcacatgacagagacagctgtgcaagtgtataaagaagcacctccggaatgaaac 360  
 Db 489 tgcacatgacagagacagctgtgcaagtgtataaagaagcacctccggaatgaaac 548  
 Oy 361 tccccaagatgtgcccgaagtgtacagagtgccctagtgggaagtcacaaagtcagt 420  
 Db 549 tccccaagatgtgcccgaagtgtacagagtgccctagtgggaagtcacaaagtcagt 608  
 Oy 421 tgtacgtccctggagatgatatccagtgtgtgaagaattgtgtccaatgcaactgtgaa 480  
 Db 609 tgtacgtccctggagatgatatccagtgtgtgaagaattgtgtccaatgcaactgtgaa 668  
 Oy 481 acccagctgtgagaggaacaatgaacacagccgggactctgtcccaagctgcgaa 540  
 Db 669 acccagctgtgagaggaacaatgaacacagccgggactctgtcccaagctgcgaa 728  
 Oy 541 gagacaatgaacacacagccagagactctgtcccaagctgtgagagacaatgacacac 600  
 Db 729 gagacaatgaacacacagccagagactctgtcccaagctgtgagagacaatgacacac 788  
 Oy 601 agcccgagatctctgcccagctgctggaagagacaatgacacacccgggactctc 660  
 Db 789 agcccgagatctctgcccagctgctggaagagacaatgacacacccgggactctc 848  
 Oy 661 gcccaagctgtgagagacaatgacacacagccgggactctgctctcattac 720

Db	849	gccccagctgcgtgaagagacaaatgaccaccagcccgaggactcctgccttccattac	908
Qy	721	ctctcatgacacatcgtaggagatcaatgtctcaatgtgctctcgtatgtgtgt 777	
Db	909	ctctcatgacacatcgtaggagatcaatgtctcaatgtgctctcgtatgtgtgt 965	
RESULT 10			
AAZ21096			
XX	AAZ21096	standard; cDNA; 1121 BP.	
XX	AAZ21096;		
XX	17-NOV-1999	(first entry)	
DE	Human	secreted protein clone j11442_1 encoding cDNA.	
XX	Human;	secreted protein; biological activity; nutritional; cytokine;	
KW	cell proliferation; differentiation; immune stimulating; vaccine;		
KM	haematopoiesis regulation; tissue growth; haemostatic; thrombolytic;		
XX	anti-inflammatory; tumour inhibition; ss.		
OS	Homo sapiens.		
PN	WO9946287-A1.		
XX	16-SEP-1999.		
PD	11-MAR-1999;	99WO-US05243.	
XX	11-MAR-1999;	98US-0077521.	
PR	14-MAY-1998;	98US-0079124.	
XX	10-MAR-1999;	99US-0266105.	
XX	(GEMV ) GENETICS INST INC.		
PA	Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;		
PI	Merberg D, Treacy M, Agostino MJ, Steinhinger RJ;		
XX	WPI; 1999-551362/46.		
DR	P-PSDB; AAY29864.		
XX	Poly nucleotides encoding secreted human proteins, derived from human		
PT	fetal brain, human adult blood, human adult bladder, or human adult		
PT	neural tissue CDNA libraries.		
XX	Claim 16; Page 103; 118pp; English.		
XX	AAZ21093 to AAZ21102 encode new human secreted proteins and AAY29861 to		
CC	AAZ29873 represent the secreted proteins encoded by the polynucleotide		
CC	sequences. AAZ21103 to AAZ21112 represent probes for the secreted		
CC	proteins. The polynucleotides and proteins are predicted to have		
CC	biological activities which would make them suitable for treating,		
CC	preventing or ameliorating medical conditions in humans and animals,		
CC	although no supporting data is given. Suggested activities include		
CC	nutritional activity, cytokine and cell proliferation/differentiation		
CC	activity, immune stimulating (e.g. as vaccines) or suppressing activity,		
CC	haematopoiesis regulating activity, tissue growth activity,		
CC	activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic		
CC	and thrombolytic activity, receptor/ligand activity, anti-inflammatory		
CC	activity, cadherin/tumour invasion suppressor activity, and tumour		
CC	inhibition activity. The polynucleotides and proteins can also be used		
CC	as nutritional sources or supplements. Such uses include use as a protein		
CC	or amino acid supplement, use as a carbon source, use as a nitrogen		
CC	source and use as a source of carbohydrate. They may also have utility		
CC	in compositions used for bone, cartilage, tendon, ligament, and/or nerve		
CC	tissue growth or regeneration, as well as for wound healing and tissue		
CC	repair and replacement, and in the treatment of burns, incisions and		
CC	ulcers. The proteins which induce cartilage and/or bone growth in		
CC	circumstances where bone is not normally formed, have application in		
CC	the healing of bone fractures and cartilage damage or defects in humans		
CC	and other animals.		

XX	Sequence	1121 BP, 289 A, 325 C, 290 G, 216 T, 1 other:
XX	Query Match	99.8%; Score 775.4; DB 20; Length 1121;
XX	Best Local Similarity	99.9%; Pred. No. 1.3e-223;
XX	Matches 776: Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 atggcccgagatcccaagacctaaagtctgcgtcgtcatctgtcggtctctgtcca	60
DB	183 atggcccgagatcccaagacctaaagtctgcgtcgtcatctgtcggtctctgtcca	242
QY	61 gttcttagcttactctgcaccaacctgcggcgaggggaagtctcccaagacagtggcc	120
DB	243 gttcttagcttactctgcaccaacctgcggcgaggggaagtctcccaagacagtggcc	302
QY	121 ccacagcaacagaggcacagcttcaagggggagagtgctccagagatctcatagatca	180
DB	303 ccacagcaacagaggcacagcttcaagggggagagtgctccagagatctcatagatca	362
QY	181 gaacatactggagcctgttaaccctgcgcacagaggggtgtggatataccaagcttccac	240
DB	363 gaacatactggagcctgtgttaaccctgcgcacagaggggtgtggatataccaagcttccac	422
QY	241 aatgacaccttctgtcttcccatgttaacagtctgttaaatcagatcaaaaataaaagtcc	300
DB	423 aatgacaccttctgtcttcccatgttaacagtctgtgttaaatcagatcaaaaataaaagtcc	482
QY	301 tgcacacatgacacagagaaacagtggtcagtggttaagaagagacaccttcggagatgaaac	360
DB	483 tgcacacatgacacagagaaacagtggtcagtggttaagaagagacaccttcggagatgaaac	542
QY	361 tccccaagagatgtgcgggaagtgtagcaggtgccctagctggggaaagtcacaagtcagtaat	420
DB	543 tccccaagagatgtgcgggaagtgtagcaggtgccctagctggggaaagtcacaagtcagtaat	602
QY	421 tgtacgtctctggatgatataccagtgtgtttgaagaatttgtgtgccaatgtccactgtgaa	480
DB	603 tgtacgtctctggatgatataccagtgtgtttgaagaatttgtgtgccaatgtccactgtgaa	662
QY	481 accccagctgtcgtgaagagacaatgagacacacagcccgaggactcctgcgccacgtctgaa	540
DB	663 accccagctgtcgtgaagagacaatgagacacacagcccgaggactcctgcgccacgtctgaa	722
QY	541 gagacatagtaacacacagcccaaggagactcctgcgccacgtctgtgaagagacaatgacacac	600
DB	723 gagacatagtaacacacagcccaaggagactcctgcgccacgtctgtgaagagacaatgacacac	782
QY	601 agcccgaggagactcctgcgccacgtctgtgaagagacaatgacacacagcccgaggagactcct	660
DB	783 agcccgaggagactcctgcgccacgtctgtgaagagacaatgacacacagcccgaggagactcct	842
QY	661 gccccagctgtcgtgaagagacaatgagacacacagcccgaggagactcctctctcatatag	720
DB	843 gccccagctgtcgtgaagagacaatgagacacacagcccgaggagactcctctctcatatag	902
QY	721 ctctcatgtcaccatgttaggagatcatagtcttaattgtgctctgattgtgttct 777	
DB	903 ctctcatgtcaccatgttaggagatcatagtcttaattgtgctctgattgtgttct 959	
XX	RESULT 11	
XX	AAK23412	
XX	AAK23412 standard; DNA; 1365 BP.	
XX	AAK23412;	
XX	18-JUN-1999 (first entry)	
XX	Human hAPO9 DNA.	
XX	Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;	
XX	developmental abnormality; gestational abnormality; prostate cancer;	





CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
CC protein. The modified nucleic acid is then transfected into a host cell,  
CC which expresses a DD-containing receptor. The absence of apoptosis of the  
CC host cell is determined following exposure of the transfected cell to an  
CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
CC apoptosis of the host cell. The modified nucleic acid encoding the  
CC modified death domain-lacking membrane-spanning protein can also include  
CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
CC the coding sequence for a FLAG-TRID clone, which was used in the method  
CC of the present invention. This sequence comprises the human TRID coding  
CC sequence and a sequence encoding the FLAG-epitope tag. The FLAG-epitope  
CC is a useful marker to purify proteins encoded by the modified DD-lacking  
CC membrane-spanning protein. The identified TM and membrane-spanning  
CC proteins may be used in defining processes involved in cell suicide and  
CC tissue homeostasis, and to evaluate, interfere and treat events, such as  
CC cell proliferation and cell-cell signalling pathways.

Sequence 1111 BP; 276 A; 315 C; 299 G; 221 T; 0 other;

Query Match	95.28;	Score 740;	DB 22;	Length 1111;
Best Local Similarity	96.68;	Pred. No. 6.3e-213;		
Matches 777; Conservative	0;	Mismatches 0;	Indels 27;	Gaps 1

OY	1	atggccggatccccaagaacctaagaattgcgtcgtatcatgtctcgggtccctgtccga	60
Db	182	atgycgcggatccccaagaacctaagaattgcgtcgtatcatgtctcgggtccctgtccga	241
OY	61	gtccctagcttactctgcgc-----acacatgcccgcag	93
Db	242	gtccctagcttactctgcgcattacaagagctgaacataaagcttaacacatgcccgcag	301
OY	94	gaggaagttccccaagacagatggtccccaagcaacagagacacaggtctcaaggggag	153
Db	302	gaggaagttccccaagacagatggtccccaagcaacagagacacaggtctcaaggggag	361
OY	154	gaggttccaagcaggtctctatagatcacagaacatactgagcctgttaaccctgacaaag	213
Db	362	gaggttccaagcaggtctctatagatcacagaacatactgagcctgttaaccctgacaaag	421
OY	214	ggtctgagattacaaccaacgccttccaacaaatgaacctctgtctccaatgtaactgtt	273
Db	422	ggtctgagattacaaccaacgccttccaacaaatgaacctctgtctccaatgtaactgtt	481
OY	274	aaatcagatcaaaaaacaataaagaattctctgcacacatgacacagacacagttgtcagt	333
Db	482	aaatcagatcaaaaaacaataaagaattctctgcacacatgacacagacacagttgtcagt	541
OY	334	aaagaagcgaaccttccggagatgaataaaatccccaagagatgtccgggaagtgtgacaggtgc	393
Db	542	aaagaagcgaaccttccggagatgaataaaatccccaagagatgtccgggaagtgtgacaggtgc	601
OY	394	cctagctgggaagtcccaagtcagataattgtacgtccctggatgagataaccagttgttga	453
Db	602	cctagctgggaagtcccaagtcagataattgtacgtccctggatgagataaccagttgttga	661
OY	454	gaattgtgtgccaatgccaatgtgggaaaaccacagctgtctgaagagagacaaatgaacacacag	513
Db	662	gaattgtgtgccaatgccaatgtgggaaaaccacagctgtctgaagagagacaaatgaacacacag	721
OY	514	ccgggggaactctctgcgccacagctgtctgaagaagacaaatgaacacacagcccaagggaactctctgc	573
Db	722	ccgggggaactctctgcgccacagctgtctgaagaagacaaatgaacacacagcccaagggaactctctgc	781
OY	574	ccaagctctgtaagagacaaatgaacacacacacccggggaaatcctgtgccccacgtctgttgaag	633
Db	782	ccaagctctgtaagagacaaatgaacacacacacccggggaaatcctgtgccccacgtctgttgaag	841
OY	634	acaatgacacacacagcccggaagactcctgtgccccacagctgtctgaagagacaaatgaacacacag	693
Db	842	acaatgacacacacagcccggaagactcctgtgccccacagctgtctgaagagacaaatgaacacacag	901
OY	694	ccgggggaactctctgcctcttcatiaactctcatgacacatcgtaaggatcatagtctta	753

Db 902 ccgggacccctgcctccctccatcaacctcgcacacatcgttaggataatagtcta 961

Oy 754 atttgacctcgatctgattgttc 777

Db 962 attgacctccgattgattgttc 985

## RESULT 14

ID AAH19326 standard; DNA; 947 BP.

AC ААН19326;

DT 23-JUL-2001 (first entry)

DE Coding sequence for FLAG-TRID clone without a transmembrane domain.

KW FLAG-epitope tag; transmembrane domain; death domain; apoptosis;

KW cell-cell signalling; Trail Receptor without Intracellular Domain; TRID;

XX

XX

FT	CDS	182..931
----	-----	----------

ET

ET

ET

ET 3

FT  
yy

PN WO200114542-A1  
vvy

01-MAR-2001.

PF 23-AUG-2000; 2000WO-US23112.  
VY

PR 25-AUG-1999; 99US-0150747.  
XX

PA  
VV  
(GENO-) GENOME THERAPEUTICS CORP.  

Denome SA, Swaln PM, Tzellias N;  
PI  
xy

DR WPI; 2001-374162/39.  
DR D-PEDP; 2AP87182

Identifying a trans

PT comprises modifying the nucleic acid encoding a death domain-lacking

**P1** membrane spanning protein

ps Disclosure; Fig 2; 38pp; English:  
xx

CC The prent invention relates tomethods for identifying a transmembrane  
CC domain (TM) of a membrane-spanning protein. The method comprises  
CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane  
CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID)  
CC by replacing the nucleic acid encoding the TM of the DD-lacking  
CC membrane-spanning protein with a candidate nucleic acid sequence to  
CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
CC protein. The modified nucleic acid is then transfected into a host cell,  
CC which expresses a DD-containing receptor. The absence of apoptosis of  
CC the host cell is determined following exposure of the transfected cell to an  
CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
CC apoptosis of the host cell. The modified nucleic acid encoding the  
CC modified death domain-lacking membrane-spanning protein can also include









GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 09:34:04 ; Search time 48.56 Seconds  
(Without alignments)  
3930.338 Million cell updates/sec

Title: US-09-826-212-1-COPY\_183\_959

Perfect score: 777  
Sequence: 1 atgcccgcgataccccaagac.....tgcttcgtatgtgtgtgt 777

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: Issued\_Patents\_NA:\*  
2: /cgn2\_6/prodata1/1na/5A\_COMB.seq:\*  
3: /cgn2\_6/prodata1/1na/5B\_COMB.seq:\*  
4: /cgn2\_6/prodata1/1na/6A\_COMB.seq:\*  
5: /cgn2\_6/prodata1/1na/6B\_COMB.seq:\*  
6: /cgn2\_6/prodata1/1na/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	777	100.0	1392	US-09-006-353A-1	Sequence 1, Appl
2	381.4	49.1	356	US-09-086-483A-1	Sequence 1, Appl
3	262.8	33.8	398	US-09-086-483A-15	Sequence 15, Appl
4	229.8	29.6	1407	US-09-505-250-2	Sequence 2, Appl
5	229.8	29.6	2152	US-09-013-895A-1	Sequence 1, Appl
6	226.2	29.1	1323	US-08-883-036A-1	Sequence 1, Appl
7	195	25.1	1799	US-09-329-633A-1	Sequence 1, Appl
8	195	25.1	1799	US-09-079-029-2	Sequence 2, Appl
9	195	25.1	3881	US-09-333-593A-1	Sequence 1, Appl
10	165.2	21.3	506	US-09-006-353A-15	Sequence 15, Appl
11	109	14.0	1062	US-09-333-593A-3	Sequence 3, Appl
12	94.6	12.2	340	US-09-006-353A-17	Sequence 17, Appl
13	91.6	11.8	241	US-09-006-353A-18	Sequence 18, Appl
14	39.4	5.1	1392	US-09-006-353A-1	Sequence 1, Appl
15	39.2	5.0	336	US-07-814-220-3	Sequence 3, Appl
16	39.2	5.0	336	US-07-814-220-3	Sequence 3, Appl
17	38	4.9	336	US-07-814-220-4	Sequence 4, Appl
18	38	4.9	336	US-07-814-220-4	Sequence 4, Appl
19	38	4.9	1147	US-08-761-277A-44	Sequence 44, Appl
20	37.8	4.9	116	US-08-986-727-14	Sequence 14, Appl
21	37.6	4.9	568	US-08-986-727-5	Sequence 5, Appl
22	37.6	4.8	173	US-08-543-020-6	Sequence 6, Appl
23	37.6	4.8	173	US-08-735-692-8	Sequence 8, Appl
24	37.6	4.8	173	US-08-542-051-5	Sequence 5, Appl
25	36.4	4.7	3292	US-09-336-447A-14	Sequence 14, Appl
26	36.4	4.7	4403765	US-09-103-840A-2	Sequence 2, Appl
27	35.8	4.6	297	US-08-767-026-8	Sequence 8, Appl

28	35.8	4.6	6889	US-08-286-740-2	Sequence 2, Appl
29	35.8	4.6	6889	PCT-US95-09576-2	Sequence 2, Appl
30	35.4	4.6	426	US-09-013-895A-6	Sequence 6, Appl
31	35.4	4.6	3489	US-08-728-323A-1	Sequence 1, Appl
32	35.4	4.6	4614	US-08-325-267A-1	Sequence 1, Appl
33	35.4	4.6	5511	US-08-928-361B-2	Sequence 2, Appl
34	35.4	4.6	7334	US-08-928-361B-1	Sequence 1, Appl
35	35.4	4.6	32207	US-08-770-379-20	Sequence 20, Appl
36	35.4	4.6	32207	US-08-757-669A-20	Sequence 20, Appl
37	35.4	4.6	32207	US-09-230-371A-20	Sequence 20, Appl
38	34.6	4.5	1460	US-09-290-640-65	Sequence 65, Appl
39	34.6	4.5	2078	US-08-785-310A-1	Sequence 1, Appl
40	34.4	4.4	2464	US-07-863-169A-4	Sequence 4, Appl
41	34.4	4.4	2464	US-08-429-96A-4	Sequence 4, Appl
42	34.4	4.4	2464	US-07-935-087-4	Sequence 4, Appl
43	34.4	4.4	2464	PCT-US93-08062-4	Sequence 4, Appl
44	34.2	4.4	2413	US-08-651-579-1	Sequence 1, Appl
45	34.2	4.4	3349	US-09-336-447A-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-09-006-353A-1  
Sequence 1, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRES:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36,373  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1392 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..959  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 183..260  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 261..959

US-09-006-353A-1

Query Match	100.0%;	Score 777;	DB 4;	Length 1392;
Best Local Similarity	100.0%;	Pred. NO. 6e-229;		
Matches 777; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	atggccggagctccccaagacccttaaaattgctgtcgtcaatcgtcggctccgtcgtgca	60
Db	183	ATGGCCGGAGCTCCCAAGACCCCTTAAAGTTGCTGTCTCATCGTCCGGTCTCGTCCCA	242
QY	61	gtcciaagtactctcgtccaccactgtccggcagagaaagtctcccaagacagatgtgcc	120
Db	243	GTCTTACTTACTGTGCGACCACTGCGCGGACGAGGAAGTTCCACGACGACGAGGCC	302
QY	121	cccaagaaacagagggcagcagcttccaaggggagagatgtctcagcagatctcatagta	180
Db	303	CCACAGGACAGAGGCGCACACTTCAAGGGGGAGAGAGTGTCCACACGAGACTCTATGATCA	362
QY	181	gaacatctctgagacccttaaccgtgtcaacagaggggtgtgatattacccaagcttccac	240
Db	363	GAACATCTGTGAGGAGCTTAAACCCGTGCACAGAGGGGTGTGATTAACCAACGGTTTCAAC	422
QY	241	aatgaaccttctgtctcccatgtacaagtttgttcaatcagatccaaaataaagaattcc	300
Db	423	AATGAACCTTCTGTGCTTCCCATGTACAGTTGTAAATCAGATCAAAAACATAAAGTTCC	482
QY	301	tgcaccatgaccagagagacagatgtgtcagtgttaaagaagcaacttcggaaatgaaac	360
Db	483	TGCACCATGACAGAGACACAGTGTGATCAATGTAAAGAAAGGCACTTCGGAGATGAACAC	542
QY	361	tcccagaagatgtgcccgaagtgtaacaggtgcctcaatgtgggaagtcccaagtcaata	420
Db	543	TCCCAGAGATGTGTCCCGGAAGTGTAGCAGGTGCTCCATGTGGGAAGTTCCAAGTCAATAAT	602
QY	421	tgtacgtctcttggatgatataccagatgtgttgaagaatttggttgccaatibccagtfgaa	480
Db	603	TGTACGTCTCTGGATGATATTCCAGTGTGTTGAAGAATTTGGTCCAAATGCCACTGTGGAA	662
QY	481	accocagctctgtaagagaaatgaacaaccaagccggggatctcttcccagctctgtaa	540
Db	663	ACCCACACTCTCTAAGAGAACAAATGAACACCAAGCCCGGGACTCTCTCCACAGTGTGTA	722
QY	541	gagacaaatgaacaaccaagccagagactcctgtcccagctctgtgaagaagaatgaacacc	600
Db	723	GAGACAAATGAACACCAAGCCAGGAGACTCTGTCCCACTGTCTGAAGAAGCAATGACACACC	782
QY	601	agcccgaggactctgtcccagctgtctgaagaagacaatgccacaagcccgaggactct	660
Db	783	AGCCCGGAGACTCTGTGCCCACTGTGTGGAAGAACAATGACCAACCAAGCCCGGAGACTCT	842
QY	661	gcccacagctctgaagagacaaatgaaccaaccaagccggggactcttgcctcttcattac	720
Db	843	GCCCACACTCTCTAAGAGAACAAATGACACCAAGCCCGGGACTCTCTCTCTCATATAC	902
QY	721	ctctcaagacaaatgttaaggatcattatgttctatattgttcttctgttgtt	777
Db	903	CTCTCAATGACCAATCGAAGGAGATCATAGTTCTAATTTGTGCTCTGTGATTTGTTTGT	959

## RESULT 2

US-09-086-483A-1  
Sequence 1, Application US/09086483A  
Patent No. 6214580  
GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD

```

1 COUNTRY: US
2 ZIP: 20850
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: Patent In Release #1.0, Version #1.30
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/09/086,483A
10 FILING DATE: May-29-98
11 CLASSIFICATION: 435
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: 60/050,936
14 FILING DATE: May-30-97
15 CLASSIFICATION: 435
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 60/069,112
18 FILING DATE: Dec-9-97
19 CLASSIFICATION: 435
20 ATTORNEY/AGENT INFORMATION:
21 NAME: BROOKES, ANDERS A.
22 REGISTRATION NUMBER: 36,373
23 REFERENCE/DOCKET NUMBER: P3379
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (301) 309-8504
26 TELEFAX: (301) 309-8439
27 INFORMATION FOR SEQ ID NO: 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 356 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: DNA (genomic)
34 FEATURE:
35 NAME/KEY: CDS
36 LOCATION: 109..1266
37 FEATURE:
38 NAME/KEY: sig_peptide
39 LOCATION: 109..271
40 FEATURE:
41 NAME/KEY: mat_peptide
42 LOCATION: 274..1266
43
44 JS-09-086-483A-1

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Query Match	49.18;	Score 381.4;	DB 4;	Length 3566;
Best Local Similarity	82.08;	Pred. No. 2.8e-107;		
Matches 452;	Conservative 0;	Mismatches 96;	Indels 3;	Gaps 1;

QY	6	ccgataccccaaagaccctaaagtcctgcgtcatcatcgtcagctcgtccgcaagtcct	65
Db	204	CCTGAGACCCCAAGATCCCTAAGTTCTGTCGTCCTTATGCTGCGGGTTCTGTCGCGGGTCCG	26
QY	6	agcttaactctgcccacactgcgcgagcagagagaattcccccagcagacagatgagccaca	12
Db	264	GGTGTACTCTCCACCATTCCTCCCGGAGAGGAAGTTTCCGAGACAGAGGGCCACCA	32
QY	126	gcaacagagagcagacttcaaggggaggtgtccagcagatctcatagatcagaca	18
Db	324	GCAACAGAGGGCGCAGGCTCAAGGAGGAGGAGATGTCCAGACAGATCTCATATGATCAGATA	38
QY	186	tactggagcctgttaaccggtgcacagaggtgtgtgattacaccaaagcttccaacaatga	24
Db	384	TACTGGAGCCCTGTAACCCGTGCACAGAGGGTGTGATTATCACCATTCCTCCAAACAATTT	44
QY	246	acctctctgcttcccatgctacagttttaaatacgatcaaaaacataaaagtctctgac	30
Db	444	GCCTTCTTGCTCGTATGTATAGTTTGTAAATCAAGTCCAAACAATAAATTTCTGTAC	50
QY	306	catgacagagacacagttgtgtcaggttaaaagaacaccttcccgaaatgaanaactccc	36
Db	504	CACACACAGAACACCGCTGTGTACGTGTGAAAAAGGAAGTCTTCACAGGTATAAAACTCCCC	56

Oy	366	agagatgtgcccgggaagtcaaca---gltgccctcagtggggaaatccaaagtcagtaattg	422
Db	554	TGAGATGTGCCCCGGACGTTAGAACAGGGGTCTCCAGAGGGATGGTCAAGGTCAAGTAATTG	623
Oy	423	tacgttccttggatgatalccacagtggtgttgaagaaatttgygtccaatgcacatgtlgyaac	482
Db	624	TACGGCCCCGGAGTGACATCAAGTGCCAAATAATGATCAAGCTGGCAGTTTCCACTGGGAAAC	683
Oy	483	cccagctgtcgtgaagagacaatgaaaccagccggggagcttcctgtccccagctgtcctaaga	542
Db	684	CCCGACAGCCGAGAGAGACAGTACACACCACTCTGGGGATGCTTGCCCTCTCCATCACTA	743
Oy	543	gacaatgaca	553
Db	744	CCTTATCATCA	754

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RESULT 3
US-09-086-483A-15
: Sequence 15, Application US/09086483A
: Patent No. 6214580
: GENERAL INFORMATION:
: APPLICANT: NI, et al.
: TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: HUMAN GENOME SCIENCES, INC.
: STREET: 9410 KEY WEST AVENUE
: CITY: ROCKVILLE
: STATE: MD
: COUNTRY: US
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/086,483A
: FILING DATE: May-29-98
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/050,936
: FILING DATE: May-30-97
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/069,112
: FILING DATE: Dec-9-97
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BROOKES, ANDERS A.
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PF379
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8439
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 398 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-09-086-483A-15

Query Match 33.8%; Score 262.8; DB 4; Length 398;
Best Local Similarity 99.2%; Pred. No. 2.5e-71;
Matches 264; Conservative 0; Mismatches 2; Indels 0; Gaps
0

1 atgacccggatcccccaagaccctaaattgctgctgcatcgtcgcgtccgcgcga 60
db 133 atggccggatcccccaagaccctaaattgctgctgcatcgtcgcgtccgcgcga 192

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Oy	61	gtccaaagttactctgcacacacgcccgcagaggaagaatctccacagagaagttggc	120
Db	193	gtccctgaagttactctgcacacactgcccgcagaggaagaatctccacagagaagttggc	252
Oy	121	ccacagacacagagagcacagcttcaagaaggagagagtgctccagcagatctcataagta	180
Db	253	ccacagacacagagagcacagcttcaagaaggagagagtgctccagcagatctcataagta	312
Oy	181	gaacatactgtagcctctgtaaacccgtgcacagagagtgctgattacaccaagcttccaac	240
Db	313	gaacatactgtagcctctgtaaacccgtgcacagagagtgctgattacaccaagcttccaac	372
Oy	241	aatgaaccttctgcttcccatgfac	266
Db	373	aatgaaccttctgcttcccatgfac	398

```

RESULT 4
US-09-505-250-2
; Sequence 2, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1407)
; OTHER INFORMATION: Human TRAIL Receptor Coding Sequence
US-09-505-250-2

Query Match          29.6%; Score 229.8; DB 4; Length 1407;
Best Local Similarity 73.2%; Pred. No. 6.2e-61;
Matches 342; Conservative 0; Mismatches 107; InDels 18; Gaps 3.

QY 6 ccgagatccccaagaccctaaagctcgtcgtcgtacatcgtcgcgtcctcgtcgcagtcct 65
Db 258 ccgggtccacaagacctccaagtgttcg-----tcgtcgggtcctcgtcgcagtcgt 311
QY 66 agcttactctgcaccactgcccggcagagagaagattccccaagcagatgtgcccaca 125
Db 312 acctgacctcagctgtaacacatc-----aaactcatgtatcctaattgacacaca 362
QY 126 gcaaacaggcgccagctccaaggggagagatgctccagcagagatctcatagatcagaaca 185
Db 363 gcaatgggaacataagcctcttgaggagatgtgtccacacagagatccatagatcagaagc 422
QY 186 tactgagacgtgtaaccccggtgacagagaggtgtgattacacaaacgtctccaacaatga 245
Db 423 tctctgagacgtgtaaccccggtgacagagaggtgtgattacacaaacgtctccaacaatga 482
QY 246 acctctctgtctcccatgtacagttgttaatatcatcatcaaaaacataaagtctcctgac 305
Db 483 gttctctgtccctcccatgtacagctgttaatatcatagataagagagagagatccctgac 542
QY 306 catgacccagagacacagatgtgtcagttgtaaaagaagcactccggatgaataactcccc 365
Db 543 cagcagccaggaacacagcatgtcagttgcaaacacaggaacttccggatgacaattctgc 602
QY 366 agagatgtgccggaagtgtacga---ggtgcctagttgggaagtcacgaatgcagtaattg 422

```





RESULT 9  
 US-09-333-593A-1  
 : Sequence 1, Application US/09333593A  
 : Patent No. 6313269  
 : GENERAL INFORMATION:  
 : APPLICANT: DEEN, KEITH C.  
 : APPLICANT: YOUNG, PETER R.  
 : APPLICANT: MARSHALL, LISA A.  
 : APPLICANT: ROSHAK, AMY K.  
 : APPLICANT: TAN, KONG B.  
 : APPLICANT: TRUENH, ALEMSSEGD  
 : TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR  
 : TITLE OF INVENTION: TR6  
 : FILE REFERENCE: GH-50008-2  
 : CURRENT APPLICATION NUMBER: US/09/333,593A  
 : CURRENT FILING DATE: 1999-06-15

QY	3	gcccgcgtatccccaagaccctaaagttctgtctgcatactgtccggctccgcgtccagat	62
Db	186	gccccggtctcccaagaacc-----ttgtctgtgttgctgcgcggtctctgcgtttggt	235
QY	63	ctcagcttactctgcaccaactctccggcgagaggaagttccccaagacagtgtccccc	122
Db	240	ctcagcttgcgtctctctgcatacccaacaagaacctctccccaagagagtcgccc	295
QY	123	acacgaacaaagaggaacagcttccaagggtgagagttgtccacagagatctctataga	187
Db	300	acaaacaaaagaggtccacgccccctcagaagagattgtgtccacctgtgaacacatctcaga	355
QY	183	acatactgtgagccctgtcaacccgtgtcacagaggtgtgtgattacacaaagcttccaaca	247
Db	360	agaagctagagattgtcatctctcgtcaaatatgagacagatcatagcatcattgaattga	415
QY	243	tgaacctctctgtctctcccaattgaatttgttaattcgatcaaaaacataaagtctctg	302
Db	420	ctctcttctctgcttgcgcgtcaccaaggtgtgattcatcagatgaggtgagctaaagctccgt	477
QY	303	caccatgtaccagagacacaaagtgtgtcagttgttaagaagagcaccctccggaattgaanaatc	367
Db	480	caccacagaccagaaacacaaagtgtgtcagttgttaagaagagcaccctccggaattgaanaatc	535
QY	363	cccagagatgtgtccgggaagtgtgaaca---agttgccttagtgtgtgggaagttccaaagtcagtaa	411
Db	540	tctcgtgagatgtgtccgggaagtgtgtcagacagaggtgtgtccccaagaggtatgtgtgtgtgtgt	595
QY	420	ttgtgattctccgtgagatgatatccagttgtgttgaagaagaatttgttcacaaagtcacactgtgtga	479
Db	600	ttgtgtacacccctggaggtgtgcatctgagattgtgtccacaaagaatcagtcatactatagaagt	655
QY	480	aaccccagctgtcgtgaag	496
Db	660	cacagttgtcagacgttag	676

RESULT 10  
 US-09-006-353A-15  
 : Sequence 15, Application US/09006535A  
 : Patent No. 6261801  
 : GENERAL INFORMATION:  
 : APPLICANT: WEI, YING-FEI  
 : APPLICANT: YU, GUO-LIANG  
 : APPLICANT: GENTZ, REINER  
 : APPLICANT: RUBEN, STEVEN  
 : TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
 : NUMBER OF SEQUENCES: 26  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: HUMAN GENOME SCIENCES, INC.,  
 : STREET: 9410 KEY WEST AVENUE

RESULT 12  
 US-09-006-353A-17  
 Sequence 17, Application US/0900653A  
 Patent No. 6261801  
 GENERAL INFORMATION:  
 APPLICANT: WEI, YING-FEI  
 APPLICANT: YU, GUO-LIANG  
 APPLICANT: GENGTZ, REINER  
 APPLICANT: RUBEN, STEVEN  
 TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 STREET: 9410 KEY WEST AVENUE  
 CITY: ROCKVILLE  
 STATE: MD  
 COUNTRY: US  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/006,353A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROOKES, ANDERS A  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PF41  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:  
LENGTH: 340 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-006-353A-17

Query Match 12.2%; Score 94.6; DB 4; Length 340;  
Best Local Similarity 91.5%; Pred. No. 1e-19;  
Matches 108; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 661 gccccagctgctgaagagaagacacccagccgggagctcctctctcatcattac 720  
|||||  
Db 8 GCCCAGCTGCTGAAGAGACATATACACGCCGGGAGCTCCGNTCTCTATATAC 67

Qy 721 ctctcatgacacatcgttaggatacatagttctaattgtg-cttctgattggttctt 777  
|||||  
Db 68 CTCCTNATCCACCATCGTAGGATCATAGTCTCAATTGCTTCAATTGTTTGT 125

## RESULT 13

US-09-006-353A-18  
Sequence 18, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PP341  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-006-353A-18

Query Match 11.8%; Score 91.6; DB 4; Length 241;  
Best Local Similarity 91.3%; Pred. No. 7e-19;  
Matches 105; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 649 ccgggagactcctgcccagctgctgaagaagaacacacccagccgggagctctcgc 708  
|||||  
Db 1 CCAGGGTCTCTNCCCACTGCTGTAAGAGACANTGACCAACGAGCCCGGAGCTCTGCC 60

Qy 709 tctt-ctcatcctcatcgtacacacatgtaggatacatagttctaattgacctt 762  
|||||  
Db 61 TCTTCTCATTAACCTCTNATGANCATGCTAGGATCATAGTCTCAATTGTCCT 115

## RESULT 14

US-09-006-353A-1/c  
Sequence 1, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PP341  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1392 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..959  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 183..260  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 261..959  
US-09-006-353A-1

Query Match 5.1%; Score 39.4; DB 4; Length 1392;  
Best Local Similarity 48.8%; Pred. No. 0.018;  
Matches 106; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 482 ccccaagctgctgaagagacacacacccagccgggagctcctgcccagctctgaga 541  
|||||  
Db 880 CCCGGCTGCTGTCATGTCCTTTCACAGCTGGGCGAGAGTCCCGGGCTGTGCT 821

Qy 542 agacaatgaacacacagccagggagctcctgcccagctgctgaagaagaatgaccacca 601  
|||||

Db 820 ATGTCTCTTCAGACAGCTGGGGCAGAGATCCCGGCTGCTGTCATGTCCTTCAGCA 761  
Qy 602 gccgggagctcctgcccagctgctgaagaagaatgaccacacagccgggagctcctg 661  
|||||



D<sub>b</sub> 760 GCTGGGAGSAGTCCCTGGGCGTGTTTCATTATCTCTTCACGACGTGGGGCAGGAGTC 701

Q<sub>y</sub> 662 CCCcagctgcTgaagagaacatgacccacccggg 698  
||| ||| | - ||| ||| |||  
D<sub>b</sub> 700 CCGGGCGTGTTCAATTGTCTCTTCAGCACGTGGG 664

RESULT 15

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US-07-814-220-3
: Sequence 3, Application US/07814220
: Patent No. 5925540
:
: GENERAL INFORMATION:
: APPLICANT: Cacecli, Thomas
: APPLICANT: Totli, Thomas E.
: APPLICANT: Szumanski, Maria B.W.
: TITLE OF INVENTION: SYNTHETIC ANTIPREZE PEPTIDE AND
: TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
: NUMBER OF SEQUENCES: 43
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WHITHAM, CURTIS & WHITHAM
: STREET: Reston Int'l. Center, 11800 Sunrise Valley Dr.,
: STREET: Suite 900
: CITY: Reston
: STATE: VA
: COUNTRY: USA
: ZIP: 20191
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/814,220
: FILING DATE: 23-DEC-1991
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/588,437
: FILING DATE: 25-SEP-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Whitham, Michael E.
: REGISTRATION NUMBER: 32,635
: REFERENCE/DOCKET NUMBER: CIT.016
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-391-2510
: TELEFAX: 703-391-9035
:
: INFORMATION FOR SEQ ID NO: 3:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 336 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
:
: NAME/KEY: CDS
: LOCATION: 31..324
:
: US-07-814-220-3

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Query Match	5.0%;	Score 39.2;	DB 2;	Length 336;
Best Local Similarity	50.5%;	Pred. No. 0.01;		
Matches 95;	Conservative 0;	Mismatches 93;	Indels 0;	Gaps 0

Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db		
526	gcccagctgtctgaagagacaatgaacacagcccagagagctctctgcccaagctgtcga	585	gcccagctgtctgaagagacaatgaacacagcccagagagctctctgcccaagctgtcga	49	gcccgggagcagcagcagctgctactgcccggcagacccagcagcagctgctgaggc	108	gcccgggagcagcagcagctgctactgcccggcagacccagcagcagctgctgaggc	56	gagcagaatgaccaccagcccgaggagctctctgcccagctgtctgaagagacaatgacacc	645	gagcagaatgaccaccagcccgaggagctctctgcccagctgtctgaagagacaatgacacc
109	gcgacccgacgacgacgctgcgcgcgacgctactgcgcgcgacccgacgacgctgcgcgcg	168	gcgacccgacgacgacgctgcgcgcgacgctactgcgcgcgacccgacgacgctgcgcgcg	646	agcccgaggactcctgtgcccaagctgtctgaagagacaatgacacacagcccgggagctcct	705	agcccgaggactcctgtgcccaagctgtctgaagagacaatgacacacagcccgggagctcct	169	accctgcttaccgacgacgctgctgcgcgcgacacacacacacacacacacacacacacac	228	accctgcttaccgacgacgctgctgcgcgcgacacacacacacacacacacacacacacac

QY	706	gcctcttc	713
Db	229	GCAGCTAC	236

Search completed: August 13, 2002, 11:26:06  
Job time: 6722 sec

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FT      /label= epitope
FT      Region      142..148
FT      /label= epitope
XX      WO9830693-A2.
XX      16-JUL-1998.
XX      13-JAN-1998; 98WO-US00152.
XX      07-AUG-1997; 97US-0054885.
XX      14-JAN-1997; 97US-0035496.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      Eimer R, Feng P, Gentz RL, Nl J, Ruben SM, Wei Y;
PI      Yu G;
XX      WPI; 1998-399141/34.
XX      N-PSDB; AAV51348.
XX      Human TRAIL receptor without an intracellular domain polypeptide -
PT      used in the diagnosis of immune system-related disorder(s)
XX      Claim 1b; Fig 1; 90pp; English.
XX      This sequence represents a human TRID (TRAIL, (TNF-related
CC      apoptosis-inducing ligand) receptor without an intracellular domain).
CC      TRID is a member of the tumour necrosis factor receptor (TNFR) family
CC      also known as TNFR-5. TRID is expressed in haematopoietic tissues and
CC      other normal human tissues. For a number of immune system-related
CC      disorders, substantially altered (whether increased or decreased) levels
CC      of TRID gene expression can be detected, therefore the TRID polypeptides,
CC      nucleic acids and antibodies are useful in the diagnosis of such immune
CC      system related disorders. Mutations of the TRID gene can also be
CC      detected. TRID can also be used to identify ligands which may be useful
CC      in the treatment of apoptosis related disorders. TRID is administered to
CC      humans at a parenteral dose of 0.01 to 1 mg/kg/day.
XX      Sequence 259 AA;

Query Match      100.0%; Score 1382; DB 19; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARIPTLTKFVVVIVAVLLPVLAYSATTAEOEYPOOTVAPQOORHSFKGECPAGSHRS 60
DB      1 maripktlktfvvivaalipvlayaltatargeevpqqlvapaqghstfkgeecpagshts 60
QY      61 EHTGACNPTCEGVVDYTNASNNPSCFPCVCKSDOKHKSCTMTRTDTCVCKEGSTFRNEN 120
DB      61 ehtgacnptcegvvdyltnasnnpescfpcvcksdokhksctmttrtdtvcvckegstfrnen 120
QY      121 SPEKCRKCSKRPSEGVQVSNKTSWDDIQCEFGANATVEFPAAEETMNTSPGPAPAAE 180
DB      121 spekcrcsksrpsegvqvsnktswdidiqceefganatvefpaaeetmntspgpapaae 180
QY      181 ETMTSTSGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGPASSHY 240
DB      181 etmtstsgtpapaaeetmtspgtpapaaeetmtspgtpapaaeetmtspgpashshy 240
QY      241 LSCITVGIIVLIVLIVFV 259
DB      241 lscitvgliivlilivfv 259

RESULT 2
ID      AAM88408
AC      AAM88408 standard; Protein; 259 AA.
XX      AAM88408;

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DT      26-APR-1999 (first entry)
XX      Human Apo-2DCR protein (amino acids 1-259).
DE      Apo-2DCR; human; apoptosis; tumour necrosis factor receptor;
XX      neurodegeneration; autoimmune disease; inflammation; cancer;
XX      therapy.
XX      Homo sapiens.
OS      Homo sapiens.
XX      Key
FH      Peptide
FT      Location/Qualifiers
FT      1..29
FT      /note= "predicted signal peptide"
FT      1..161
FT      /note= "extracellular domain, this domain is
FT      specifically claimed in Claim 5"
FT      Domain
FT      68..109
FT      /note= "cysteine-rich domain"
FT      110..149
FT      /note= "cysteine-rich domain"
FT      Peptide
FT      162..176
FT      /note= "tandem repeat peptide"
FT      177..191
FT      /note= "tandem repeat peptide"
FT      192..206
FT      /note= "tandem repeat peptide"
FT      207..221
FT      /note= "tandem repeat peptide"
FT      222..236
FT      /note= "tandem repeat peptide"
FT      237..259
FT      /note= "hydrophobic C-terminal region"
FT      Modified-site
FT      77
FT      /note= "N-glycosylation"
FT      Modified-site
FT      140
FT      /note= "N-glycosylation"
FT      Modified-site
FT      156
FT      /note= "N-glycosylation"
FT      Modified-site
FT      169
FT      /note= "N-glycosylation"
FT      Modified-site
FT      184
FT      /note= "N-glycosylation"
FT      Modified-site
FT      184
FT      /note= "N-glycosylation"

XX      WO9858062-A1.
XX      23-DEC-1998.
XX      12-JUN-1998; 98WO-US12456.
XX      18-JUN-1997; 97US-0878168.
XX      (GETH ) GENENTECH INC.
XX      Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;
PI      Kim KJ, Wood WI;
XX      WPI; 1999-095340/08.
XX      N-PSDB; AAV84347.
XX      New Apo-2DCR polypeptide - used for modulation and diagnosis of
PT      apoptosis, e.g. in neurodegeneration
XX      Claim 1; Page 50-51; 88pp; English.
XX      This polypeptide comprises human Apo-2DCR, a novel member of the
CC      tumour necrosis factor receptor family that binds to Apo-2 ligand.
CC      Its amino acid sequence was deduced from the nucleotide sequence
CC      of an isolated cDNA clone (see AAV84347); an alternative translation
CC      initiation site in this clone will encode a polypeptide (see
CC      AAM88409) comprising amino acid residues -40 to 269 of Apo-2DCR.
CC      Apo-2DCR shows more sequence identity to DR4 (60%) and Apo-2 (50%)
CC      than to other apoptosis-linked receptors. The polypeptide can be
CC      obtained by expression in host cells using the vector deposited as

```

CC ATCC 209087. The invention provides vectors and host cells for  
 CC recombinant production of Apo-2Dcr polypeptides, antibodies, and  
 CC transgenic and knockout animals (useful e.g. for screening and  
 CC developing drugs that protect against excessive apoptosis).  
 CC Apo-2Dcr, or chimeras comprising Apo-2Dcr or its (claimed)  
 CC extracellular domain fused to a heterologous polypeptide are used  
 CC to modulate apoptosis of mammalian cells (claimed) and/or NF-kappaB  
 CC activation by Apo-2 ligand, and may be expressed in vivo or ex vivo  
 CC for gene therapy. They can be used in methods for the modulation  
 CC and diagnosis of apoptosis e.g. in cases of neurodegeneration,  
 CC autoimmune diseases and inflammation. Most human tumour cells do  
 CC not express Apo-2Dcr transcripts, but normal tissues do, suggesting  
 CC that Apo-2Dcr may permit selective killing of cancer cells by Apo-2  
 CC ligand, possibly by protecting normal, but not cancerous, cells.  
 CC  
 XX Sequence 259 AA;

Query Match 100.0%; Score 1382; DB 20; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPKTLKFFVYIVAVLLPVLAISATTARQEEVPOQTVAPQOQRHSFGEECPAGSHRS 60  
 Db 1 maripkltkffvviavallpvlaysattarqeevpqqtvpqqrhsfkgcecpagshrs 60  
 QY 61 EHTGACNPGCTEGVDYTNASNNPSCFPGTVCKSDOKHKSCTMTPTDYCOCKEGTFRNEN 120  
 Db 61 ehtgacnpgctegvdytnasnnepscfcptcvcksdqkhksctmtptdycockegtlfrnen 120  
 QY 121 SPENCRKSCRCPGSEVOYNSCTSMDDIOCEFEFGANATVETPAAEEMNTSPGTPAPAAE 180  
 Db 121 spencrkscrcpsgevyvnsctsmddiocefefganavetpaaeemntspgtpapaae 180  
 QY 181 EMTNRSPTGTPAPAAEEMTTSPTGTPAPAAEEMTTSPTGTPAPAAEEMTTSPTGTPAAS 240  
 Db 181 emtnrspgtppapaaeemttsptgtpapaaeemttsptgtpapaaeemttsptgtpasshy 240  
 QY 241 LSCRTVGITLVLLILVIFV 259  
 Db 241 lscrtvgitlvllilvifv 259

RESULT 3  
 AAU12321  
 ID AAU12321 standard; Protein: 259 AA.  
 XX  
 AC AAU12321;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO366 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.  
 XX  
 OS Homo sapiens.  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US32678.  
 XX  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerilsen ME, Goddard A, Godowski PJ, Gunney AU, Sherwood S;  
 PI Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPT: 2001-408281/43.  
 DR N-P5DB; AAS21393.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 PS  
 XX  
 PS Claim 12: Fig 300; 813pp: English.  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, or the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 XX  
 XX Sequence 259 AA;

Query Match 100.0%; Score 1382; DB 22; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPKTLKFFVYIVAVLLPVLAISATTARQEEVPOQTVAPQOQRHSFGEECPAGSHRS 60  
 Db 1 maripkltkffvviavallpvlaysattarqeevpqqtvpqqrhsfkgcecpagshrs 60  
 QY 61 EHTGACNPGCTEGVDYTNASNNPSCFPGTVCKSDOKHKSCTMTPTDYCOCKEGTFRNEN 120  
 Db 61 ehtgacnpgctegvdytnasnnepscfcptcvcksdqkhksctmtptdycockegtlfrnen 120



ID	AB36696 standard; Protein; 259 AA.
XX	
XX	AB36696;
XX	
DT	15-MAR-2001 (first entry)
XX	
DE	Human tumour necrosis factor receptor 5 (TRID) protein SEQ ID NO:2.
XX	
KW	Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nontropic;
KW	TRAIL receptor without intracellular domain; diagnosis; cytosolic;
KW	tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW	immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW	anticonvulsant; antiparasitic; caducant; anti-HIV; antiparkinsonian;
KW	gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW	apoptotic cell death related disease; autoimmune disorder;
KW	cardiovascular disorder; viral infection.
XX	
OS	Homo sapiens.
XX	
PN	WO20071150-A1.
PD	
XX	30-NOV-2000.
XX	
PF	18-MAY-2000; 2000WO-US13515.
XX	
PR	20-MAY-1999; 99US-0135164.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Wei Y, Ruben SM, Gentz RL, Ni J;
DR	WPI: 2001-041051/05.
XX	
DR	N-PSDB: AAC90774.
XX	
PT	Nucleic acid encoding a TRID polypeptide, also referred to as tumor;
PT	necrosis factor receptor 5; useful in the diagnosis, treatment or
XX	prevention of cancer, autoimmune disorders and viral infection -
PS	
XX	Claim 15; Fig 1; 285pp; English.
XX	
CC	The present sequence represents the human TRID protein (tumour necrosis
CC	factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC	intracellular domain, also referred to as tumour necrosis factor
CC	receptor 5 (TNFR-5 or TR5)). TRID has cytosolic, immunosuppressive,
CC	nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC	antiparasitic, cardiac, anti-HIV, antiparkinsonian and vasotropic
CC	activities, and can be used in gene therapy. The TRID polynucleotides
CC	are useful for detecting complementary polynucleotides. TRID proteins and
CC	polynucleotides are useful in the treatment of tumours, resistance to
CC	parasite, bacteria and viruses, restenosis and graft versus host disease.
CC	They are also useful for inducing proliferation of T-cells, endothelial
CC	cells and certain haematopoietic cells, to regulate antiviral responses
CC	and to prevent certain autoimmune diseases after stimulation of TRID by
CC	an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC	polypeptides are useful for treating and/or preventing diseases
CC	associated with increased or decreased apoptotic cell death. The TRID
CC	polynucleotides, proteins, antibodies, agonists and antagonists are
CC	useful in the diagnosis, treatment or prevention of: (a) cancer;
CC	(b) autoimmune disorders; (c) diseases associated with increased
CC	apoptosis; (d) cardiovascular disorders; and (e) viral infection.
XX	
XX	
XX	Sequence 259 AA:
XX	
Query Match	100.0%; Score 1382; DB 22; Length 259;
Best Local Similarity	100.0%; Pred. No. 2.5e-86;
Matches 259; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
0Y	1 MARIKTLKEVVVIAVLLPLVATSAATPAROEVEVPOQTVAPOOQRHSFGECGPAGSHRS 60
dbb	1 maripktlkfvvviavllplvatsatargvevpqqtavapqqrntstfgcecpagshrs 60
0Y	61 EHTGACNPTCEGVDTNANNNPSCFPCVACKSDCKHKSSCTMTBTPVQCCEGTFRNN 120

Db	61	ehltgacnpteeydvdytnasamepscictvcksdqkhkssctumtrdvcqckeglfnen	120
QY	121	SEMWKRCSSRCPSGCVQVSNCTSMNDIQCEVFGNATVTPAAEEFMNTTSPGTPAAAE	180
Db	121	spemrckscircpsgcvqsnctswddlqcveefiganavevcpaeetmnttspgtpapae	180
QY	181	ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY	240
Db	181	etmntspgtpapaeetmnttspgtpapaeetmnttspgtpapaeetmnttspgtpasshy	240
QY	241	LSCTIVGIIVLIVLIVFV	259
Db	241	lsctivgiivlilivlifr	259
RESULT 6			
ID	AAB53091	standard; Protein; 259 AA.	
AC	AAB53091;		
DT	28-FEB-2001	(first entry)	
DE	Human	angiogenesis-associated protein PRO366, SEQ ID NO:152.	
XX	Human	angiogenesis-associated protein; PRO: endothelial cell growth;	
KW	cardiac hypertrophy; cardiovascular disorder; endothelial disorder;		
KW	angiogenic disorder; atherosclerosis; osteoporosis; hypertension;		
KW	myocardial infarction; diabetic retinopathy; Rheumatoid arthritis;		
KW	Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; Canc		
KW	Alzheimer's disease; Huntington's disease; stroke; drug screening;		
XX	gene therapy; transgenic animal.		
OS	Homo sapiens.		
XX	WO200053753-A2.		
XX	14-SEP-2000.		
PD	05-JAN-2000; 2000WO-US00219.		
PF	08-MAR-1999; 99WO-US05028.		
PR	12-MAR-1999; 99US-0123957.		
PR	14-MAY-1999; 99US-0134287.		
PR	02-JUN-1999; 99WO-US12252.		
PR	23-JUN-1999; 99US-0141037.		
PR	20-JUL-1999; 99US-0144758.		
PR	26-JUL-1999; 99US-0145698.		
PR	01-SEP-1999; 99WO-US20114.		
PR	08-SEP-1999; 99WO-US20594.		
PR	15-SEP-1999; 99WO-US21090.		
PR	15-SEP-1999; 99WO-US21547.		
PR	05-OCT-1999; 99WO-US23089.		
PR	30-NOV-1999; 99WO-US28313.		
PR	30-NOV-1999; 99WO-US28409.		
PR	02-DEC-1999; 99WO-US28564.		
PR	02-DEC-1999; 99WO-US28565.		
XX	(GETH ) GENENTECH INC.		
PA	Asuhkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;		
XX	Asuhkenazi PJ, Gurney AJ, Hillan KJ, Kuo SS, Mark MR, Maisters SA,		
PI	Paoni NF, Pletti RM, Watanabe CK, Williams PM, Wood WI;		
PI	WPI; 2001-090793/10.		
DR	N-PSDB; AAC97488.		
XX	New isolated nucleic acid for producing a PRO polypeptide, analyzing		
PT	genetic disorders and treating cardiovascular, endothelial or		
PT	angiogenic disorders, such as atherosclerosis, wounds or cancer -		
PS	Claim 69; Fig 56; 293pp; English.		

Query Match	Similarity	100.0%	Score 1387	DB 22	Length 259
Best Local	Similarity	100.0%	Pred. No. 2,5e-86		
Matches 259	Conservative	0	Mismatches 0	Indels	Gaps 0
QY	1	MARIPTLKEFVVVIVIAVLLPLVLAYSATTAAROEVEVPOQVFAPOQOHRHSFGEECPAGSHRS	60		
Db	1	maripkltkfvyvviyaavllpviayattarargeevpqglvapqqrhnsfigeepagshrs	60		
QY	61	EHTGACNPCTEGVDYTNASNNNEPSCFPTVCKSDOKHRS SCTMTDPTVQCCKEGTFRRMEN	120		
Db	61	ehgtgacnpctegvdytnasnnnepscfptcvcksdqkhkssccmtrdtvqcckegtfrrmen	120		
QY	121	SPEMKRKSRCRPSGSGVOVSNCTSWDIDOCVEEFGANAIATVEYPAAEIYMTNTSGTPAPAAE	180		
Db	121	spemkrkscrcrpsgsgevsnctswddiqveefganaetvcpaaeetmtntspgtpapaae	180		
QY	181	ETMTNTSPCTPAPAAEETMTNTSGTPAPAAEETMTNTSGTPAPAAEETMTNTSGTPAASHX	240		
Db	181	etmtntspgtpapaaeetmtntspgtpapaaeetmtntspgtpapaaeetmtntspgtpaashx	240		
QY	241	LSCITVGIIVLIVLLIVFV	259		
Db	241	lscitvgiivlilivllivfv	259		
RESULT 7					
AAW76331					
AAW76331 standard; Protein; 299 AA.					
AAW76331:					
11-JAN-1999 (first entry)					
Human tumour necrosis related receptor TR5.					

Query Match	100.0%;	Score 1382;	DB 19;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 2.9e-86;		
Matches 259;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0



QY 1 MARIPKTLKFVYVIVAVLLPVLAYSATTAROEENVPQQTVAPOOQRHSEFKGECPCGASHRS 60  
 CC |  
 CC |  
 Db 41 maripkltklfvvivaavllpvlaysattarqeavpqrvtvppqqrhskfgeecpgashrs 100  
 CC |  
 CC |  
 QY 61 EHTGACNCTEGVDYTNASNNPSCFPCTVCKSDOKHKSSCTMTRTDYCOCKEGTFRNEN 120  
 CC |  
 CC |  
 Db 101 ehtgacnptcgvdytnasnepscfctvcvsdqkhksacmtltdvcqcegftrfren 160  
 CC |  
 CC |  
 QY 121 SPEMCRKSRCPGSEVOVSNCTSMDDIQCEBFGANATVETPAPAEETMNTSPGTPAPAAE 180  
 CC |  
 CC |  
 Db 161 spemcrksrpsgevgvsnctswddiqceefgenatvecpaaeetmtspgtpapaae 220  
 CC |  
 CC |  
 QY 181 ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY 240  
 CC |  
 CC |  
 Db 221 etmntspgtpapaaeetmttspgtpapaaeetmttspgtpapaaeetmttspgtpasshy 280  
 CC |  
 CC |  
 QY 241 LSCITVGIIVLIVLIVFV 259  
 CC |  
 CC |  
 Db 281 lscitvgliivlilivfv 299  
 CC |  
 CC |  
 RESULT 8  
 AAY29864  
 ID AAY29864 standard; Protein; 299 AA.  
 AC AAY29864;  
 XX  
 DT 17-NOV-1999 (first entry)  
 XX  
 DE Human secreted protein clone ljl1442.1.  
 XX  
 KW Human; secreted protein; biological activity; nutritional; cytokine;  
 KW cell proliferation; differentiation; immune stimulating; vaccine;  
 KW haematopoiesis regulation; tissue growth; haemostatic; thrombolytic;  
 KW anti-inflammatory; tumour inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WC09946287-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PE 11-MAR-1999; 99WO-US05243.  
 XX  
 PR 11-MAR-1998; 98US-0077521.  
 PR 14-MAY-1998; 98US-0079124.  
 PR 10-MAR-1999; 99US-0266105.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ;  
 XX  
 DR WPI: 1999-551362/46.  
 DR N-PSDB: AAZ21096.  
 XX  
 PT Polynucleotides encoding secreted human proteins, derived from human  
 PT fetal brain, human adult blood, human adult bladder, or human adult  
 PT neural tissue cDNA libraries.  
 XX  
 PS Claim 17; Page 104; 118pp; English.  
 CC  
 CC AAZ21093 to AAZ21102 encode new human secreted proteins and AAY29861 to  
 CC AAY29873 represent the secreted proteins encoded by the polynucleotide  
 CC sequences. AAZ21103 to AAZ21112 represent probes for the secreted  
 CC proteins. The polynucleotides and proteins are predicted to have  
 CC biological activities which would make them suitable for treating,  
 CC preventing or ameliorating medical conditions in humans and animals,  
 CC although no supporting data is given. Suggested activities include  
 CC nutritional activity, cytokine and cell proliferation/differentiation  
 CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cachectin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity. The polynucleotides and proteins can also be used  
 CC as nutritional sources or supplements. Such uses include use as a protein  
 CC or amino acid supplement, use as a carbon source, use as a nitrogen  
 CC source and use as a source of carbohydrate. They may also have utility  
 CC in compositions used for bone, cartilage, tendon, ligament, and/or nerve  
 CC tissue growth or regeneration, as well as for wound healing and tissue  
 CC repair and replacement, and in the treatment of burns, incisions and  
 CC ulcers. The proteins which induce cartilage and/or bone growth in  
 CC circumstances where bone is not normally formed, have application in  
 CC the healing of bone fractures and cartilage damage or defects in humans  
 CC and other animals.  
 CC  
 CC Sequence 299 AA:  
 SQ  
 Query Match 100.0%; Score 1382; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MARIPKTLKFVYVIVAVLLPVLAYSATTAROEENVPQQTVAPOOQRHSEFKGECPCGASHRS 60  
 Db 41 maripkltklfvvivaavllpvlaysattarqeavpqrvtvppqqrhskfgeecpgashrs 100  
 QY 61 EHTGACNCTEGVDYTNASNNPSCFPCTVCKSDOKHKSSCTMTRTDYCOCKEGTFRNEN 120  
 Db 101 ehtgacnptcgvdytnasnepscfctvcvsdqkhksacmtltdvcqcegftrfren 160  
 QY 121 SPEMCRKSRCPGSEVOVSNCTSMDDIQCEBFGANATVETPAPAEETMNTSPGTPAPAAE 180  
 Db 161 spemcrksrpsgevgvsnctswddiqceefgenatvecpaaeetmtspgtpapaae 220  
 QY 181 ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY 240  
 Db 221 etmntspgtpapaaeetmttspgtpapaaeetmttspgtpapaaeetmttspgtpasshy 280  
 QY 241 LSCITVGIIVLIVLIVFV 259  
 Db 281 lscitvgliivlilivfv 299  
 RESULT 9  
 AAY05744  
 ID AAY05744 standard; Protein; 299 AA.  
 AC AAY05744;  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DE Tumour necrosis factor receptor TR5.  
 XX  
 KW Tumour necrosis factor receptor; TR5; TRID; DCRI; agonist;  
 KW antagonist; screening; human; cancer; AIDS; Alzheimer's disease;  
 KW inflammation; arthritis; septicemia; autoimmune disease;  
 KW psoriasis; inflammatory bowel disease; transplant rejection;  
 KW graft versus host disease; infection; stroke; ischaemia;  
 KW acute respiratory disease syndrome; restenosis; brain injury;  
 KW bone disease; atherosclerosis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP911633-A1.  
 XX  
 PD 28-APR-1999.  
 XX  
 PF 02-OCT-1998; 98EP-0203332.  
 PR 08-OCT-1997; 97US-0061334.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI McDonnell PC, Young PR, Zou J;

XX WP1: 1999-246560/21.  
XX  
XX Identifying agonists and antagonists of tumor necrosis factor  
PT related receptors TR1, TR3 and TR5, and of ligand TL3, useful for  
PT treatment of cancer, AIDS, Alzheimer's disease, bone disease etc  
XX  
XX Disclosure: Page 13-14; 23pp; English.  
XX  
XX The present sequence represents tumour necrosis factor receptor  
CC (TNFR) TR5, also known as TR1D or DcR1. The invention relates  
CC to TNFR related polypeptides TR1, TR3 and TR5 (see AA05042-44) and  
CC their ligand TL3 (see AA050745). TR1, TR3, TR5 and TL3 are used in  
CC claimed methods of identifying agonists and antagonists, i.e.  
CC compounds that bind to the receptors or ligand, and which activate  
CC (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or  
CC TL3. A screening kit for identifying agonists, antagonists,  
CC ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or  
CC TL3 polypeptides is provided. The agonists and antagonists are  
CC useful for treatment of chronic and acute inflammation, arthritis,  
CC septicemia, autoimmune disease e.g. inflammatory bowel disease,  
CC psoriasis, transplant rejection, graft versus host disease,  
CC infection, stroke, ischemia, acute respiratory disease syndrome,  
CC resection, brain injury, AIDS, bone diseases, cancer (e.g.  
CC lymphoproliferative disorders), atherosclerosis and Alzheimer's  
CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.  
XX  
SQ Sequence 299 AA:  
  
Query Match 100.0%; Score 1382; DB 20; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2,9e-86;  
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MARIKTLKFWVIVAVLPLVATYSATTAROEYVPOQTVPAPQOORHSFKGECPPAGSHRS 60  
Db 41 maripkltkfivvivaavlplvaysattarqeevpqqlvapgqqrhstkgcecpagshrs 100  
  
QY 61 EHTGACNPCTEGVDYTNASNNPSCFCTVCKSDOKRHSCTMTDRIVCOCKEGTFRNEN 120  
Db 101 ehtgacnpctegvdyltnasnepscfctvcksdqkhksctumtrdvcoqkegffnen 160  
  
QY 121 SPEMKRKSRCPSGEGVOYNSCTSMDDIOCVEEFGANATVEPPAAEETMTNTSGTPASSHY 180  
Db 161 spemckrksrcpsgevgvsnctswddiqveefganatvecpaaeeetmtntspgtpapaae 220  
  
QY 181 ETMTNTSGTPAPAAEETMTNTSGTPAPAAEETMTNTSGTPASSHY 240  
Db 221 etmtntspgtpapaaeeetmtntspgtpapaaeeetmtntspgtpasshy 280  
  
QY 241 LSCITVIGIIVLIVLIVFV 259  
Db 281 lscitvgiivlilvllivfv 299  
  
RESULT 10  
AA00933  
ID AA00933 standard; Protein: 299 AA.  
XX  
XX AA00933:  
XX  
DT 02-JUN-1999 (first entry)  
XX  
XX Human TRAIL-R3 protein sequence.  
XX  
KW Human; DR5; DR5s; TRAIL-R3; apoptosis related condition; cancer; therapy;  
KW autoimmune disease; viral infection; degenerative disorder;  
KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischemic injury;  
KW cerebellar degeneration; myelodysplastic syndrome.  
XX  
OS Homo sapiens.  
XX  
XX FN W09909165-A1.

XX 25-FEB-1999.  
PD  
XX  
XX 14-AUG-1998; 98WO-US16945.  
PE  
XX  
XX 15-AUG-1997; 97US-0055906.  
PR  
XX  
XX (IDUN-) IDUN PHARM INC.  
PA  
XX  
XX Alnemrl ES;  
PI  
XX  
XX WP1: 1999-181035/15.  
DR  
DR N-PSDB: AAX27280.  
XX  
XX Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
PT protein - useful in for screening for (antagonists that modulate  
PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
XX  
XX Claim 16; Page 62-63; 71pp; English.  
XX  
XX This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An  
CC antibody against the TRAIL receptors is useful for detecting mammalian  
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
CC bioassays for screening for (antagonists of DR5 or TRAIL-R3 proteins.  
CC (Ant)agonists identified by the assay are useful for modulating the  
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
CC related conditions which are treated in this way, include cancer  
CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
CC erythematosus and immune-mediated glomerulonephritis), viral infections  
CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
CC syndromes (e.g. aplastic anaemia) and ischemic injury (e.g. myocardial  
CC infarction and stroke). The polynucleotides can also be used to treat  
CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
CC used to form a composition that is useful for inhibiting expression of a  
CC human DR5 or TRAIL-R3 protein.  
XX  
SQ Sequence 299 AA:  
  
Query Match 100.0%; Score 1382; DB 20; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2,9e-86;  
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MARIKTLKFWVIVAVLPLVATYSATTAROEYVPOQTVPAPQOORHSFKGECPPAGSHRS 60  
Db 41 maripkltkfivvivaavlplvaysattarqeevpqqlvapgqqrhstkgcecpagshrs 100  
  
QY 61 EHTGACNPCTEGVDYTNASNNPSCFCTVCKSDOKRHSCTMTDRIVCOCKEGTFRNEN 120  
Db 101 ehtgacnpctegvdyltnasnepscfctvcksdqkhksctumtrdvcoqkegffnen 160  
  
QY 121 SPEMKRKSRCPSGEGVOYNSCTSMDDIOCVEEFGANATVEPPAAEETMTNTSGTPAPAAE 180  
Db 161 spemckrksrcpsgevgvsnctswddiqveefganatvecpaaeeetmtntspgtpapaae 220  
  
QY 181 ETMTNTSGTPAPAAEETMTNTSGTPAPAAEETMTNTSGTPASSHY 240  
Db 221 etmtntspgtpapaaeeetmtntspgtpapaaeeetmtntspgtpasshy 280  
  
QY 241 LSCITVIGIIVLIVLIVFV 259  
Db 281 lscitvgiivlilvllivfv 299  
  
RESULT 11  
AAW94671  
ID AAW94671 standard; Protein: 299 AA.  
XX  
XX AAW94671:  
XX  
DT 04-MAY-1999 (first entry)

XX Human TNF-related apoptosis-inducing ligand binding protein.  
 DE  
 XX  
 XX Human: TNF-related apoptosis-inducing ligand binding protein; clotting;  
 KW TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy;  
 KW thrombotic microangiopathy; thrombotic thrombocytopenic purpura;  
 KW hemolytic-uraemic syndrome; systemic lupus erythematosus.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W09900423-A1.  
 XX  
 XX 07-JAN-1999.  
 XX  
 XX 25-JUN-1998; 98WO-US13491.  
 XX  
 XX 26-JUN-1997; 97US-0883529.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 XX  
 XX Smith CA, Walczak H;  
 XX  
 XX WPI; 1999-095685/08.  
 XX  
 XX N-PSDB; AAX16692.  
 XX  
 XX New isolated TRAIL binding protein - which binds to a tumour  
 PT necrosis factor-related apoptosis inducing ligand, used in the  
 PT diagnosis and treatment of TRAIL-mediated disorders  
 PT  
 XX  
 XX Claim 1; Fig 1; 47pp; English.  
 XX  
 XX The present sequence is human tumour necrosis factor (TNF)-related  
 CC apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be  
 CC used for inhibiting the biological activities of TRAIL or for purifying  
 CC TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated  
 CC disorder such as T cell death in HIV-infected patients. They can be used  
 CC for treating thrombotic microangiopathies such as thrombotic  
 CC thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small  
 CC blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic  
 CC acids can also be used for gene therapy. They can also be used as  
 CC carriers for delivering attached agents to cells bearing TRAIL.  
 CC  
 XX  
 XX Sequence 299 AA;  
 SQ  
 Query Match 100.0%; Score 1382; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2,9e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 AC AAW8409;  
 XX  
 XX 26-APR-1999 (first entry)  
 DT  
 XX Human Apo-2Dcr protein (amino acids -40 to 259).  
 DE  
 XX  
 XX Apo-2Dcr: human; apoptosis; tumour necrosis factor receptor;  
 KW neurodegeneration; autoimmune disease; inflammation; cancer;  
 KW therapy.  
 XX  
 XX Homo sapiens.  
 XX  
 XX  
 XX Key  
 FH Peptide  
 FT Location/Qualifiers  
 FT 1..40  
 FT /note= "-40 to -1 region of Apo-2Dcr"  
 FT 41..69  
 FT /note= "predicted signal peptide"  
 FT 41..201  
 FT /note= "extracellular domain, this domain is  
 specifically claimed in Claim 5"  
 FT 108..149  
 FT /note= "cysteine-rich domain"  
 FT 150..189  
 FT /note= "cysteine-rich domain"  
 FT 202..216  
 FT /note= "tandem repeat peptide"  
 FT 217..231  
 FT /note= "tandem repeat peptide"  
 FT 232..246  
 FT /note= "tandem repeat peptide"  
 FT 247..261  
 FT /note= "tandem repeat peptide"  
 FT 262..276  
 FT /note= "tandem repeat peptide"  
 FT 265..299  
 FT /note= "hydrophobic C-terminal region"  
 FT 117  
 FT /note= "N-glycosylation"  
 FT 180  
 FT /note= "N-glycosylation"  
 FT 196  
 FT /note= "N-glycosylation"  
 FT 209  
 FT /note= "N-glycosylation"  
 FT 224  
 FT /note= "N-glycosylation"  
 FT  
 XX W09858062-A1.  
 XX  
 XX 23-DEC-1998.  
 XX  
 XX 12-JUN-1998; 98WO-US12456.  
 XX  
 XX 18-JUN-1997; 97US-0878168.  
 XX  
 XX (GENENTECH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;  
 PI Kim KJ, Wood WI;  
 XX  
 XX WPI; 1999-095340/08.  
 XX  
 XX N-PSDB; AAV84347.  
 XX  
 XX New Apo-2Dcr polypeptide - used for modulation and diagnosis of  
 PT apoptosis, e.g. in neurodegeneration  
 PT  
 PS Claim 9; Page 53-54; 88pp; English.  
 XX  
 CC This polypeptide comprises human Apo-2Dcr, a novel member of the  
 CC tumour necrosis factor receptor family that binds to Apo-2 ligand.  
 CC Its amino acid sequence was deduced from the nucleotide sequence  
 CC of an isolated cDNA clone (see AAV84347); an alternative translation

CC inflammation site in this clone will encode apolipoprotein (see  
CC AAH88408) lacking the first 40 amino acid residues of this sequence  
CC Apo-2DCR shows more sequence identity to DR4 (608) and Apo-2 (508)  
CC than to other apoptosis-linked receptors. The polypeptide can be  
CC obtained by expression in host cells using the vector deposited as  
CC ATCC 209087. The invention provides vectors and host cells for  
CC recombinant production of Apo-2DCR polypeptides, antibodies, and  
CC transgenic and knockout animals (useful e.g. for screening and  
CC developing drugs that protect against excessive apoptosis).  
CC Apo-2DCR or chimeras comprising Apo-2DCR or its (claimed)  
CC extracellular domain fused to a heterologous polypeptide are used  
CC to modulate apoptosis of mammalian cells (claimed) and/or NF-kappaB  
CC activation by Apo-2 ligand, and may be expressed *in vivo* or *ex vivo*  
CC for gene therapy. This can be used in methods for the modulation  
CC and diagnosis of apoptosis e.g. in cases of neurodegeneration,  
CC autoimmune diseases and inflammation. Most human tumour cells do  
CC not express Apo-2DCR transcripts, but normal tissues do, suggesting  
CC that Apo-2DCR may permit selective killing of cancer cells by Apo-2  
CC ligand, possibly by protecting normal, but not cancerous, cells.

Query Match	100.0%;	Score 1382;	DB 20;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 2.9e-86;		
Matches 259;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MARIPKTLKEFWVVLVAVALLLPLATASANTTAROEEVPPOOTVAPPOORHSFKSECPAGSHRS	60
Dd	41	maripkltlkfvyvvaavlpylajysattaqeevpqqvtapqqrhsfkjeeccpaghrs	1000
QY	61	EHTGACNCEPTGEVDYTNAASNNEPSCFCTCYCKSDQKHKSOCMTMRDTVCOCKEETFNEN	1200
Dd	101	ehtgacnmpctegvydtasnamnepscfpcctcycksdqhksocmtmrldtvcqkegfnn	1600
QY	121	SPEMCRKCSRRPSEEVONYNSDMDIQCVEEFANNTVTTPAAEETMMNTSPGTPAAAE	1800
Dd	161	spermcrkcscrpsgevgvsncltsddiqcvееfanaatvtelpaaeeetmmntspgpapaae	2200
QY	181	ETMMNTSPGPAAEETMMNTSPGTPAAAEETMMNTSGCTPAPA AEETMMNTSPGTASSHY	2400
Dd	221	etmmtspgtppapaaeelmtitpgtpapaaeelmtitpgtpapaaeelmtitspgtasshy	2800
QY	241	LSCITGVIGIIVILLIIVFV	259
Dd	281	lsctivglivilivillivfv	299

```

RESULT 13
AAB01343
ID AAB01343 standard; Protein; 299 AA

```

AC	AAB01343;
XX	
DT	25-SEP-2000 (first entry)
XX	
DE	Death receptor.
XX	
KW	U114; death receptor; apoptosis; programmed cell death; FAS;
KW	TRF-R; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW	human.
XX	
OS	Homo sapiens.
XX	
PN	WO200034335-A2.
XX	
PD	15-JUN-2000.
XX	
PF	03-DEC-1999; 99WO-US26035.
XX	
PR	04-DEC-1998; 98US-0205018.
XX	
PA	(SCHE ) SCHERING CORP.

XX  
PI    Leong C, Phillips JH;  
XX  
DR    WPL; 2000-423383/36.  
XX

A pure recombinant polypeptide which binds to a polyclonal antibody specific for the mature U144 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known which include the CD95 (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.

Query Match	100.0%;	Score 1382;	DB 21;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 2.9e-86;		
Matches 259;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MARIPKTLKFFVVVIVAVVLLPLVLAASATTAROEVEVPQOTVAPQOO RHSEFKBCECPAGSHRS	60
Db	41	maripkltkffvvvivaavllpylajysaltatgaeevppqgtvabpqgrhsfkbcecpagshrs	100
QY	61	EHTGACNCFTEGVDTYNASNNPESCFCPTYCKSDOKRHSCTMTRDTVCOCKBEGTFENEN	120
Db	101	ehtgacnctegvdytnasnnepscfpcptycksdqkhksctmttrdtvcqckegtfen	160
QY	121	SPEWCRKCSRCPSEVEQYNSNTSMDDDIQCVEEFANATVTPRAAEETMTTSPGTPAPAAE	180
Db	161	spemcrksrpsvsgvqnsctlsddiqcveefgaatvtpraaeetmttspgtpapaae	220
QY	181	ETMTNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASHY	240
Db	221	etmtntspgtpapaaeetmttspgtpapaaeetmttspgtpapaaeetmttspgtpashy	280
QY	241	LSCTIVGIVIVIVLIVFV	259
Db	281	lscitvgtivivivlivi	299

RESULT	14
AAW93578	
ID	AAW93578 standard; Protein; 259 AA

AC	AAW93578;
XX	
DT	18-JUN-1999 (first entry)
XX	
DE	Human hAP09 protein.
XX	
KW	Tumour necrosis factor receptor; signal transducer molecule; TNF; Ap04;
KW	developmental abnormality; gestational abnormality; prostate cancer;
KW	Ap06; Ap08; Ap09; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW	cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW	apoptosis; human.
XX	
OS	Homo sapiens.
XX	
PN	W09911791-A2.
XX	
PD	11-MAR-1999.
XX	



```
QY 1 MARIPKILKEVVIVAVILLPVLAISATTAROEVPQOTVADPOQORHSFKGECPAGSHRS 60
Db 1 maripkilkfvvvavavllpvlaysattarqevvpqglvapqgrhsfkgeecpagshrs 60
QY 61 EHTGACNPCTEGVDYTNASNNEPSCFCTVCKSDOKHKSCTMTMDTYCCKEGETFRNEN 120
Db 61 ehlgacnpctegvdytnasnnepscfcctvcksdqkhkssctmtrdlvcgckeglfirvn 120
QY 121 SPENCRCSCRCPSEVQVSNCTSMDDIQVEEFGANATVETPAAEETMNTSPGTPAPAAE 180
Db 121 spencrkscrcpsgevgvsnctswddiqveefganatvetpaaeelmtlspgtpapaae 180
QY 181 ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPASSHY 240
Db 181 etmntspgtpapaaeelmtlspgtpapaaeelmtlspgtpapaaeelmtlspgtpasshy 240
QY 241 LSCPIVGIIVLIVLIVFV 259
Db 241 lsctlvglivlivlivfv 259
```

Search completed: August 13, 2002, 08:31:29  
Job time: 123 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 13, 2002, 08:29:26 ; Search time 28.27 seconds  
(without alignments)  
880.337 Million cell updates/sec

Title: US-09-826-212-2

Perfect score: 1382

Sequence: 1 MARIPTLKEFVVIVAVLLP.....YLSCTIVGIIVLLIVFV 259

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR\_71:\*  
2: PIR:\*  
3: PIR:\*  
4: PIR:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201.5	14.6	427	1	GOHUN
2	200.5	14.5	425	1	A26431
3	192	13.9	651	2	JC7705
4	188.5	13.6	461	2	JC4302
5	184.5	13.4	416	1	JN0006
6	178	12.9	801	2	T29018
7	169.5	12.3	461	1	A35356
8	166.5	12.0	271	2	S12783
9	166.5	12.0	272	2	I37552
10	166	12.0	272	2	I48700
11	164.5	11.9	314	2	I37383
12	163.5	11.8	335	2	A40036
13	163	11.8	327	2	A46484
14	157	11.4	326	1	GOVZML
15	156	11.3	324	2	F36791
16	153.5	11.1	324	2	JC2385
17	149.5	10.8	535	2	A42086
18	147.5	10.7	455	1	GOHUT1
19	146	10.6	474	2	B38634
20	145	10.5	459	2	I48854
21	144	10.4	454	1	GOMST1
22	143.5	10.4	98	2	H81072
23	141.5	10.2	292	2	S24169
24	141.5	10.2	348	2	T28623
25	141.5	10.2	349	2	D72175
26	141.5	10.2	349	2	D36858
27	141.5	10.2	493	2	JC5486
28	140.5	10.2	325	2	B43692
29	139.5	10.1	1367	1	S48478

30	134.5	9.7	93	2	S04157	outer membrane pro
31	133.5	9.7	577	2	A60501	thrombomodulin pre
32	133	9.6	888	2	T46726	secreted acid phos
33	132	9.6	307	1	GSEF3	salivary glue prot
34	132	9.6	607	2	S27776	80K protein (allel
35	132	9.6	3020	2	A43932	80K protein (allel
36	132	9.6	1506	2	T30886	integumentary muc
37	129.5	9.4	88	2	S02720	outer membrane pro
38	129.5	9.4	461	1	GORTM1	tumor necrosis fac
39	129	9.3	393	2	S62335	tumor necrosis fac
40	127.5	9.2	135	2	T49996	IT1-7 protein - tr
41	127.5	9.2	1459	2	T32271	ALAGP4 - Arabidops
42	127	9.2	1802	2	S69703	hypothetical prote
43	126	9.1	138	2	D96715	HKR1 protein precu
44	126	9.1	514	2	A31643	protein F4N2.10 [l
45	126	9.1	571	2	T43456	cell adhesion 80K
						hypothetical prote

## ALIGNMENTS

RESULT 1

GOHUN

nerve growth factor receptor precursor, low affinity [validated] - human

N:Alternate names: NGF receptor

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1988 #sequence,revision 31-Mar-1988 #text\_change 08-Dec-2000

C:Accession: A25218; A60204; S21689; I57638

R:Johnson, D.; Lananhan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, Cell 47, 545-554, 1986

A:Title: Expression and structure of the human NGF receptor.

A:Reference number: A25218; MUID:87051725

A:Accession: A25218

A:Molecule type: mRNA

A:Residues: 1-427 <JUH>

A:Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205

R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, J. Neurochem. 48, 225-232, 1987

A:Title: Purification and amino terminal sequencing of human melanoma nerve growth fa

A:Reference number: A60204; MUID:87085574

A:Accession: A60204

A:Molecule type: protein

A:Residues: 29-31,'T',33-42,'TP',45-46,'TX',50-51,'XX',54-56 <MAR>

A:Experimental source: melanoma cell line A875

R:Visavajjhala, P.; Leszyk, J.D.; Lin-Geerke, J.; Ross, A.H. Arch. Biochem. Biophys. 294, 244-252, 1992

A:Title: Structural domains of the extracellular domain of human nerve growth factor

A:Reference number: S21689; MUID:92198017

A:Accession: S21689

A>Status: preliminary

A:Molecule type: protein

R:Sengal, A.; Patil, N.; Chao, M. Mol. Cell. Biol. 8, 3160-3167, 1988

A:Title: A constitutive promoter directs expression of the nerve growth factor recept

A:Reference number: I57638; MUID:89096903

A:Accession: I57638

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-22 <RES>

A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom

C:Comment: The cysteine-rich region of the extracellular domain may form part or all

C:Comment: This protein is thought to form a high-affinity receptor when it associate

C:Comment: This receptor undergoes both N- and O-linked glycosylation.

C:Genetics:

A:Gene: GDB:NGFR

A:Cross-references: GDB:120234; OMIM:162010

A:Map position: 17q21-17q22

C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-427/Product: nerve growth factor receptor #status experimental <MAT>  
F:29-250/Domain: extracellular #status predicted <EXT>  
F:32-65/Domain: NGF receptor repeat homology <NG>  
F:67-108/Domain: NGF receptor repeat homology <NG2>  
F:109-147/Domain: NGF receptor repeat homology <NG3>  
F:149-169/Domain: NGF receptor repeat homology <NG4>  
F:197-248/Region: serine/threonine-rich  
F:251-272/Domain: transmembrane #status predicted <TRM>  
F:273-427/Domain: intracellular #status predicted <INT>  
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.6%, Score 201.5; DB 1; Length 427;  
Best Local Similarity 24.4%; Pred. No. 2.9e-05;  
Matches 64; Conservative 25; Mismatches 92; Indels 81; Gaps 9;

Qy 51 EECFAG--SHREHTGACN-----PCEGVDYNNASNNPSCPTVC 91  
Db 30 EACPFGLTHSGECKKACLGAVAPCGANOTVCEPCLDVSTFSDVSAPECKPCTEC 89  
Qy 92 KSDOKHKSSCTWTRDTVCQCKEGTFRNENSP--EMCR-----KCSRC 131  
Db 90 VGLQSMSPCVAEADAVRCAGYQDETFGRCEACRVCESGLVFSQDKQNTVCCEC 149  
Qy 132 PSG-----EVQVSNCTSMDDICVEEFGANAVETPPAAETMT 170  
Db 150 PDGTSDEANHVDPCLPTVCEEDTERQLRECTRMADAECEIPIGRNITRSTP-PEGSDST 208  
Qy 171 SPGTPAPAAETMTSPGTPAPAAETMTSPGTPAPAAETMTSPGTPAPAAETMT 230  
Db 209 APSTDEPEA-----PEQDLASTVAG-----VVTVMGSSQPVVTRG--TT 248  
Qy 231 SPGTPASSHYLSCTIVGIIVLI 252  
Db 249 DNLIPVYCSILAAYVGLVAYI 270

RESULT 2  
A26431  
nerve growth factor receptor precursor, low affinity - rat  
N:Alternate names: NGF receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 10-Sep-1999  
C:Accession: A26431; PH1229  
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
Nature 325, 593-597, 1987  
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
A:Reference number: A26431; MUID:87115859  
A:Accession: A26431  
A:Molecule type: mRNA  
A:Residues: 1-425 <RAD>  
R:Metzls, M.; Timms, T.; Allikmets, R.; Saarma, M.; Persson, H.  
Gene 121, 247-254, 1992  
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoid  
A:Reference number: PH1229; MUID:93077038  
A:Accession: PH1229  
A:Molecule type: DNA  
A:Residues: 1-20 <MEP>  
A:Cross-references: GB:X61269  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C:Comment: This protein is thought to form a high-affinity receptor when it associates  
C:Genetics:  
A:Introns: 20/3  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-427/Product: nerve growth factor receptor #status predicted <MAT>  
F:30-251/Domain: extracellular #status predicted <EXT>  
F:33-66/Domain: NGF receptor repeat homology <NG1>  
F:66-109/Domain: NGF receptor repeat homology <NG2>  
F:110-148/Domain: NGF receptor repeat homology <NG3>

F:150-190/Domain: NGF receptor repeat homology <NG4>  
F:198-249/Domain: serine/threonine-rich  
F:252-273/Domain: transmembrane #status predicted <TRM>  
F:274-425/Domain: intracellular #status predicted <INT>  
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%, Score 200.5; DB 1; Length 425;  
Best Local Similarity 23.9%; Pred. No. 3.4e-05;  
Matches 68; Conservative 32; Mismatches 107; Indels 77; Gaps 9;

Qy 17 VLLPVLAYSATTARQEEVPOQTAPQOQRHSKGECPA---GSHREHTGA---CNPC 69  
Db 17 LLLILGVSSGCAK-----ETCSTGLYTHS--GECCKACNLGEGVAPCGANOTVCCEC 68  
Qy 70 TEGVDYNNASNNPSCPTVCCKSDOKHKSSCTWTRDTVC----- 109  
Db 69 LDNTFSDVYSATPECKPCTECLGLQSMSPCVAEADAVRCAGYQDETFGRCEACSV 128  
Qy 110 -----QCKEGTFRNE--NSPCKRCKSCRCPSGEVQVSNCTSMDDIQ 148  
Db 129 CEVSGGLVFSQDKQNTVCCEBCECTYSDEANHVDPCLPTVCEEDTERQLRECTRMADAE 188  
Qy 149 CVEEFGANAVETPPAAETMTSPGTPAPAAETMTSPGTPAPAAETMTSPGTPAPA 208  
Db 189 CEIIPGRMIPRSTP-PEGSDSTAPSTOPEVPEPDOLVPSVTA----- 230  
Qy 209 AEETMTSPGTPAPAAETMTSPGTPASSHLSCTIVGIIVLI 252  
Db 231 --DMVTVMGSSQPVVTRG--TTDNLIPYCSILAAYVGLVAYI 271

RESULT 3  
JC7705  
death receptor-6 - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 09-Nov-2001 #sequence, revision 09-Nov-2001 #text, change 09-Nov-2001  
C:Accession: JC7705  
R:Bridgman, J.T.; Bode, J.; Goetz, F.W.; Johnson, A.L.  
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001  
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.  
A:Reference number: JC7705; MUID:21308433; PMID:11414698  
A:Accession: JC7705  
A:Molecule type: mRNA  
A:Residues: 1-651 <BRI>  
A:Cross-references: GB:AF349908  
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belo  
tresa, activates a cell death and/or survival signaling cascade.  
C:Genetics:  
A:Gene: dr-6  
C:Keywords: ovary  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>  
F:332-350/Domain: transmembrane #status predicted <TRM>  
F:410-475/Domain: death domain #status predicted <DED>  
F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 13.9%, Score 192; DB 2; Length 651;  
Best Local Similarity 23.9%; Pred. No. 0.00015;  
Matches 68; Conservative 35; Mismatches 110; Indels 72; Gaps 12;

Qy 14 IVAVLPLVLAYSATTARQEEVPOQTVA-----PQOQRHSKGECPAGSHSEH 62  
Db 5 VLAVALPLVLVLGTRADAPKLTSDONAVSLPAGKYLHDKRTNDBLIDCKCPAGTYSKH 64  
Qy 63 -----TGACNCPCTGVDYNNASNNPSCFPC--TVCKSDOKHKSSCTWTRDTVCQCKEGTF 116  
Db 65 CTKSLRRCSPCPDGT-FTKHENGIERCHPCRKPCOLPMIKTCTALTDRCTCLSTGF 123  
Qy 117 R-----NENSPCKRCKSCRCPSGEV--QVSNCTSMDDICVEEF 153  
Db 124 QINDTCVPTVCYGVGWRKKGTEDEDVRCRKLRTGFTFSDVPSVMCKKTYTD--C--F 178



```

OY      154 GANAVTEPPAAEETNTSPGTPAPAAEETMTTSPGTAPAAEETWTSP-----202
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       179 GKMMVMVPRGRKESDNVC-XSAPSAPNTSLSS---DKADQGETYEAPPATVLPGLNNS 234
OY      203 ----GTPAAPAEETMTTSPGTAPAAEETMTTSPGTAPASSHYLS 242
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       235 VFDLSSSPAP-----RVSNNGTAPEPTVDYNDSANGVTGAPGSLSS 273

RESULT          4
JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor
A:Reference number: JC4302; MUID:96011645
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
A:Accession: PC4093
A:Molecule type: Protein
A:Residues: 1-7 <SU2>
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: Enfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domin: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F:44-194/Domin: extracellular cysteine rich #status predicted <EXT>
F:44-82/Domin: NGF receptor repeat homology <NGF>
F:84-126/Domin: NGF receptor repeat homology <NGF>
F:211-231/Domin: transmembrane #status predicted <TM>
F:361-447/Domin: signal transduction #status predicted <ST>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      13.6%; Score 188.5; DB 2; Length 461;
Best Local Similarity 22.8%; Pred. No. 0.00018;
Matches 69; Conservative 30; Mismatches 94; Indels 109; Gaps 11;

OY      42 OOOHRISFFGECEPAG--SHRSHTGACNPCTGCV-----DYINA 78
              :::: | | | | | | | | | | | | | | | | | | | | |
Db       37 REKRRLS----CPQKYSHPNRSLICCTKCHKGTLHLNDCLPGIDTDRCRECDNGTFAS 92
OY      79 SNNESECPPTVCKKD--QKHKSCTMTRDVYCQCKEGFRNENSPEM--CRKCSRPCSG 134
              : | : | : | : | : | : | : | : | : | : | : | : |
Db       93 ENHLLQGCLSCSKREMNOVELSPCTVDRDLYCGGKRNDYRKRYSETFLQCLNCSLCPNG 152
OY      135 EVO-----VSNCYSM-----DIQCVEEFGAMATVETPAAEETWN-----169
              || | | | | | | | | | | | | | | | | | | | |
Db       153 TVQLCLEKODITICHGHGFLELRKEVCVSNCKNAACKNLCPATSETRNDPDGTIVL 212
OY      170 -----ISPGRPAAL-ETINTSPG-----188
              || | | | | | | | | | | | | | | | | | | | |
Db       213 LPLVIFFGLCAFLFLVGLACRYQRMKPKLYSIICGKSTPVKEGEDEPLATAPSGPIITV 272
OY      189 -TPAPAAEETMTTSP-----GTPAPAAEETMTTSPGTAPAAEETWTTSPTGTPA 236
              : | : | | | | | | | | | : | : | | | | | |
Db       273 FSPIRSFSPPTTFSPVPSPSPSSPTFPDCMSNKIYVSPKEINAPPOGACPILMPFA 332
OY      237 SS 238
              : |
Db       333 SP 334

RESULT          5
JN0006

```

nerve growth factor receptor, low affinity precursor - chicken  
N.Alternate names: NGF receptor  
C.Species: Gallus gallus (chicken)  
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
A.Accession: JN0006; A60504  
R.Laage, T.H.; Weiskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R  
Neuron 2, 1123-1134, 1989  
A.Title: Structure and developmental expression of the nerve growth factor receptor 1  
A.Reference number: JN0006; MUID:90166579  
A.Accession: JN0006  
A.Molecule type: mRNA  
A.Residues: 1-416 <LAR>  
A.Experimental source: embryonic chick brain  
R.Heuer, J.G.; Faemle-Mainie, S.; Wheeler, E.F.; Bothwell, M.  
Dev. Biol. 137, 287-304, 1990  
A.Title: Structure and developmental expression of the chicken NGF receptor.  
A.Reference number: A60504; MUID:90152140  
A.Accession: A60504  
A.Status: preliminary; not compared with conceptual translation  
A.Molecule type: mRNA  
A.Residues: 21-35,'Y','37'-172,'K','174'-275,'S','277'-395,'R','397'-416 <HEU>  
C.Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom  
C.Comment: The cysteine-rich region of the extracellular domain may form part or all  
C.Keyword: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor  
F.1-20/Domain: signal sequence #status predicted <SIG>  
F.21-416/Product: nerve growth factor receptor #status predicted <MNT>  
F.21-239/Domain: extracellular #status predicted <EXT>  
F.24-57/Domain: NGF receptor repeat homology <NG1>  
F.59-100/Domain: NGF receptor repeat homology <NG2>  
F.101-139/Domain: NGF receptor repeat homology <NG3>  
F.141-181/Domain: NGF receptor repeat homology <NG4>  
F.189-237/Region: serine/threonine-rich  
F.240-261/Domain: transmembrane #status predicted <MEM>  
F.262-416/Domain: intracellular #status predicted <INT>  
F.52/Binding site: carbohydrate (Asn) (covalent) #status predicted

A:Reference number: Z20553  
A:Accession: T29018  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-801 <KIR>  
A:Cross-references: EMBL:U23181, PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZK84.1  
A:Experimental source: strain Bristol N2; clone ZK84  
C:Genetics:  
A:Gene: CESP:ZK84.1  
A:Map position: 2  
A:Introns: 22/2; 45/3; 108/1  
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 12.9%; Score 178; DB 2; Length 801;  
Best Local Similarity 26.6%; Pred. No. 0.0012;  
Matches 74; Conservative 27; Mismatches 111; Indels 66; Gaps 10;

Oy 16 AVLLPVLVYSAPTAAQEEPPQQTVPAPOOO---RHSPFGKEECPAGSHRSEHTGACNPCTE 71  
Db SVPAIVADAAAGDYDPSSSIPETPAPAEDDPAPASAAAEETPAPAPAEETPAPETAISA 435  
Oy 72 GVDTYNASNANNEPCPPCYCKSKDKHKSSCTMTKDTVCQCKEGTF-----RNENSPENC 125  
Db 436 APDAAGCAPADPADVAAPADV-----ATTAPETSQAOSAAGSYDVSEPSEAVETATIV 486  
Oy 126 RKCSRCPGEVGVNSCTSD-----DICVEEGRGANATVEPTPA----- 164  
Db 487 ESATETAPDSNAARICTPAASEPAPATIEAPTADAITLETAPAAPAPAPAPAEAAAGYDAPS 546  
Oy 165 ---EETMNTSPG----TPAPAEETMNTSPG----TPAPAEETMNTSPG----TPA 206  
Db 547 SVPEETPAPAPADETPAPAEETPAPAPAEETPAPAPAEETPAPAPAEETPAPA 606  
Oy 207 PAEETMNTSPG----TPAPAEETMNTSPG----TPA 236  
Db 607 PAADETPAPAPAEETPAPAPAEETPAPAPAEETPAPA 644

RESULT 7  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dover, S.K.  
Science 248; 1019-1023; 1990  
A>Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SN1>  
A:Cross-references: GB:M2315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,  
Proc. Natl. Acad. Sci. U.S.A. 87; 8331-8335; 1990  
A>Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195; 'R' 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.  
Cytokine 2; 231-237; 1990  
A>Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <GB>  
A:Cross-references: NID:g235648; PIDN:AAB19824.1; PID:g235649

```

A.Note: sequence extracted from NCBI backbone (NCBIN:63366, NCBIPI:63371)
R.Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A.Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A.Reference number: A36007; MUID:90349572
A.Accession: A36007
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 116-140, 'P',142-195,'R',197-362,'T',364-461<HEL>
A.Cross-references: GB:M5857; NID:g339751; PIDN:AA63262.1; PID:g339752
R.Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus,
J. Biol. Chem. 265, 1531-1536, 1990
A.Title: Purification and partial amino acid sequence analysis of two distinct tumor
A.Reference number: A23666; MUID:91056048
A.Accession: A23666
A.Status: preliminary
A.Molecule type: protein
A.Residues: 23-40;65-69;136-141;300-306<LOE>
R.Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A.Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A.Reference number: A35010; MUID:90110215
A.Accession: A35010
A.Status: preliminary
A.Molecule type: protein
A.Residues: 27-31<ENG>
R.Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A.Title: Cloning, sequencing and partial functional characterization of the 5' region
A.Reference number: I38094; MUID:95121934
A.Accession: I38094
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-37<RES>
A.Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C.Genetics:
A.Gene: GDB:TNFR2
A.Cross-references: GDB:I25914; OMIM:191191
A.Map position: 1p36.2-1p36.2
A.Introns: 26/3
A.Note: the list of introns is incomplete
C.Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C.Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:123-416/Domain: signal sequence #status predicted <SIG>
F:123-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-279/Domain: transmembrane #status predicted <TM>
F:280-461/Domain: intracellular #status predicted <INT>
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.3% Score 169.5; DB 1; Length 461;
Best Local Similarity 22.3%; Pred. No.0.0025;
Matches 66; Conservative 40; Mismatches 123; Indels 67; Gaps 13;

11 VVVIYAVLLPLVLAISATTARQEEVPOQTVAPO-----QQRSHFKGECCPAGSH- 58
DB 4 VAVVMAALAVGLELWMAAHLPAQVAFPPYAPDEPSTCLRREYDQTGMQMSCSPQGH 63
QY 59 -----RSEHTGACNPCTGSDVYTNAASNNBPCFC-IVYCKSDQKHKSSCTMTBTVQCC 112
DB 64 KVFCTKTSDT-VCOSC-EDSYTYTOLMMVWPCLSCGSKSSDQVETQACTREQNRICTCR 121
QY 113 EGTFFENSPEMCRKCS---RC-----PSEGVQVSNCTSWDDIQ- 149
DB 122 PGWYCALSKQGBCRCLARKCRPGFGVARGCTETSDYVCKPCAPRGFFSNITSTDI-CR 180
QY 150 -----VEEFGANATVET--PAAEETMNTSPT--PAPAAETMNTSPTGAPAAEETM 198
DB 181 PHQICNVVAIGNMSADVCTSTSPTRSMAGVAHLLPQVSTRQHNOP--TPREST----- 235

```

QY 199 TTSPGTPAPAEETMTTSPGTPAPAEETMTTSPGTPASSHYLSCTVIGIIVL 254  
DB 236 -----APSTSLPLPKPGSPRPAAGSGTODFALPGLIVGVALGLIIGVNCVIM 284

RESULT 8  
S12783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence,revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Mallett, S.; Fossun, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte  
A:Reference number: S12783; MUID:90214614  
A:Accession: S12783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:X17037; NID:957830; PIDN:CA934897.1; PID:957831  
C:Superfamily: CD27 antigen; NGF receptor repeat homolog  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 12.0%; Score 166.5; DB 2; Length 271;  
Best Local Similarity 28.4%; Pred. No. 0.0024;  
Matches 63; Conservative 25; Mismatches 93; Indels 41; Gaps 11;

QY 52 ECPAGS---HRSEHT--GACNPTGEGVDYTNASNNPSCFCTVC--KSDQKHKSCTMT 104  
DB 40 ECGGHHGAVSCDHTRTDVCPCPCRG--FYNEAVNYDTCKCTQCNHRSGSELKONCTPT 97  
QY 105 RDIVCOCKEGTF-RNENSPENCRCRCRCPGSEVOVSN---CTSMDDIQCVEFGANATVE 160  
DB 98 EDTVCCQCRPGTQPRQDSHKLGVDCVPCPGHFGSPGNOACKPW-----TNCITLS 147  
QY 161 TPAAETMTTSPGTPAPAEETMTTSPGTPAPAEETMTTSPGTPAPAEETMTTSPGTP 217  
DB 148 GKQIRH-----PASNSLDTVCEDRSILATLMEIQTFRPTVSTVWPRTSOLP 199  
QY 218 GTPAPAEETMTTSPGTPASSHYLSCTVIGIIVLIVIV 259  
DB 200 STPLVA-----PEGPAFAVILGLIGLAPLVLLALYL 234

RESULT 9  
S13752  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence,revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: S13752  
R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat  
Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A:Reference number: S13752; MUID:94170844  
A:Accession: S13752  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CA53536.1; PID:9472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homolog

Query Match 12.0%; Score 166.5; DB 2; Length 277;  
Best Local Similarity 26.2%; Pred. No. 0.0024;  
Matches 59; Conservative 36; Mismatches 83; Indels 47; Gaps 14;

QY 52 ECPAGS---HRSEHTGACNPTGEGVDYTNASNNPSCFCTVC--KSDQKHKSCTMT 103  
DB 40 ECGGHHGAVSCDHTRTDVCPCPCRG--FYNEAVNYDTCKCTQCNHRSGSELKONCTPT 97

DB 45 ECRPGNGVNSRCSRSQNT-VCRPGPGF-YNDVYSSKP-CKPCTWMLRSGSERKOLCTA 101  
QY 104 TRDIVCOCKEGTFRNENSPENCRCRCRCPGSEVOVSN---CTSMDDIQCVEFGANATVE 160  
DB 102 TQDTVRCRCRAGT-QPLDSYKPGVDCAPCPGHHFSPGNOACKPW-----TNCITL- 149  
QY 161 TPAAETMTTSPGTPAPAEETMTTSPGTPAPAEETMTTSPGTPAPAEETMTTSPGTP 220  
DB 150 --ACKHTIQ-----PASNSDAICEDRPAPATQOETQ-----GPPA-----RPITYQPIEA 194  
QY 221 APAAETMTTSP-GTPASSHYLSCTVIGIIV-----LIVLIVIV 259  
DB 195 WPRTSQGPSTPRVEPGGAAVALIGLIGLIVLGLLPLALLALYL 239

RESULT 10  
S148700  
gene ox40 protein - mouse  
N:Alternate names: OX40 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence,revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I48700; I48334; S34377  
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.  
J. Immunol. 151, 5261-5271, 1993  
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell  
A:Reference number: I48700; MUID:94044750  
A:Accession: I48700  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <RES>  
A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CA97772.1; PID:9312828  
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.  
Eur. J. Immunol. 25, 926-930, 1995  
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX  
A:Reference number: I48334; MUID:95235413  
A:Accession: I48334  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-14,'G',16-272 <RE2>  
A:Cross-references: EMBL:X85214; NID:9732818; PIDN:CA59476.1; PID:9732819  
C:Genetics:  
A:Gene: ox40  
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homolog

Query Match 12.0%; Score 166; DB 2; Length 272;  
Best Local Similarity 25.8%; Pred. No. 0.0026;  
Matches 67; Conservative 37; Mismatches 106; Indels 50; Gaps 13;

QY 16 AVLLPVLAYSATTARQEEVPOQTVAPOQQRHSFKG-----ECPAGS---HRSEHT--GA 65  
DB 10 ALLLALTLGYTARLNCV-----KHTYPSGHKCCRCRCOPGHGAVSCDHTRTPL 59  
QY 66 CNPCTGEGVDYTNASNNPSCFCTVC--KSDQKHKSCTMTRTDVCQCKEGTF-RNENSP 122  
DB 60 CHPCGTG--FYNEAVNYDTCKCTQCNHRSGSELKONCTPTQDTVRCRCRPGTQPRQDSGY 117  
QY 123 EMCRKCSRCPSGSEVOVSN---CTSMDDIQCVEFGANATVEPAPAEETMTTSPGTPAPAA 179  
DB 118 KLGVDCVPCPGHFGSPGNOACKPW-----TNCITL---SGKQIRH-----PASDS 159  
QY 180 EETMTTSPGTPAPAEETMTTSPGTPAPAEETMTTSPGTPAPAEETMTTSPGTPASSH 239  
DB 160 LDVAVEDSLATLMEIQRP---TFRPTVOSTVWPRTSLSLPPPLVIVPEG-PARAV 215

QY 240 YLSCITVIGIIVLIVIV 259  
DB 216 LLGLIGLILAPLVLLALYL 235

RESULT 11  
S137383



Db 122 KCKCKPDFCYDCSPGCEHCVCRCASCEHGLE--PCTATSNMTCRKQSPRN 168

## RESULT 14

GOVZML T2 protein - myxoma virus (strain Lausanne)

C:Species: myxoma virus

C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999

C:Accession: A40566

R:Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.

Virology 184, 370-382, 1991

A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis

A:Reference number: A40566; MUID:91335768

A:Accession: A40566

A:Molecule type: DNA

A:Residues: 1-326 <UPT>

A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

C:Keywords: glycoprotein

F:64-105/Domain: NGF receptor repeat homology <NG3>

F:106-147/Domain: NGF receptor repeat homology <NG3>

F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.4%; Score 157; DB 1; Length 326;

Best Local Similarity 24.7%; Pred. No. 0.01;

Matches 42; Conservative 19; Mismatches 61; Indels 48; Gaps 6;

QY 53 CPAGSHNSEHTG-----ACNPTGEGVDYTNASNNPSCFECT-VCKSDQKHKSCTMRD 106

Db 43 CPDSYASRLCGPCSDYVCSPC-KNETFTASTNHAPACVSCRCRGTGHLSESQCDKTRD 101

QY 107 TVCCCKGEGTENENSPKCRK---SRCP-----SGEYQVSNCTSW----- 144

Db 102 RVCCDSAGNYCLKGQBCRCICAPKTCGAGYGVSGHTRTDVLCCKPCRYTSDAVSST 161

QY 145 -----DDIOCVEEFGANATVETPAAEETMNTSPGTP 175

Db 162 ETCSSFNYSIVERNLYPVNDTSCCTTTAGPNEVYKTSSEFSVTLNHTDCDP 211

## RESULT 15

F36791

hypothetical protein ORF50 - ictalurid herpesvirus 1 (strain auburn 1)

C:Species: ictalurid herpesvirus 1

A:Note: host ictalurid punctatus (channel catfish)

C:Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 31-Jan-2000

C:Accession: F36791

R:Davidson, A.J.

submitted to GenBank, January 1992

A:Description: Channel catfish virus: a new type of herpesvirus.

A:Reference number: A36804

A:Accession: F36791

A:Molecule type: DNA

A:Residues: 1-670 <DAV>

A:Cross-references: GB:M75136; NID:g331209; PIDN:AAA88153.1; PID:g331260

R:Davidson, A.J.

Virology 186, 9-14, 1992

A:Title: Channel catfish virus: a new type of herpesvirus.

A:Reference number: A39447; MUID:92087490

A:Contents: annotation

A:Note: neither protein nor nucleic acid sequence is given

C:Genetics:

A:Gene: 50

C:Superfamily: period clock protein; EGF homology

Query Match 11.3%; Score 156; DB 2; Length 670;

Best Local Similarity 43.3%; Pred. No. 0.021;

Matches 39; Conservative 15; Mismatches 30; Indels 6; Gaps 4;

QY 155 ANAIVETPA-AEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETM 213

Db 152 ANITTAIPAGANDTANITTTATPA-GANDTANITTTATPAAGANDTAVTTTSATPAGANDTAV 210

QY 214 TTSPGTPAPA---AEET-MTTSPTGPASSH 239

Db 211 TTPATPAGANDTANDTAVTTTPAMPAGAN 240

Search completed: August 13, 2002, 08:30:04  
Job time: 38 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:30:11 ; Search time 15.81 Seconds

(without alignments)  
634.305 Million cell updates/sec

Title: US-09-826-212-2

Sequence: 1 MARIKTLKFFVIVIVALLP.....YLSCTIVGIVLVIVLVFV 259

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1382	100.0	259 1 T10C_HUMAN	O14798 h tumor nec
2	634	45.9	386 1 T10D_HUMAN	Q9ubn6 homo sapien
3	472	34.2	468 1 T10A_HUMAN	O00220 homo sapien
4	448	32.4	440 1 T10B_HUMAN	O14763 homo sapien
5	201.5	14.6	427 1 T16_HUMAN	P08138 homo sapien
6	200.5	14.5	425 1 T16_HUMAN	P07174 rattus norv
7	194	14.0	332 1 TNR6_PIG	O77736 sus scrofa
8	188.5	13.6	461 1 T1A_PIG	P50555 sus scrofa
9	187	13.5	323 1 TNR6_BOVIN	P51867 bos taurus
10	184.5	13.4	416 1 T16_CHICK	P18519 gallus gall
11	171.5	12.4	471 1 T1A_BOVIN	O19131 bos taurus
12	169.5	12.3	461 1 T1B_HUMAN	P20333 homo sapien
13	166.5	12.0	271 1 TNR4_HUMAN	P15725 rattus norv
14	166.5	12.0	277 1 TNR4_HUMAN	P43468 homo sapien
15	166	12.0	272 1 TNR4_MOUSE	P47741 mus musculu
16	163.5	11.8	335 1 TNR6_HUMAN	P25445 homo sapien
17	163	11.4	327 1 TNR6_MOUSE	P25446 mus musculu
18	157	11.4	326 1 VT2_MYXVL	P29825 myxoma viru
19	156	11.3	670 1 VG50_HSV1	O00130 ictaluriid h
20	153.5	11.1	324 1 TNR6_RAT	O63199 rattus norv
21	152	11.0	5179 1 MOC2_HUMAN	Q02817 homo sapien
22	149.5	10.8	595 1 TNR8_HUMAN	P28908 homo sapien
23	147.5	10.7	455 1 T1A_HUMAN	P19438 homo sapien
24	146	10.6	474 1 T1B_MOUSE	P25118 mus musculu
25	144	10.4	454 1 T1A_MOUSE	P25118 mus musculu
26	141.5	10.2	349 1 VC22_VARY	P34015 variola vir
27	140.5	10.2	325 1 VT2_SFVA	P25943 shope fibro
28	139.5	10.1	1367 1 AMYR_YEAST	P08640 saccharomyc
29	137.5	9.7	577 1 TRBM_MOUSE	P15306 mus musculu
30	133.5	9.7	1453 1 CA11_CHICK	P02457 gallus gall
31	132	9.6	307 1 SGS3_DROME	P02840 drosophila
32	129.5	9.4	88 1 H82_NEICO	P11910 neisseria g
33	129.5	9.4	461 1 T1A_RAT	P22934 rattus norv

34	128.5	9.3	1637 1 MRSP_STAU	P80544 staphylococ
35	128	9.3	1802 1 HKR1_YEAST	P41809 saccharomyc
36	126	9.1	514 1 CSA_DICDI	P08796 dictyostell
37	125	9.0	1723 1 AIM1_HUMAN	Q9Y4K1 homo sapien
38	124	9.0	450 1 CYL_PARDE	P13627 paracoccus
39	124	9.0	1959 1 AGRI_RAT	P25304 rattus norv
40	121.5	8.8	634 1 HMP1_CANAL	P46593 candida alb
41	121	8.8	283 1 T14_HUMAN	Q92956 homo sapien
42	120.5	8.7	255 1 TNR9_HUMAN	O07011 homo sapien
43	119.5	8.6	1162 1 TCNA_TRYCR	P23253 trypanosoma
44	119	8.6	412 1 SEPL_HUMAN	Q14242 homo sapien
45	117.5	8.5	435 1 TNR3_HUMAN	P36941 homo sapien

## ALIGNMENTS

RESULT	ID	SEQUENCE	STANDARD	PRT	259 AA.
1	T10C_HUMAN	O14798: 014755:			
2	T10D_HUMAN	Q9ubn6: 000220:			
3	T10A_HUMAN	O14763: 014730:			
4	T10B_HUMAN	P08138: 008100:			
5	T16_HUMAN	P07174: 007140:			
6	T16_HUMAN	P07174: 007140:			
7	TNR6_PIG	O77736: 077700:			
8	T1A_PIG	P50555: 050520:			
9	TNR6_BOVIN	P51867: 051830:			
10	T16_CHICK	P18519: 018500:			
11	T1A_BOVIN	O19131: 019100:			
12	T1B_HUMAN	P20333: 020300:			
13	TNR4_HUMAN	P15725: 015700:			
14	TNR4_HUMAN	P43468: 043430:			
15	TNR4_MOUSE	P47741: 047710:			
16	TNR6_HUMAN	P25445: 025410:			
17	TNR6_MOUSE	P25446: 025410:			
18	VT2_MYXVL	P29825: 029800:			
19	VG50_HSV1	O00130: 000100:			
20	TNR6_RAT	O63199: 063170:			
21	MOC2_HUMAN	Q02817: 002800:			
22	TNR8_HUMAN	P28908: 028900:			
23	T1A_HUMAN	P19438: 019410:			
24	T1B_MOUSE	P25118: 025100:			
25	T1A_MOUSE	P25118: 025100:			
26	VC22_VARY	P34015: 034000:			
27	VT2_SFVA	P25943: 025910:			
28	AMYR_YEAST	P08640: 008610:			
29	TRBM_MOUSE	P15306: 015300:			
30	CA11_CHICK	P02457: 002430:			
31	SGS3_DROME	P02840: 002810:			
32	H82_NEICO	P11910: 011900:			
33	T1A_RAT	P22934: 022900:			

RA Tschopp J.;  
 RT "Characterization of two receptors for TRAIL.";  
 RL FEBS Lett. 416:329-334(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98211672; PubMed=9551946;  
 RA Moriguchi-Sapaya J., Cowper A.E., Xu X.-N., Morris G., McMichael A.J.,  
 RA Bell J.I., Screaton G.R.;  
 RT "Lymphocyte inhibitor of TRAIL (TNF-related apoptosis-inducing  
 RT ligand): a new receptor protecting lymphocytes from the death ligand  
 RT TRAIL.";  
 RL Immunol. 160:3-6(1998).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a  
 CC cytoplasmic death domain and hence is not capable of inducing  
 CC apoptosis. May protect cells against TRAIL mediated apoptosis by  
 CC competing with TRAIL-R1 and R2 for binding to the ligand.  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -1- TISSUE SPECIFICITY: Higher expression in normal tissues than in  
 CC tumor cell lines. Highly expressed in peripheral blood  
 CC lymphocytes, spleen, skeletal muscle, placenta, lung and heart.  
 CC -1- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED.  
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; AF020502; AAB71413.1; ALT\_INIT.  
 DR EMBL; AF014794; AAC05593.1; ALT\_INIT.  
 DR EMBL; AF012629; AAB67110.1; -  
 DR EMBL; AF012536; AAB67104.1; -  
 DR EMBL; AF016267; AAB81181.1; -  
 DR EMBL; AF033854; AAB87506.1; -  
 DR HSSP; P19438; TEXT.  
 DR MIM; 603613; -  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 1.  
 DR SMART: SMO0208; TNFR; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; Apoptosis; Glycoprotein; Repeat; GPI-anchor; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 236  
 FT FTRES 24 236  
 FT PROPEP 237 259  
 FT REPEAT 69 109  
 FT REPEAT 110 149  
 FT DOMAIN 162 236  
 FT REPEAT 162 176  
 FT REPEAT 177 191  
 FT REPEAT 192 206  
 FT REPEAT 207 221  
 FT REPEAT 222 236  
 FT REPEAT 222 236  
 FT DISULFID 69 85  
 FT DISULFID 88 101  
 FT DISULFID 91 109  
 FT DISULFID 111 125  
 FT DISULFID 128 141  
 FT DISULFID 131 149  
 FT LIPID 236 236  
 FT CARBOHYD 77 77  
 FT CARBOHYD 140 140  
 FT CARBOHYD 156 156  
 FT CONFLICT 119 119  
 FT SEQUENCE 259 AA; 27395 MW; FE3BF7FCEEA50B8 CRC64;

Query Match 100.0%; Score 1382; DB 1; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 7, 4e-78;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 MARIKTKLKVYVIVAVLLPVLANSATTAROEVEPQGTVAPOQOHRSGKEBCPAGSHRS 60  
 Db 1 MARIKTKLKVYVIVAVLLPVLANSATTAROEVEPQGTVAPOQOHRSGKEBCPAGSHRS 60  
 Oy 61 EHTGACNCTGEGVDYTNASNNNEPSCFCTVCKSDQKHSSCGMTMDYVCOCKEGFRHEN 120  
 Db 61 EHTGACNCTGEGVDYTNASNNNEPSCFCTVCKSDQKHSSCGMTMDYVCOCKEGFRHEN 120  
 Oy 121 SPEMKRCSRCPSGEGVSNCTSMDDIOCEBFGANATVEPAPAEETMTNTSPGTPAPAE 180  
 Db 121 SPEMKRCSRCPSGEGVSNCTSMDDIOCEBFGANATVEPAPAEETMTNTSPGTPAPAE 180  
 Oy 181 ETMTNTSPGTPAPAEETMTNTSPGTPAPAEETMTNTSPGTPAPAEETMTNTSPGTPASSHY 240  
 Db 181 ETMTNTSPGTPAPAEETMTNTSPGTPAPAEETMTNTSPGTPAPAEETMTNTSPGTPASSHY 240  
 Oy 241 LSCITVGIIVLIVLIVFV 259  
 Db 241 LSCITVGIIVLIVLIVFV 259  
 RESULT 2  
 T10D\_HUMAN STANDARD: PRT: 386 AA.  
 AC QGUBN6; Q9Y604;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10D precursor (Decoy  
 DE receptor 2) (DCR2) (TNF-related apoptosis-inducing ligand receptor 4)  
 DE (TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death  
 DE domain).  
 GN TNFRSF10D OR DCR2 OR TRAILR4 OR TRUND.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND VARIANT.  
 RP TISSUE-Fetal lung;  
 RX MEDLINE=98044290; PubMed=9382840;  
 RA Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P.,  
 RA Askenazi A.;  
 RT "A novel receptor for Apo2L/TRAIL contains a truncated death domain.";  
 RT Curr. Biol. 7:1003-1006(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANTS S-35 AND L-310.  
 RP TISSUE-Forebrain fibroblast, and Peripheral blood lymphocytes;  
 RX MEDLINE=9809091; PubMed=9430226;  
 RA Degli-Esposti M.A., Dougall W.C., Smolak P.J., Waugh J.V., Smith C.A.,  
 RA Goodwin R.G.;  
 RT "The novel receptor TRAIL-R4 induces NF-kappaB and protects against  
 RT TRAIL-mediated apoptosis, yet retains an incomplete death domain.";  
 RT Immunity 7:813-820(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RP MEDLINE=98196860; PubMed=9537512;  
 RA Pan G., Ni J., Yu G.-L., Wei Y.-F., Dixit V.M.;  
 RT "TRUND, a new member of the TRAIL receptor family that antagonizes  
 RT TRAIL signalling.";  
 RT FEBS Lett. 424:41-45(1998).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains a  
 CC truncated death domain and hence is not capable of inducing  
 CC apoptosis but protects against TRAIL-mediated apoptosis. Reports  
 CC are contradictory with regards to its ability to induce the NF-  
 CC kappaB pathway (According to ref.1 it cannot but according to  
 CC ref.2 it can induce the NF-kappaB pathway).



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CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed, in particular in fetal
CC kidney, lung & liver and in adult testis and liver. Also expressed
CC in peripheral blood leukocytes, colon and small intestine, ovary,
CC prostate, thymus, spleen, pancreas, kidney, lung, placenta and
CC heart.
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN (TRUNCATED).
CC -----
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CC -----
DR EMBL: AF029761; AAC03477.1; -
DR EMBL: AF021232; AAC32765.1; -
DR EMBL: AF021233; AAC32766.1; -
DR EMBL: AF023849; AAC52053.1; -
DR HSSP: P19438; 1NCF.
DR MIM: 603614; -.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM000208; TNFR_2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;
KW Polymorphism.
FT STGNAL 1 55
FT CHAIN 56 386
FT FT
FT DOMAIN 56 211 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSMEM 212 232 EXTRACELLULAR (POTENTIAL).
FT REPEAT 233 386 POTENTIAL.
FT REPEAT 233 386 CYTOPLASMIC (POTENTIAL).
FT REPEAT 233 386 TNFR-CYS 1.
FT REPEAT 233 386 TNFR-CYS 2.
FT REPEAT 233 386 DEATH (TRUNCATED).
FT DOMAIN 245 250 POLY-GLY.
FT DOMAIN 245 250 POLY-VAL.
FT DISULFID 99 115 POTENTIAL.
FT DISULFID 118 131 POTENTIAL.
FT DISULFID 121 139 POTENTIAL.
FT DISULFID 141 155 POTENTIAL.
FT DISULFID 158 172 POTENTIAL.
FT DISULFID 162 180 POTENTIAL.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 35 35 P -> S (IN TRAIL-R4-B).
FT VARIANT 35 35 /FTID=VAR_011417.
FT VARIANT 35 35 S -> L (IN TRAIL-R4-B).
FT VARIANT 35 35 /FTID=VAR_011418.
FT SEQUENCE 386 AA; 41823 MW; 77A93577CAAF2632 CRC64;
SQ

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Query Match 45.9%; Score 634; DB 1; Length 386;  
 Best Local Similarity 51.8%; Pred. No. 2.9e-33;  
 Matches 132; Conservative 22; Mismatches 41; Indels 60; Gaps 3;

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QY 5 PKTKFVYVAVLLPYLVANSATTAROEVEPQGTVAPOQSHRSKGECPAGSHRSEHTG 64
DB 35 PKTKFVYVAVLLPYLVANSATTAROEVEPQGTVAPOQSHRSKGECPAGSHRSEHTG 94
QY 65 ACNCTGVDYTNASNNBPSCFCTVCKSDOKHSSCGMTDTYCOCKEGFRNENSGEM 124
DB 95 ACNCTGVDYTNASNNBPSCFCTVCKSDOKHSSCGMTDTYCOCKEGFRNENSGEM 154
QY 125 CRKC-SRCPGSEGVONCSWDIDQCEEFGANATVETPAAEETMNTSPGTPAPAAEETM 183
DB 155 CRTRCTGCPRMKAVKVNCTPRSDIKCKNESASSTGKTPAAEEVITLLG----- 204
QY 184 NTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPASSHYLSC 243

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DB 205 -----MLASP-----YHYLI 215
QY 244 TIVGIVLVILVIF 258
DB 216 IIVLVILVAVVWGF 230

RESULT 3
T10A_HUMAN STANDARD; PRT; 468 AA.
AC 000220;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10A precursor (Death
DE receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL
DE receptor-1) (TRAIL-R1).
GN TNFRSF10A OR DR4 OR TRAILR1 OR APO2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97238921; Pubmed=9082980;
RA Pan G., O'Rourke K., Chinnaiyan A.M., Gentz R., Ebner R., Ni J.,
RA Dixit V.M.;
RT "The receptor for the cytotoxic ligand TRAIL.";
RL Science 276:111-113(1997).
RN [2]
RN FUNCTION.
RX MEDLINE=98090092; Pubmed=9430227;
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce
RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";
RL Immunity 7:821-830(1997).
CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates
CC apoptosis in a caspase-dependent manner. Can trigger the nuclear
CC factor kappaB-pathway and can bind the cytoplasmic adapter
CC molecule FADD/MORT1 which engages activation of effector caspases
CC caspase 8 leading to subsequent activation of effector caspases
CC that execute apoptotic death of the cell.
CC -1- SUBUNIT: Can interact with TRADD and RIP.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed. High levels are found in
CC spleen, peripheral blood leukocytes, small intestine and thymus,
CC but also in K562 erythroleukemia cells, MCF7 breast carcinoma
CC cells and activated T-cells.
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL: U90875; AAC51226.1; -
DR HSSP: P19438; 1EXT.
DR MIM: 603611; -.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.

```

FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 468 TUMOR NECROSIS FACTOR RECEPTOR  
FT DOMAIN 24 239 SUPERFAMILY MEMBER 10A.  
FT TRANSMEM 240 262 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 263 468 POTENTIAL.  
FT REPEAT 147 188 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 189 229 TNFR-CYS 1.  
FT DOMAIN 365 448 TNFR-CYS 2.  
FT DOMAIN 29 32 DEATH.  
FT DISULFID 132 145 POLY-ALA.  
FT DISULFID 148 164 POTENTIAL.  
FT DISULFID 167 180 POTENTIAL.  
FT DISULFID 170 188 POTENTIAL.  
FT DISULFID 190 204 POTENTIAL.  
FT DISULFID 207 221 POTENTIAL.  
FT DISULFID 211 229 POTENTIAL.  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 468 AA; 50025 MM; 1E85DDC2C8760E7 CRC64;

Query Match 34.2%; Score 472; DB 1; Length 468;  
Best Local Similarity 58.7%; Pred.No.2.4e-22;  
Matches 91; Conservative 16; Mismatches 42; Indels 6; Gaps 3;

QY 3 RIPPTLKEVVYIVAVLLPVLAYSATTAROEVPQOTVAPQOORHSFKGEGCPAGSHRSEH 62  
DB RHVHTFKFVV--VGVLLQVPSASATIKLHD--QSISTQGMHSPGLGELCPGSHRSEH 141  
QY 63 TGACNPGCEGYDTNMSNNEPSCFCPCYCKSDQKHKSCTMTROTVCCKRGTFRNENSP 122  
DB 142 PGACNRCRCEGYGVYTNMNNLFCACLPCTACKSDEERSPCTTNTACOCKPGTFRDNESA 201

QY 123 EMCRCRSC-CPGSEGYOVNCTSMDDIOCVEEFGAN 156  
DB 202 EMCRCRSTGCPRGKVKYKDCIPMSDIECVKESGN 236

RESULT 4  
T10B\_HUMAN STANDARD: PRT: 440 AA.  
ID T10B\_HUMAN  
AC 014763: 015531; 015508; 015517; 014720; Q9BVE0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL receptor-2) (TRAIL-R2)  
GN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF N-TERMINUS.  
RC TISSUE=foreskin fibroblast;  
RX MEDLINE=97459925; PubMed=931198;  
RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y., Bolani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Goodwin R.G., Rauch C.T.;  
RA "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";  
RT EMBO J. 16:5386-5397(1997).  
RL [2]  
RN SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE RP SPLICING.  
RX MEDLINE=97431692; PubMed=9285725;  
RA Screaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E., McMichael A.J., Bell J.I.;  
RT "TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL.";  
RL Curr. Biol. 7:693-696(1997).  
RN [3]  
RN SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.

RC TISSUE=Liver, and Spleen;  
RX MEDLINE=98039016; PubMed=9373179;  
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschopp J.;  
RT "Characterization of two receptors for TRAIL.";  
RL FEBS Lett. 416:329-334(1997).  
RN [4]  
RN SEQUENCE FROM N.A. (SHORT ISOFORM).  
RC TISSUE=ovary;  
RX MEDLINE=97467719; PubMed=9326928;  
RA Wu G.S., Burns T.F., McDonald E.R., III, Jiang W., Meng R., Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R., Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;  
RT "Killer/DR5 is a DNA damage-inducible p53-regulated death receptor gene.";  
RL Nat. Genet. 17:141-143(1997).  
RN [5]  
RN SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=97390508; PubMed=9242610;  
RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;  
RT "An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";  
RL Science 277:815-818(1997).  
RN [6]  
RN SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=97467318; PubMed=9325248;  
RA MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;  
RT "Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";  
RL J. Biol. Chem. 272:25417-25420(1997).  
RN [7]  
RN SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=9809092; PubMed=9430227;  
RA Chaudhary P.M., Eby M., Jasmán A., Bookwalter A., Murray J., Hood L.;  
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
RL Immunity 7:821-830(1997).  
RN [8]  
RN SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=97390509; PubMed=9242611;  
RA Sheridan J.P., Walters S.A., Pletl R.M., Gurney A., Skubatch M., Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I., Goddard A.D., Godowski P., Ashkenazi A.;  
RT "Control of TRAIL-induced apoptosis by a family of signalling and decoy receptors.";  
RL Science 277:818-821(1997).  
RN [9]  
RN SEQUENCE FROM N.A. (LONG ISOFORM).  
RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yusa Y.;  
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2 gene in colorectal carcinoma.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RN SEQUENCE FROM N.A. (SHORT ISOFORM).  
RA Cao X., Zhang W., Wan T.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RN SEQUENCE FROM N.A. (SHORT ISOFORM).  
RA Farrah T., Yu T., Gilbert T., Gross J., O'Hara P.;  
RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RN SEQUENCE FROM N.A. (LONG ISOFORM).  
RC TISSUE=Cervix;  
RA Strausberg R.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
RX MEDLINE=20017054; PubMed=10549288;  
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.;  
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a

RT complex with death receptor 5.";  
 RL MOL. Cell 4:563-571(1999).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
 RX PubMed-10542098.  
 RA Mongkolkeha J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Sreelax G.R.;  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates  
 CC apoptosis in a caspase-dependent manner. Can trigger the nuclear  
 CC factor kappaB-pathway and can bind the cytoplasmic adapter  
 CC molecule FADD/MORT1 which engages initiator caspases such as  
 CC caspase 8 leading to subsequent activation of effector caspases  
 CC that execute apoptotic death of the cell.  
 CC -1- SUBUNIT: Homotrimer (Potential). Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/TRICK2B (SHOWN HERE)  
 CC AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
 CC very highly expressed in tumor cell lines such as HeLa S3, K562,  
 CC Hs-60, SM480, A549 and G361; highly expressed in heart, peripheral  
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
 CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
 CC the intestinal tract; not detectable in brain.  
 CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.  
 CC -1- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell  
 CC carcinoma of the head and neck.  
 CC -1- SIMILARITY: CONTAINS 1 ILA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC  
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 CC  
 DR EMBL: AF016849; AAC51778.1; -  
 DR EMBL: AF018657; AAB70577.1; -  
 DR EMBL: AF018658; AAB70578.1; -  
 DR EMBL: AF018658; AAB70578.1; -  
 DR EMBL: AF016266; AAB81180.1; -  
 DR EMBL: AF022386; AAB71949.1; -  
 DR EMBL: AF012628; AAB67109.1; -  
 DR EMBL: AF020501; AAB71412.1; -  
 DR EMBL: AF016268; AAC01565.1; -  
 DR EMBL: AF012535; AAB67103.1; -  
 DR EMBL: AF014718; BAA33723.1; -  
 DR EMBL: AB014710; BAA33723.1; JOINED.  
 DR EMBL: AB014712; BAA33723.1; JOINED.  
 DR EMBL: AB014711; BAA33723.1; JOINED.  
 DR EMBL: AB014712; BAA33723.1; JOINED.  
 DR EMBL: AB014713; BAA33723.1; JOINED.  
 DR EMBL: AB014714; BAA33723.1; JOINED.  
 DR EMBL: AB014715; BAA33723.1; JOINED.  
 DR EMBL: AB014716; BAA33723.1; JOINED.  
 DR EMBL: AB014717; BAA33723.1; JOINED.  
 DR EMBL: AF153687; AAF75587.1; -  
 DR EMBL: AF192548; AAF07175.1; -  
 DR EMBL: BC001281; AAH01281.1; -  
 DR EMBL: BC001281; AAH01281.1; -  
 DR MIM: 603612; -  
 DR MIM: 601400; -  
 DR PDB: 1D0G; 22-OCT-99.  
 DR PDB: 1D4V; 01-NOV-99.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 2.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 2.  
 DR PROSITE: PSS0017; DEATH\_DOMAIN; 1.  
 DR PROSITE: PSS0052; TNFR\_NGFR\_1; 2.

DR PROSITE: PSS0050; TNFR\_NGFR\_2; 2.  
 KW Receptor: Apoptosis; Transmembrane; Repeat; Signal;  
 KW Alternative splicing; 3D-structure.  
 FT SIGNAL 1 55  
 FT CHAIN 56 440  
 FT  
 FT DOMAIN 56 210 TUMOR NECROSIS FACTOR RECEPTOR  
 FT TRANSMEM 211 231 SUPERFAMILY MEMBER 10B.  
 FT DOMAIN 232 440 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 97 137 POTENTIAL.  
 FT REPEAT 138 178 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 192 206 TNFR-CYS 1.  
 FT DOMAIN 339 422 TNFR-CYS 2.  
 FT DOMAIN 250 253 TAPE.  
 FT DISULFID 81 94 DEATH.  
 FT DISULFID 97 113 POLY-GLY.  
 FT DISULFID 116 129  
 FT DISULFID 119 137  
 FT DISULFID 139 153  
 FT DISULFID 156 170  
 FT DISULFID 160 178  
 Query Match 32.48; Score 448; DB 1; Length 440;  
 Best Local Similarity 40.7%; Pred. No. 6,5e-21;  
 Matches 105; Conservative 23; Mismatches 68; Indels 62; Gaps 4;  
 QY 3 RIPTLKVYVIVVLLPYLAYSATTAEROEVPQOTVAPQOQRHFRGECBPAGSHRSEH 62  
 DB 33 RVPKTL-VLVVAVALLVSAESALITQODLAPQORAPQOKRSPSGLCPPGHHSSE 90  
 QY 63 TGACNPCTEGVYVYTNASNEPSCPCCTVCKSDQKHKSCCTWRDYPVCCCKEGTFRNENSP 122  
 DB 91 GRDIDICKYGGDDYTHNMWDLFCRLCRPCDSCGEVLSCTTTRNTVCCCEGTREDESP 150  
 QY 123 EMCRC-K-SRCSGGEVOYNSCTSMWDICQVEEFGANATVETPAABETMTSPGTPAAAE 181  
 DB 151 EMCRCRCGCGRGVXKQDCTPWSIDICVH----- 180  
 QY 182 TMTNTPGPPAPAEETMTSPGTPAPAEETMTSPGTPAPAEETMTSPGTPASSHYL 241  
 DB 181 -----KESGTRHSG-EAPVAVETVTSPTGTPASSCL 211  
 QY 242 SCTIVGIIVLLVLLVFEV 259  
 DB 212 SGIIIGTVAAVVLIVAV 229  
 RESULT 5  
 TR16\_HUMAN STANDARD; PRT; 427 AA.  
 ID TR16\_HUMAN  
 AC P08138;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-  
 DE affinity nerve growth factor receptor) (NGF receptor) (gp80-LINGER)  
 DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).  
 GN NGFR OR TNFRSF16.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87051725; PubMed=3022937;  
 RA Johnson D., Lanhahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,  
 RA Botwell M., Chao M.;  
 RT "Expression and structure of the human NGF receptor.";  
 RL Cell 47:545-554(1986).  
 RN [2]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=89096903; PubMed=2850481;  
 RA Sehgal A., Patil N., Chao M.;

RT		"A constitutive promoter directs expression of the nerve growth factor receptor gene."
RH	MOL. CELL. BIOL.	8:3160-3167(1988).
CC	-1-	FUNCTON: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,
CC	AND NT-4.	CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF NEURAL CELLS.
CC	-1-	SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
CC	-1-	INTERACTS WITH P75NTR-ASSOCIATED CELL DEATH EXECUTOR.
CC	-1-	SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1-	PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC	-1-	SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC	-1-	SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC		-----
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CC		-----
DR	EMBL;	M14764; AAB59544.1; .
DR	EMBL;	M21621; AAA36363.1; .
DR	PIR;	A25218; GOHUN.
DR	HSSP;	P07174; INGR.
DR	MIM;	162010; .
DR	InterPro;	IIPRO00488; Death.
DR	InterPro;	IIPRO01368; TNFR_C6.
DR	Pfam;	PF00531; death; 1.
DR	Pfam;	PF00020; TNFR_C6; 4.
DR	SMART;	SMO0005; DEATH; 1.
DR	SMART;	SMO0208; TNFR; 3.
DR	PROSITE;	PS00652; TNFR_NGFR_1; 3.
DR	PROSITE;	PS50050; TNFR_NGFR_2; 4.
DR	PROSITE;	PS50017; DEATH_DOMAIN; 1.
KW	Receptor;	Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW	Phosphorylation;	Signal; Apoptosis.
FT	SIGNAL	1 .. 28
FT	CHAIN	29 .. 427
FT	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 16, EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN	29 .. 250
FT	TRANSMEM	251 .. 272
FT	DOMAIN	273 .. 427
FT	REPEAT	31 .. 64
FT	REPEAT	66 .. 107
FT	REPEAT	108 .. 146
FT	REPEAT	148 .. 188
FT	DOMAIN	344 .. 421
FT	DOMAIN	197 .. 248
FT	DISULFD	32 .. 43
FT	DISULFD	44 .. 57
FT	DISULFD	47 .. 64
FT	DISULFD	67 .. 83
FT	DISULFD	86 .. 99
FT	DISULFD	107 .. 122
FT	DISULFD	109 .. 122
FT	DISULFD	125 .. 138
FT	DISULFD	128 .. 146
FT	DISULFD	149 .. 164
FT	DISULFD	167 .. 180
FT	DISULFD	170 .. 188
FT	CARBONYD	60 .. 60
SO	SEQUENCE	427 AA; 45183 MW; BO9FA143FB30625B CXC64; N-LINKED (GLCNAC... ) (POTENTIAL).

Query Match	14.6%;	Score 201.5;	DB 1;	Length 427;
Best Local Similarity	24.4%;	Pred. No. 6e-06;		
Matches 64;	Conservative 25;	Mismatches 92;	Indels 81;	Gaps 9;

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QY      51 EECFAG--SHSSEHTGACN-----PTEGVDYTNASNNPSPFPCTVC 91
      |||  :|  |||  |||  :|  :|  :|  :|  :|  :|  :|  :|  :|
Db      30 EACFGLYTHSGECKKACNLGEGVAQPCGANQTVCECECLDSTYFSDVVSATEPCPCTEC 89

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QY 92 KSDQKHSSCTMTBDYVQCKEGRFRNESP--EMCR-----RCSR 131
Db 90 VGLQSMASPCVEADDAVRCRAYGYDDETTGRCACRVCESGLVFCODKONTVCERC 149
QY 132 PSG-----EYVSNCTSMDDIQCEEFGANATVETPAAEEMNT 170
Db 150 PDGTYSDANHVDPCLPCTCEEDTERQRLRETRNADACECEIGRWITRTP--PESSDS 208
QY 171 SPGTAPAPAAEETMTMSPGTPAPAAEETMTTSPGTPADAPAEETMTTSPGTAPAPAAEETMT 230
Db 209 APSTQEPER-----PPEODLLASTFVAG-----VTTVWGSSQPVVTRG--TY 248
QY 231 SPGTPASSHYLSCTIYGIIVLI 252
Db 249 DNLIPVYCSIIAAVYVGLVAYI 270

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RESULT	6			
ID	TR16_RAT	STANDARD:	PR:	425 AA.
AC	PO7174.			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-APR-1988 (Rel. 07, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 16 precursor (Low-			
DE	affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)			
DE	(p75 ICD) (Low affinity neurotrophin receptor p75NTR).			
GN	NGFR OR TNFRSF16.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87115859; PubMed=3027580;			
RA	Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;			
RT	"Gene transfer and molecular cloning of the rat nerve growth factor			
RT	receptor.";			
RL	Nature 325:593-597(1987).			
RN	[2]			
RP	SEQUENCE OF 1-22 FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=93077038; PubMed=1446821;			
RA	Welsis M., Timmusk T., Allikmeets R., Saarma M., Persson H.;			
RT	"Regulatory elements and transcriptional regulation by testosterone			
RT	and retinoic acid of the rat nerve growth factor receptor promoter.";			
RL	Gene 121:247-254(1992).			
RN	[3]			
RP	STRUCTURE BY NMR OF 334-418.			
RX	MEDLINE=97449145; PubMed=9305641;			
RA	Liepinsh E., Illeg L.L., Oetting G., Ibanez C.F.;			
RT	"NMR structure of the death domain of the p75 neurotrophin receptor.";			
RL	EMBO J. 16:4999-5005(1997).			
CC	-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,			
CC	AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF			
CC	NEURAL CELLS.			
CC	-1- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.			
CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; X05137; CAA28783.1; -			
DR	EMBL; X61269;-; NOT_ANNOTATED_CDS.			
DR	PIR; A26431; A26431.			



Db	96	SSKCRRCRC--DGEHGLEVEKNCRTQNTCKRCANPFCNHSQCEHCNPCTCCEHGYE	153
Oy	138	VSNCRTSMDIOCVEEF	153
Dd	154	--NCPTSTNCKREVF	167

RESULT 8

ID	TRIA_PIG	STANDARD:	PRT:	461 AA.
AC	P50555:			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-R1) (p55).			
GN	TNFRSF1A OR TNFR1.			
OC	Sus scrofa (pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxId=9823;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
KX	MEDLINE=96011645; PubMed=7590278;			
RA	Suter B., Pauli U.H.;			
RT	"Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor".;			
RL	Gene 163:263-266(1995).			
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).			
CC	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
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CC	EMBL: U19994; AAC48499.1; -.			
DR	HSSP: P19438; TNFR.			
DR	InterPro: IPR000488; Death.			
DR	InterPro: IPR001368; TNFR_C6.			
DR	Pfam: PF00531; death. 1.			
DR	Pfam: PF00020; TNFR_C6; 3.			
DR	ProDom: PD000771; TNFR_C6; 1.			
DR	SMART: SMO0005; DEATH. 1.			
DR	SMART: SMO0208; TNFR. 3.			
DR	PROSITE: PS00652; TNFR_NGR_1; 3.			
DR	PROSITE: PS50050; TNFR_NGR_2; 2.			
DR	PROSITE: PS50017; DEATH_DOMAIN. 1.			
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.			
FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	461	TUMOR NECROSIS FACTOR RECEPTOR 1.
FT	DOMAIN	22	210	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	211	233	POTENTIAL.

Query Match	Best Local Similarity	Matches	Conservative	Score	DB 1	Length	461
FT	DOMAIN	234	461		CYTOPLASMIC (POTENTIAL).		
FT	REPEAT	43	82		TNFR-CYS 1.		
FT	REPEAT	83	125		TNFR-CYS 2.		
FT	REPEAT	126	166		TNFR-CYS 3.		
FT	REPEAT	167	195		TNFR-CYS 4.		
FT	DOMAIN	340	350		N-SHASE ACTIVATION DOMAIN (MSD).		
FT	DOMAIN	362	447		DEATH.		
FT	DISULFID	44	58		BY SIMILARITY.		
FT	DISULFID	59	72		BY SIMILARITY.		
FT	DISULFID	62	81		BY SIMILARITY.		
FT	DISULFID	84	99		BY SIMILARITY.		
FT	DISULFID	102	117		BY SIMILARITY.		
FT	DISULFID	105	125		BY SIMILARITY.		
FT	DISULFID	127	143		BY SIMILARITY.		
FT	DISULFID	146	158		BY SIMILARITY.		
FT	DISULFID	149	166		BY SIMILARITY.		
FT	DISULFID	168	179		BY SIMILARITY.		
FT	DISULFID	182	190		BY SIMILARITY.		
FT	DISULFID	185	194		BY SIMILARITY.		
FT	CARBOHYD	54	54		N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	86	86		N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	145	145		N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	151	151		N-LINKED (GLCNAC. . .) (POTENTIAL).		
SEQ	SEQUENCE	461 AA:	50696 MM;	CD72361EC60C9D43	CRC64;		
Query Match	Best Local Similarity	Matches	69;	Conservative	30;	Mismatches	94;
						Indels	109;
						Gaps	11.
QY	42 QOORHSFKGEPRAG--SIRSEHTGACNCTGY-----DYTA 78						
DB	37 RKRRL-----CPOKRYSHPNRSLICPKRCHGYLHNDLCPGLDTPDCRECDNGFTFS 92						
QY	79 SNNESECFPCYTCCKSD--OHKSSCTMTPTDYCOCKEGRFNRNSPEM--CRKSCRCPG 134						
DB	93 EHHILQCLSCSKCRBMSGVLEISPTCVDRDYCGGCRKNYRKRYNSETTLFQCLNCSLCPNG 152						
QY	135 EVO-----VSNCTSN-----DIOCVEEFGANATVETPAAEETYN----- 169						
DB	153 TVOLCLEKODPTICNCHSGFLRDEKCVSCVNCKNADCNLCPATSETENDPDQGTIVL 212						
QY	170 -----ISPGPAPAAE-ETMTSPG----- 188						
DB	213 LPLVTFPGICLAFPLFVGLACRYQRMKPKLYSLICGKSTPVKEGEPEPLATAPSPGPIIT 272						
QY	189 -TPAPAAEETMTSP-----GTPAPAAEETMTSPGTPAPAAEETMTSPGTPA 236						
DB	273 FSPISFSPITTFSPVSPSPISPSPTFFPCDMSNIKYVSPREINAPPPGAGPILMPMPA 332						
QY	237 SS 238						
DB	333 SP 334						
RESULT	9						
TNR6_BOVIN	TNR6_BOVIN	STANDARD:	PRT:	323	AA.		
AC	P51867:						
DT	01-OCT-1996 (Rel. 34, Created)						
DT	01-OCT-1996 (Rel. 34, Last sequence update)						
DT	16-OCT-2001 (Rel. 40, Last annotation update)						
DE	Tumor necrosis factor receptor superfamily member 6 precursor (FAST receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).						
DE	TNFRSF6 OR APT1 OR FAS.						
GN	Bos taurus (bovine).						
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;						
OC	Bovidae; Bovinae; Bos.						
OX	NCBI_TaxID=9913;						
NP	[1]						
FP	SEQUENCE FROM N.A.						

RX MEDLINE-96226401; PubMed-8634151;  
 RA Yoo J., Stone R.T., Beattie C.W.;  
 RT "Cloning and characterization of the bovine Fas. ";  
 RL DNA Cell Biol. 15:227-234(1996).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE  
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED  
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING  
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC  
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF  
 CC CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING  
 CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE  
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U34794; AAC48546.1; -  
 DR HSSP: P25445; IDPF.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 323  
 FT DOMAIN 17 170  
 FT TRANSMEM 171 188  
 FT DOMAIN 189 323  
 FT REPEAT 45 80  
 FT REPEAT 81 124  
 FT REPEAT 125 163  
 FT DOMAIN 238 306  
 FT SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;  
 SQ  
 Query Match 13.5%; Score 187; DB 1; Length 323;  
 Best Local Similarity 31.9%; Pred. No. 3.6e-05;  
 Matches 37; Conservative 21; Mismatches 44; Indels 14; Gaps 4;  
 QY 44 QRSFGKECPAGSH-----RSEHTGACNPCTEGVDTNANNNPSCFCTVCKSKPOKH 97  
 Db 51 RHHQFCQCPKRRKNGCKRGDPTPEVLCSEGNFTYTKSHSDKCRKCSIC--DEEH 108  
 QY 98 ----KSSCTWTRDYQCKEGTFRNENSPKCRKSRCPGGEVQVNSCTGMDWIDQC 149  
 Db 109 GLEVEQNCFTRTMTKCRKSNFCNSPCHNCBCTTCEHGITE--KCTPTSNK 162  
 RESULT 10  
 TR16-CHICK STANDARD; PRT; 416 AA.  
 AC P18519;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-

DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LINGFR)  
 DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).  
 GN NGFR OR TNFRSF16.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE-9016579; PubMed-2560385;  
 RX Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,  
 RA Shooter E.M., Reichardt L.F.;  
 RT "Structure and developmental expression of the nerve growth factor  
 RT receptor in the chicken central nervous system.";  
 RL Neuron 2:1123-1134(1989).  
 RN [2]  
 RP SEQUENCE OF 21-416 FROM N.A.  
 RX MEDLINE-90152140; PubMed-2154393;  
 RA Heuer J.G., Patemie-Nainie S., Wheeler E.F., Bothwell M.;  
 RT "Structure and developmental expression of the chicken NGF receptor.";  
 RL Dev. Biol. 137:287-304(1990).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,  
 CC AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF  
 CC NEURAL CELLS (BY SIMILARITY).  
 CC -1- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 DR PIR: JN0006; JN0006.  
 DR PIR: A60504; A60504.  
 DR HSSP: P07174; INGR.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 DR Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;  
 FT SIGNAL 1 19  
 FT CHAIN 20 416  
 FT DOMAIN 29 239  
 FT TRANSMEM 240 261  
 FT DOMAIN 262 416  
 FT REPEAT 23 57  
 FT REPEAT 58 98  
 FT REPEAT 100 138  
 FT REPEAT 140 180  
 FT DOMAIN 333 410  
 FT SEQUENCE 410 AA; 46445 MW; 4D88A90E9E1F4892 CRC64;  
 SQ  
 Query Match 13.5%; Score 187; DB 1; Length 323;  
 Best Local Similarity 31.9%; Pred. No. 3.6e-05;  
 Matches 37; Conservative 21; Mismatches 44; Indels 14; Gaps 4;  
 QY 44 QRSFGKECPAGSH-----RSEHTGACNPCTEGVDTNANNNPSCFCTVCKSKPOKH 97  
 Db 51 RHHQFCQCPKRRKNGCKRGDPTPEVLCSEGNFTYTKSHSDKCRKCSIC--DEEH 108  
 QY 98 ----KSSCTWTRDYQCKEGTFRNENSPKCRKSRCPGGEVQVNSCTGMDWIDQC 149  
 Db 109 GLEVEQNCFTRTMTKCRKSNFCNSPCHNCBCTTCEHGITE--KCTPTSNK 162  
 RESULT 10  
 TR16-CHICK STANDARD; PRT; 416 AA.  
 AC P18519;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-

FT CONFLICT 396 396 K -> R (IN REF. 2).  
 SQ SEQUENCE 416 AA; 44654 MW; 6BCEAB54F4D2D56 CRC64;  
 Query Match 13.4%; Score 184.5; DB 1; Length 416;  
 Best Local Similarity 23.4%; Pred. No. 6,4e-05;  
 Matches 69; Conservative 36; Mismatches 93; Indels 97; Gaps 14;  
 QY 15 VAVLLPVLASATTAAROEYVPOQTVAPOQORHSFKGEECPAGSHRSEHT 63  
 DB 5 VPLLILLPAGPTMGSKK-----LTKMYTSGECKKCNLGEVYQCGVNGT--- 54  
 QY 64 GACNPGTEGYDYNASNNPSCFCTVC-----KSDQ----- 95  
 DB 55 -VEPCIDSVTSDVTSATEPCKCTCQVGLHSMAPCVESDDAVCRACAYGFODELSGS 113  
 QY 96 -KHKSSCTM-----TRDTVC--CKEETFRNE--NSPEMKKCRCPGSEGYVSCT 142  
 DB 114 CKECISCEVGBGLMPCRDSDVYCEPCPESTFSDENFVDPCLPTICEENEVVAECT 173  
 QY 143 SMDIQCEVEFGANATVETPAAEETMTNTSPGTAPAAEETMTTSP 202  
 DB 174 ATSDAEC-RDLHPWTHTTSL-----AGSDSPETITRDPT-----EGMATF- 216  
 QY 203 GTPAPAAEETMTTSPGTAPAAEETMTTSPGT-----PASSHYISCTIVGIIVLI 252  
 DB 217 -----LADIVTYMGSSQP-----VYSRGTADNLIIPVCSILAAYVGLVAYI 259  
 RESULT 11  
 ID TRIA\_BOVIN STANDARD; PRT; 471 AA.  
 AC 019131;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-RI)  
 DE (p53).  
 GN TNFRSF1A OR TNFR1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Arteria;  
 RA Lee E.-K., Taylor M.J., Kehrl M.E.;  
 RT "Cloning of cDNA encoding bovine tumor necrosis factor-receptor I  
 (TNF-R1).";  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DIS)  
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 HOMOMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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 CC -----  
 DR EMBL: U90937; AAB65143.1; -.  
 DR HSSP; P19438; TNFR.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR ProDom; PD000771; TNFR\_c6; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.  
 FT SIGNAL 1 21  
 FT CHAIN 22 471  
 FT DOMAIN 22 210  
 FT TRANSMEM 211 233  
 FT DOMAIN 234 471  
 FT REPEAT 83 82  
 FT REPEAT 126 125  
 FT REPEAT 126 166  
 FT REPEAT 167 195  
 FT DOMAIN 340 360  
 FT DOMAIN 372 457  
 FT DISULFID 44 56  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 190  
 FT DISULFID 185 194  
 FT CARBOHYD 54 54  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 SQ SEQUENCE 471 AA; 51367 MW; 5243EF514DF81C4 CRC64;  
 Query Match 12.4%; Score 171.5; DB 1; Length 471;  
 Best Local Similarity 21.1%; Pred. No. 0.00044;  
 Matches 75; Conservative 32; Mismatches 118; Indels 131; Gaps 14;  
 QY 14 VAVLLPVLASATTAAROEYVPOQTVAPOQORHSFKGEECPAGSHRSEHTGACNPCTE 71  
 DB 6 VPGILLP-LVLPALLADVYPAGVGIVPHRDLKRESQCGKYNHPQNTICTCKKH 64  
 QY 72 GV-----DYTNASNNPSCFCTVCSD--QKHKSSCTMTDPTV 108  
 DB 65 GTLYLNDPCPGGRDTCRCVCAPTALENLARCLSCSRCDMEFVEISPCVVDRTV 124  
 QY 109 CCKEETFRN--ENSPKCRKCRCPGSEGYV-----SNQTSMD 146  
 DB 125 CGCKRNOYREYGEFGRLNCSLCPNGTVNIPQERODTICHHMGFFLGAKCISCHD 184  
 QY 147 IQ-----CVEEFGA----- 155  
 DB 185 CKNNECEKICTRSTGKDSODPGTYVLLPVIYFGCLAFASVAVLACRYORMKPKLYS 244  
 QY 156 ----NATVEPAAEETMTNTSPG---TPAPAAEETMTNTSP-----GTPAPAA 194  
 DB 245 IICGOSTLVKGEPELLVAPAGFNPPTTICSSPSSSPVSIPIYISCDRSNFGAVASPS 304  
 QY 195 EET-----MTTSPGTAPAAEETMTTSPGTAPAAEETMTTSPGTAPAAEETMTTSP 246  
 DB 305 SETAPPHLAKAPILPGPASTHICT-PGPPA-----STHLCTPPGPASTHIL--CTPV 353



RESULT 12  
 ID TRIB\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20335;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor binding protein 2) (TNFR2) (p80) (TNF-R2) (p75) (CD120B) (Etanercept).  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; Pubmed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";  
 RL Science 248:1019-1023(1990).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9104591; Pubmed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., Kling M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299745; Pubmed=8661109;  
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RL Genomics 35:94-100(1996).  
 RN  
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=90349572; Pubmed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 RN  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE=90110215; Pubmed=2153136;  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN  
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE=91056048; Pubmed=2173696;  
 RA Loetscher H., Schlaeger E.J., Lamm H.-W., Pan Y.-C.E., Lesslauer W., Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN  
 RP CHARACTERIZATION.  
 RX MEDLINE=93016040; Pubmed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor phosphorylation.";  
 RL J. Biol. Chem. 267:21172-21178(1992).

[8]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
 RP TRAF2.  
 RX MEDLINE=99221490; Pubmed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of human TRAF2.";  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- LEVEL: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACEUTICAL: Available under the name Embrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Embrel consist of the extracellular ligand-binding portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to TNF-alpha and blocks its interactions with receptors.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".  
 CC -1- DATABASE: NAME=Embrel; NOTE=Clinical information on Embrel;  
 CC WWW="http://www.embrelinfo.com/".  
 CC -----  
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 CC -----  
 DR EMBL: M32315; AAA59929.1; -;  
 DR EMBL: M35857; AAA63262.1; -;  
 DR EMBL: U52165; AAC50622.1; -;  
 DR EMBL: U52156; AAC50622.1; JOINED.  
 DR EMBL: U52157; AAC50622.1; JOINED.  
 DR EMBL: U52158; AAC50622.1; JOINED.  
 DR EMBL: U52159; AAC50622.1; JOINED.  
 DR EMBL: U52160; AAC50622.1; JOINED.  
 DR EMBL: U52161; AAC50622.1; JOINED.  
 DR EMBL: U52162; AAC50622.1; JOINED.  
 DR EMBL: U52163; AAC50622.1; JOINED.  
 DR EMBL: U52164; AAC50622.1; JOINED.  
 DR EMBL: M55994; AAA36755.1; -;  
 DR PIR: A35356; A35356.  
 DR PIR: A36007; A36007.  
 DR PIR: A36475; A36475.  
 DR PIR: B35010; B35010.  
 DR PIR: A23666; A23666.  
 DR PDB: 1CA9; 12-APR-99.  
 DR MIM: 191191; -;  
 DR InterPro: IPR001368; TNFR\_C6.  
 DR Pfam: PF00020; TNFR\_C6; 4.  
 DR ProDom: PD000771; TNFR\_C6; 1.  
 DR SMART: SM00208; TNFR; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461  
 FT DOMAIN 23 257  
 FT TRANSMEM 258 287  
 FT DOMAIN 288 461  
 FT REPEAT 39 76  
 FT REPEAT 77 118  
 FT REPEAT 119 162  
 FT REPEAT 163 201  
 FT DISULFID 40 53  
 FT DISULFID 54 67  
 FT DISULFID 57 75  
 FT DISULFID 78 93  
 FT  
 FT TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TNFR-CYS 1.  
 FT TNFR-CYS 2.  
 FT TNFR-CYS 3.  
 FT TNFR-CYS 4.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.



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RX MEDLINE-95219871; PubMed-7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M.L., Seidlin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor.";
RL Circ. Shock 44:30-34(1994).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X75962; CAAS3576.1; -.
DR EMBL: S76792; AAB3944.1; ALT_INIT.
DR HSSP: P25942; LCDP.
DR MIM: 600315; -.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 3.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 28
FT CHAIN 29 277
FT DOMAIN 29 214 POTENTIAL.
FT TRANSEM 215 235 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 236 277 SUPERFAMILY MEMBER 4.
FT REPEAT 30 65 CYTOPLASMIC (POTENTIAL).
FT REPEAT 66 107 TNFR-CYS 1.
FT REPEAT 108 126 TNFR-CYS 2.
FT REPEAT 127 167 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 146 166 TNFR-CYS 4.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 29340 MW; 49F1525941550BF CRC64;

Query Match 12.0%; Score 166.5; DB 1; Length 277;
Best Local Similarity 26.2%; Pred. No. 0.00055;
Matches 59; Conservative 36; Mismatches 83; Indels 47; Gaps 14;

QY 52 ECPAGS-----HRESEHTGACNPCTEGVDYTNASNNPSCFCTVC--KSDOKHKSCGM 103
DB 45 ECRONGNVAKCSRSQNT-VCRPGCGF-YNDVYSSKP-CRPTCTCNLRSSGSRKOLCTA 101
QY 104 TRDVCQCKESTFRNENSPENCRKCRCPSEVOVSN---CTSWDDICVEBFGANATVE 160
DB 102 TQDVCRCRACGT-CPLDISYKPGVDCAPCPGPHSPGDQACKPW-----TNCITL- 149
QY 161 TPAAEETMTSPGTAPAPAEETMTNTSPGTAPAPAEETMTSGTAPAPAEETMTTSPGT 220
DB 150 --AGRHITLQ-----PASNSSAIDCEDRDPPTAQDETQ-----GPDA-----RPITVQPTGA 194
QY 221 APAAEETMTSP-GTPASSHYLSCTIVGIV-----LIVLILFV 259
DB 195 WPRTSQSGSTRPVEYVPGRAVAAILGLVLTGLGLPLAILLALYL 239

RESULT 15
TNRA_MOUSE STANDARD; PRT: 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)

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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4, precursor (OX40L
DE receptor) (OX40 antigen).
CN TNFRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE-94044750; PubMed-8228223;
RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Fell H.;
RT "Cloning of mouse OX40: a T cell activation marker that may mediate
RT T-B cell interactions.";
RL J. Immunol. 151:5261-5271(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
RT of rat OX40 protein.";
RL Eur. J. Immunol. 23:926-930(1993).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z21674; CAA79772.1; -.
DR EMBL: X85214; CAAS9476.1; -.
DR HSSP: P19438; IEXT.
DR MGD: MGI:104512; Tnfrsf4.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 3.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 272
FT DOMAIN 20 211 POTENTIAL.
FT TRANSEM 212 236 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 237 272 SUPERFAMILY MEMBER 4.
FT REPEAT 26 61 CYTOPLASMIC (POTENTIAL).
FT REPEAT 62 103 TNFR-CYS 1.
FT REPEAT 104 124 TNFR-CYS 2.
FT REPEAT 125 165 TNFR-CYS 3 (INCOMPLETE).
FT CARBOHYD 144 144 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06B7BB4156F0D08E CRC64;

Query Match 12.0%; Score 166; DB 1; Length 272;
Best Local Similarity 25.8%; Pred. No. 0.00058;
Matches 67; Conservative 37; Mismatches 106; Indels 50; Gaps 13;

QY 16 AVLLPVLYASATTARQEEPPQOTVAPQOQRHSFKG-----ECPAGS---HRESEHT--GA 65
DB 10 ALLLALTLGVTARLNCV-----KHYPGSHKCRRCQPGHGKGVSRCHDTROTLL 59

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RESULT	2			
09QZM4	09QZM4	PRELIMINARY:	PRT:	381 AA.
ID	09QZM4			
AC	09QZM4			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	KILLER/DR5 TRAIL DEATH-INDUCING RECEPTOR.			
CN	TNFRSF10B.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99310501; PubMed=10383128;			
RA	Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;			
RT	"Molecular cloning and functional analysis of the mouse homologue of			
RT	the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand			
RL	(TRAIL) death receptor.";			
DR	Cancer Res. 59:2770-2775 (1999).			
DR	EMBL; AF176833; AAD52656.1; ..			
DR	HSSD; 014763; IDOG.			
DR	MGP; MG1:1341090; Tnf1sf10b.			
DR	InterPro: IPR001368; TNFR_c6.			
DR	Pfam; PF00531; death.1.			
DR	Pfam; PF00020; TNFR_c6; 2.			
DR	SMART; SM00005; DEATH; 1.			
DR	SMART; SM00208; TNFR; 2.			
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.			
DR	PROSITE; PS00652; TNFR_NGFR.1; UNKNOWN_2.			
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.			
DR	Receptor			
SW	SEQUENCE 381 AA; 42164 MW; 222531758F4ADE0A CRC64;			
Query Match,	20.7%; Score 285.5; DB 11; Length 381;			
Best Local Similarity	39.2%; Pred. No.5.5e-16;			
Matches	58; Conservative 27; Mismatches 42; Indels 21; Gaps			
QY	11 VVVIVAVLLPVLIAYSAT*-----ARQEEVPRQGTVAPOQORHSFKGECPAGSHSEHTGA 65			
DB	40 LAVLDQAVFVPYTPANPAHNRPAGLQRPESPSPR-----GPCLAGQYLSE--GN 84			
QY	66 CNPCEGSDYDTYASNNP-PSCRPCTVYCKSDQKHNKSCSTMTPTVYQCKEGTFRNENSPRM 124			
DB	85 CKPCEGGIDYTSNHSNLSDCILCYCKEDKVKVETRCNITMTVCRCKRGTFEDKDSPEI 144			
QY	125 CRKSCRPSGEVQVQVNCSTWMDIQVEE 152			
DB	145 COSGNCITDGEDEELTCTPRENRKCVSK 172			
RESULT	3			
09JUL6	09JUL6	PRELIMINARY:	PRT:	381 AA.
ID	09JUL6			
AC	09JUL6			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	TRAIL RECEPTOR KILLER/DR5 HOMOLOGUE.			
CN	TNFRSF10B OR MK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SPLEEN;			
RA	Nakamura Y., Tamari M., Watanabe O.;			
RT	"Mouse TRAIL receptor.";			

[illegible]

OY	66	CNPCEGVDYNNANNE..PSCPCEVVCVKSDOKHSSCMTBPTVOCKEGFRNNSPEM	124
Dd	85	KCPKEGGIDYTRSRSNHSLSDCILCTVCKEDKDKVYETRCNITTFEBCRCKGFIEDXOSPFI	144
OY	125	CRCSCRPSGEVOVSNCTSMWDIOCVEE	152
Dd	145	COSCSNCVTDEBELTSCTPRENRKCYSK	172
RESULT	5		
ID	057408	PRELIMINARY;	PRT; 368 AA.
AC	057408;		
DT	01-JUN-1998	(TREMBLrel. 06, Created)	
DT	01-JUN-1998	(TREMBLrel. 06, last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)	
DE	SUGROOP E ALV RECEPTOR.		
OC	Melaegris gallopavo (Common turkey).		
CC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OX	Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.		
RN	NCHI_TaxID=9103;		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97471016; PubMed=9326659;		
RA	Ackins H.B., Brojatsch J., Naughton J., Rolfs M.M., Pesola J.M.,		
RT	Young J.A.;		
RT	"Identification of a cellular receptor for subgroup E avian leukosis		
RT	virus";		
RL	Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).		
DR	EMBL; AF006002; AAB93987.1;-.		
DR	HSSP; O14763; IDOG.		
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.		
DR	InterPro; IPR000488; Death.		
DR	InterPro; IPR001368; Tnfr_c6.		
DR	Pfam; PF00531; death_1.		
DR	Pfam; PF00020; TNFR_c6; 2.		
DR	SMART; SM00005; DEATH; 1.		
DR	SMART; SM00208; TNFR; 2.		
DR	PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.		
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.		
DR	PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.		
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.		
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.		
KW	Receptor.		
SO	SEQUENCE	368 AA; 41020 MW; 5701AAC2A6D4F87E2 CRC64;	
Query Match	18.3%; Score 253; DB 13;	Length 368;	
Best local similarity	34.7%; Pred. No. 2.6e-13;		
Matches	50; Conservative 27; Mismatches 59; Indels 8; Gaps		
OY	8	LKFVVIVAVILLPVLAYSATTAROEVEVPQQTVAPOOQRHSFGECBPAGSHSEHTGACN	67
Dd	6	LFCFVLLILLAKVHGSAANAAYKRAVKSDYLKPDPY-----SKKCPMGTYLANDSSRCL	60
OY	68	PTEGVDTMANSNNPESPCTVCCKSDOKHKSSCMTRPTVOCKEGFRNNSP_EMKR	126
Dd	61	PEKKP-EETEPNDPKCGCTCRKEDDOEVSPCNSTRMTRACKNGTGFLPDHPCEMCQ	119
OY	127	KC-SRPCSGEVOVSNCTSMWDIOG	149
Dd	120	KQOTRCRGQVRIAACTQGSDLRC	143
RESULT	6		
O9IAR7		PRELIMINARY;	PRT; 368 AA.
AC	O9IAR7;		
DT	01-OCT-2000	(TREMBLrel. 15, Created)	
DT	01-OCT-2000	(TREMBLrel. 15, last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)	
DE	TVB51.		

GN TVER.  
OS Gallus gallus (chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RP MEDLINE=20193796; PubMed=10729132;  
RA Adkins H.B., Brojatsch J., Young J.A.T.;  
RT "Identification and Characterization of a TNFR-related Receptor for  
RT Subgroups B/D/E Avian Leukosis Viruses Reveals Cysteine Residues  
RT Required Specifically for Subgroup E Virus Entry.";  
RL J. Virol. 74:3572-3578(2000).  
DR EMBL: AF161713; AAF60221.1; -.  
DR HSSP: O14763; IDOG.  
DR InterPro: IPR001450; 4Fe4S\_ferredoxin.  
DR InterPro: IPR000488; Death.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00531; death; 1.  
DR Pfam: PF00020; TNFR\_c6; 2.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; UNKNOWN\_1.  
DR PROSITE; PS00117; DEATH\_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
SQ SEQUENCE 368 AA; 41531 MW; 0533CE531DEB47C6 CRC64;

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Query Match Similarity      16.1%; Score 222; DB 13; Length 368;
Best Local Similarity      32.6%; Pred. No. 9, 3e-11;
Matches      47; Conservative      24; Mismatches      65; Indels      8; Gaps

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OY	8	LKEVVVIVAVLLPVLATASATTAROEVEVPOQTVAPOOQRHSFSGEECPAGSHRSEHTGACN	67
DB	6	LRLCPVLLLLFLFAEVLQGSAAVKKRADRSDDLQKPDLYR-----RKCPMGTYEANDSIQCL	60
OY	68	PCTEGVDYITNASNNBSPCPTCYVCKSDQKHKSSCYTRTQCYCCKGTFRNENSP-EMKR	126
DB	61	PKRKO-EYIEYENDPFKCLGCRTCREDQVEVSPICPTNTQCAKCKNGTCLPDPCEMCO	119
OY	127	KC-SRCPGSEVOVSNCTSMDDIQ	149
DB	120	KCTECPKQVRLAPCTQHSDLLC	143

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RESULT      7
O9PW79      PRELIMINARY;      PRT;      368 AA.
AC      O9PW79:
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      TVBS3.
GN      TVB.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97100985; PubMed=8945512;
RA      Brojatsch J., Naughton J., Rollis M.M., Zingler K., Young J.A.;
RT      "CAI", a TNFR-related protein, is a cellular receptor for cytopathic
RT      avian leukosis-sarcoma viruses and mediates apoptosis.";
RN      Cell 87:845-855(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Brojatsch J., Naughton J., Young J.A.T.;
RT      Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AF1617712; AAA47256.1; -.

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DB	235	VFDLSSSPAP-----RVSNNGTAETVYXNDISANGTVGAGSLS	273
RESULT	10		
Q9Z0W1	09Z0W1	PRELIMINARY;	PRT; 417 AA.
AC	09Z0W1		
DT	01-MAY-1999	(TREMBLrel. 10. Created)	
DT	01-MAY-1999	(TREMBLrel. 10. Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19. Last annotation update)	
DE	NERVE GROWTH FACTOR RECEPTOR.		
GN	NGFR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090.		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-A;		
RX	MEDLINE=99077793; PubMed=9857182;		
RA	Tuffreau C., Benjean J., Blondel D., Kieffer B., Flaimand A.,		
RT	"Low-affinity nerve-growth factor receptor (P75NTR) can serve as a		
RL	receptor for rabies virus."		
RL	EMBO J. 17:7250-7259(1998).		
DR	EMBL; AF105292; AAD17943.1; .		
DR	HSSP; P07174; INGR.		
DR	MGD; MGI:97323; NGF.		
DR	InterPro; IPR000488; Death.		
DR	InterPro; IPR000561; EGF-like.		
DR	InterPro; IPR000734; Lipase.		
DR	InterPro; IPR001368; TNFR_C6.		
DR	Pfam; PF00531; death; 1.		
DR	Pfam; PF00020; TNFR_C6; 4.		
DR	SMART; SMO0005; DEATH; 1.		
DR	SMART; SMO0208; TNFR; 3.		
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.		
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.		
DR	PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.		
DR	PROSITE; PS00562; TNFR_NGFR_1; 3.		
DR	PROSITE; PS50050; TNFR_NGFR_2; 4.		
KW	Receptor.		
SEQUENCE	417 AA; 44686 MW; 5D7AA510DB8A9B2	CNC64;	
Query Match	14.4%;	Score 198.5;	DB 11; Length 417;
Best Local Similarity	24.7%;	Pred. No. 9.2e-09;	
Matches	71; Conservative	35; Mismatches	104; Indels 77; Gaps 11;
OY	14	IVAVLLPLVLAASATTARQDEVPQQTVAQQQSHSKSGECPA---GSHRSEHTGA-----C	66
DB	6	LILLILLILLIGVSGGAK-----ETCSIGMTYHS--GECCKACNLGEGVAQPCGANQTVG	57
OY	67	NPCTEGVDVYTNASNNPSCFCTVCKSDQKHKSCTMTRDYVC-----	109
DB	58	EECLDSVTFSDVVSATPECKPCTECLGLQSMGAPCEVDAACRQSYGYODEETGRCEA	117
OY	110	-----QKEGTFRNE-NSPEMCRKCSKCPGSEGVQVNSCTSD	145
DB	118	CSVCGVSGGLVFSCKDKONTVCEDECPREGYSDENAHVDPCLFCTVCEPDERQLRCTPWA	177
OY	146	DIOQVEEGGANTVEPTPAAEETMTNSPGTPAPAAEETMTNSGTPAPAAEETMTNSPGTP	205
DB	178	DAECCEIGRMTTRITRP-PEGSDVTTPTSGQEPAPERPDLIASITYA-----DIVTTVMGSS	232
OY	206	APAAEETMTNSPGTPAPAAEETMTNSGTPAPAAEETMTNSGTPAPAAEETMTNSGTP	252
DB	233	QP-----VTRGT-----ADNLI-----PYVCSIIAAVAVGLAVYI	263
RESULT	11		
Q9PRG7	Q9PRG7	PRELIMINARY;	PRT; 401 AA.

Query Match	Best Local	Similarity	Score	DB	Length
Matches	58: Conservative	34: Mismatches	104: Indels	42: Gaps	
45	RSHFSGE---ECPASHRSEHTG---ACNPCTEGVDYTNASNNPSCFPCTCKSDOKH	97			
26	QYTAGGECICISQVGBGVKRCGVNQYVCEPLDSVYTSIDTISHNEACKPCPECCHKRM	85			
98	KSSCMTTRDTVCQCKEGFTFRNENSPDMCKSCRCPGSEYVNGTSMWDIQCEEFGANA	157			
86	EAPCVDSEDAVACAYGYFTDKKSGQ-CKLCKSCPEGFGMMMSCTNIDPTIC-----EK	138			
158	TYETPAEETMTTSGCTPAPAAE-----TMTNSPGTPAPAAEETMTTS-----P	202			
139	CPEGTVSDSDNDRDCLPCTICEDDEIEAKECTFTSDYVCYDNPVRVSSVTPASSDFPYT	198			
203	GTPAP---AAEETMTTSPGT---PAPAAEETMTTSPGTASSHLSCTIVGIIYLIY	253			
199	GTSVPEPDLSSSSATTSBGSKVLPPTGVAENLI-----PVICSIILAVIAGLVAFIV	250			



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Db      39  ECQGYGVASHRNSQDT-ICHPCPEG--FYNEAVNYOACKPCYQCNRRSGSEPOQECTH 95
Qy      104 TRDVTVCCKBETFRNENSPKCRKSCRCPSGEVQVSN---CTSWDDIOCVEEFGANATVE 160
Db      96  TRDVTVCRCRPGT-PLNGYKRGVDCAPCPQGHSEGNRRACRPW-----TNCITL- 143
Qy      161 TPAAEETMTSPGTPAPAAEE--TMNTSP-GTP-APAAEETMTSPGTPAPAAEETMTTS 216
Db      144 --ACKRTLOPRASSISDAVCEDRSSLATQPMETPSAPYRPRTARTSTAMPRTA-----QG 195
Qy      217 PGTPAPAAEETMTSPGTPASSHYLSCTI-VGIIVLIVLLI 256
Db      196 PSTP-----TLFASKG-PQLAIVLSIGLIGLIALL 229

RESULT 15
Q9DF34  Q9DF34  PRELIMINARY;  PRT;  357 AA.
AC  Q9DF34;
DT  01-MAR-2001 (TREMblrel. 16, Created)
DT  01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT  01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE  DEATH RECEPTOR.
OS  Brachydanio rerio (zebrafish) (zebra danio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC  Cypriniformes; Cyprinidae; Danio.
OX  NCBI_TaxID=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;
RT  "Stimulation of erythropoiesis by inhibiting a new hematopoietic death
RT  receptor in transgenic zebrafish.";
RL  Nat. Cell Biol. 0:0-0(2000).
DR  EMBL; AF302789; AAC21396.1; -.
DR  HSSP; P19438; IEXT.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; death; 1.
DR  SMART; SM00020; TNFR_c6; 3.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 3.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR  PROSITE; PS50050; TNFR_NGFR_2; 2.
KW  Receptor.
SQ  SEQUENCE 357 AA; 40662 MW; 1652B4840D9EEDBA CRC64;

Query Match 12.9%; Score 178.5; DB 13; Length 357;
Best Local Similarity 25.4%; Pred. No. 3.5e-07;
Matches 43; Conservative 31; Mismatches 58; Indels 37; Gaps 6;

Qy      8  LKVVVIVAVLLPV-----LAYSATTAROE-----EVPQQTVAPOQQRHS 47
Db      1  MRYITLIVLLNLTINARSHGDLAMHRSYKNRLSRDVSRCREGLFYPHENICCL----- 55
Qy      48  FKGEBCPAGSH-----RSEHTGACNPCTEGVDYTNASNNBSCFPCTVCKSDQKHKSSC 101
Db      56  ---NCPAGTYVVKRACAAAEKGYCAPC-EFDYTEHDHGLKLCISCDKRIDQETIEKC 110
Qy      102 TMTBDTVQCKEGTF-RNENSPKCRKSCRCPSGEVQVSNCTSMDDIOC 149
Db      111 TSTONTKCKRNGSFCLPDQACEVCKCKCKEDETETKSCTAISNTVC 159
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Search completed: August 13, 2002, 08:37:06  
Job time: 390 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:29:26 ; Search time 20.64 Seconds  
(Without alignments)  
306.503 Million cell updates/sec

Title: US-09-826-212-2  
Perfect score: 1382  
Sequence: 1 MARIPKTLKFVVIVAVLLP.....YLSCTIVGIVLIVLLVFPV 259

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5a\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5b\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6a\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6b\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Deckfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1382	100.0	259	4	US-09-006-353A-2
2	1382	100.0	239	4	US-09-153-927-3
3	634	45.9	386	4	US-09-086-483A-2
4	472	34.2	467	4	US-09-086-483A-6
5	472	34.2	468	4	US-09-013-895A-2
6	448	32.4	440	3	US-08-883-036A-2
7	398.5	28.8	424	4	US-09-333-593A-8
8	380.5	27.5	412	4	US-09-333-593A-2
9	379.5	27.5	411	4	US-09-329-633A-2
10	379.5	27.5	411	4	US-09-079-029-1
11	236.5	17.1	303	4	US-09-333-593A-4
12	212	15.3	368	2	US-08-651-579-2
13	201.5	14.6	427	4	US-09-086-483A-4
14	201.5	14.6	427	4	US-09-041-886-2
15	201.5	14.6	427	4	US-09-006-353A-5
16	201.5	14.6	455	4	US-09-527-236A-4
17	184.5	13.4	224	3	US-08-974-022-50
18	184.5	13.4	224	4	US-08-795-445A-50
19	184.5	13.4	224	4	US-08-795-447A-50
20	184.5	13.4	224	4	US-08-974-186-50
21	184.5	13.4	224	4	US-08-795-446B-50
22	184.5	13.4	376	4	US-09-180-100-22
23	183.5	13.3	438	1	US-08-097-827-11
24	183.5	13.3	438	1	US-08-494-574-11
25	178.5	12.9	360	4	US-09-180-100-11
26	178.5	12.9	358	1	US-08-385-229-4
27	173.5	12.6	159	4	US-09-180-100-23

28	173.5	12.6	486	1	US-08-243-010-1	Sequence 1, Appl
29	169.5	12.3	461	1	US-08-385-229-2	Sequence 2, Appl
30	169.5	12.3	461	2	US-08-650-000-2	Sequence 2, Appl
31	169.5	12.3	461	4	US-09-042-785A-7	Sequence 1, Appl
32	169.5	12.3	461	4	US-08-477-347-3	Sequence 3, Appl
33	169.5	12.3	461	4	US-09-006-353A-4	Sequence 4, Appl
34	169.5	12.3	461	4	US-08-476-862-2	Sequence 2, Appl
35	169.5	12.3	461	6	5395760-2	Patent No. 5395760
36	169	12.2	144	4	US-09-180-100-21	Sequence 21, Appl
37	167.5	12.1	143	4	US-09-180-100-10	Sequence 10, Appl
38	167.5	12.1	335	4	US-08-815-469-6	Sequence 6, Appl
39	166.5	12.0	277	2	US-08-147-784-2	Sequence 2, Appl
40	166.5	12.0	277	4	US-08-195-967-2	Sequence 2, Appl
41	166.5	12.0	277	4	US-09-006-353A-12	Sequence 12, Appl
42	166.5	12.0	277	4	US-08-472-940-2	Sequence 2, Appl
43	165.5	12.0	669	4	US-09-013-885A-3	Sequence 3, Appl
44	164.5	11.9	314	1	US-08-444-231-19	Sequence 19, Appl
45	164.5	11.9	314	1	US-08-152-443A-19	Sequence 19, Appl

## ALIGNMENTS

```
RESULT 1
US-09-006-353A-2
: Sequence 2, Application US/09006353A
: Patent No. 6261801
:
GENERAL INFORMATION:
: APPLICANT: WEI, YING-PEI
: APPLICANT: YU, GUO-LING
: APPLICANT: GENTZ, REINER
: APPLICANT: RUBEN, STEVEN
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: HUMAN GENOME SCIENCES, INC.
: STREET: 9410 KEY WEST AVENUE
: CITY: ROCKVILLE
: STATE: MD
: COUNTRY: US
: ZIP: 20850
:
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/006.353A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BROOKES, ANDERS A
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PE341
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 259 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-09-006-353A-2
:
Query Match 100.0%; Score 1382; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 5.3e-102;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MARIPKTLKFVVIVAVLLPVLAYSATTAROEVEPQQTAVAPDQQRHSFGKECPAGSHRS 60
Db 1 MARIPKTLKFVVIVAVLLPVLAYSATTAROEVEPQQTAVAPDQQRHSFGKECPAGSHRS 60
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QY 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYCOCKEGTFRNEN 120  
|||||  
Db 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYCOCKEGTFRNEN 120  
QY 121 SPEMCRKCSRCPGSEGVQVSNCTSMDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAE 180  
|||||  
Db 121 SPEMCRKCSRCPGSEGVQVSNCTSMDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAE 180  
QY 181 ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPASSHY 240  
|||||  
Db 181 ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPASSHY 240  
QY 241 LSCITVGIIVLIVLIVFV 259  
|||||  
Db 241 LSCITVGIIVLIVLIVFV 259

RESULT 2  
US-09-153-927-3  
; Sequence 3, Application US/09153927A  
; Patent No. 6297022  
; GENERAL INFORMATION:  
; APPLICANT: McDonnell, Peter C.  
; APPLICANT: Young, Peter R.  
; TITLE OF INVENTION: A Method of Identifying Agonists and  
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3  
; TITLE OF INVENTION: and TR5  
; FILE REFERENCE: GH50031  
; CURRENT APPLICATION NUMBER: US/09/153,927A  
; CURRENT FILING DATE: 1998-09-16  
; EARLIER APPLICATION NUMBER: 60/061,334  
; EARLIER FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PASTSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 299  
; TYPE: PRT  
; ORGANISM: Human  
US-09-153-927-3

Query Match 100.0%; Score 1382; DB 4; Length 299;  
Best Local Similarity 100.0%; Pred. No. 6.3e-102;  
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPTLKEFVVIVAVLLPVLAASATTAROEVEVPOQTVAPOOQRHSFKGECPPAGSHRS 60  
|||||  
Db 41 MARIPTLKEFVVIVAVLLPVLAASATTAROEVEVPOQTVAPOOQRHSFKGECPPAGSHRS 60  
QY 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYCOCKEGTFRNEN 120  
|||||  
Db 101 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYCOCKEGTFRNEN 160  
QY 121 SPEMCRKCSRCPGSEGVQVSNCTSMDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAE 180  
|||||  
Db 161 SPEMCRKCSRCPGSEGVQVSNCTSMDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAE 220  
QY 181 ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPASSHY 240  
|||||  
Db 221 ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPASSHY 280  
QY 241 LSCITVGIIVLIVLIVFV 259  
|||||  
Db 281 LSCITVGIIVLIVLIVFV 299

RESULT 3  
US-09-086-483A-2  
; Sequence 2, Application US/09086483A  
; Patent No. 6214580  
; GENERAL INFORMATION:

APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/086,483A  
FILING DATE: May-29-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,936  
FILING DATE: May-30-97  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,112  
FILING DATE: Dec-9-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF379  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
FAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 386 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-086-483A-2

Query Match 45.9%; Score 634; DB 4; Length 386;  
Best Local Similarity 51.8%; Pred. No. 9.7e-43;  
Matches 132; Conservative 22; Mismatches 41; Indels 60; Gaps 3;

QY 5 PKTLKEFVVIVAVLLPVLAASATTAROEVEVPOQTVAPOOQRHSFKGECPPAGSHRS 64  
|||||  
Db 35 PKTLKEFVVIVAVLLPVLAASATTAROEVEVPOQTVAPOOQRHSFKGECPPAGSHRS 94  
QY 65 ACNPCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYCOCKEGTFRNENSPM 124  
|||||  
Db 95 ACNPCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYCOCKEGTFRNENSPM 154  
QY 125 CRKC-SRCPGSEGVQVSNCTSMDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAEETM 183  
|||||  
Db 155 CRCTGTCGPRMVKVSNCTSPRSDICKNESAASTGKTPAAEETVTTILG----- 204  
QY 184 NTSPTGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPASSHYLSC 243  
|||||  
Db 205 -----MLASP-----YHYLTI 215  
QY 244 TVIGIIVLIVLIVFV 258  
|||||  
Db 216 IVLVIIIVLVVGV 230

RESULT 4  
US-09-086-483A-6  
; Sequence 6, Application US/09086483A  
; Patent No. 6214580  
; GENERAL INFORMATION:

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? APPLICANT: NI, et al.
? TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
? NUMBER OF SEQUENCES: 15
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: HUMAN GENOME SCIENCES, INC.
? STREET: 9410 KEY WEST AVENUE
? CITY: ROCKVILLE
? STATE: MD
? COUNTRY: US
? ZIP: 20850
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/086,483A
? FILING DATE: May-29-98
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/050,936
? FILING DATE: May-30-97
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/069,112
? FILING DATE: Dec-9-97
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: BROOKES, ANDERS A.
? REGISTRATION NUMBER: 36,373
? REFERENCE/DOCKET NUMBER: PF379
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (301) 309-8504
? TELEFAX: (301) 309-8439
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 467 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-086-483A-6

Query Match          34.2%; Score 472; DB 4; Length 467;
Best Local Similarity 58.7%; Pred. No. 7.5e-30;
Matches 91; Conservative 16; Mismatches 42; Indels 6; Gaps 3;

QY 3 RIPTLKFVVYIVAVLLPVLAYSATFARQEEVPOQTVAPOQQRHSFKGECPAGSHRSEH 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 RVHRTKFFVY--VGLLQVVPSSAATIKLHD---QSIGTQWHSPLGELCPPSHRSEH 141

QY 63 TGACNPTCEGVDTYNASNNESCFPCYVCKSDOKHKSSCTTRTYVCCCKGCTFRNENSP 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 PGACNRCTEGVGYTNASNNLFACLPCTACKSDDEERSCTTTRNTACOCKGCTFRNDNSA 201

QY 123 EMCRCRSR-CPSEGVQVSNCTSMDDICVEEFGAN 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 202 EMCRCSTGCPGRGVKVKDCTPMSDIECVHRESGN 236

RESULT 5
US-09-013-895A-2
; Sequence 2, Application US/09013895A
; Patent No. 6342363
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
```

```

? TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
? NUMBER OF SEQUENCES: 12
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: HUMAN GENOME SCIENCES, INC.
? STREET: 9410 KEY WEST AVENUE
? CITY: ROCKVILLE
? STATE: MD
? COUNTRY: US
? ZIP: 20850
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/013,895A
? FILING DATE: 27-JAN-1998
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: STEEFE, ERIC K.
? REGISTRATION NUMBER: 36,688
? REFERENCE/DOCKET NUMBER: 1488,1300002
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)371-2540
? TELEFAX: (202)371-2600
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 468 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-013-895A-2

Query Match          34.2%; Score 472; DB 4; Length 468;
Best Local Similarity 58.7%; Pred. No. 7.5e-30;
Matches 91; Conservative 16; Mismatches 42; Indels 6; Gaps 3;

QY 3 RIPTLKFVVYIVAVLLPVLAYSATFARQEEVPOQTVAPOQQRHSFKGECPAGSHRSEH 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 RVHRTKFFVY--VGLLQVVPSSAATIKLHD---QSIGTQWHSPLGELCPPSHRSEH 141

QY 63 TGACNPTCEGVDTYNASNNESCFPCYVCKSDOKHKSSCTTRTYVCCCKGCTFRNENSP 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 PGACNRCTEGVGYTNASNNLFACLPCTACKSDDEERSCTTTRNTACOCKGCTFRNDNSA 201

QY 123 EMCRCRSR-CPSEGVQVSNCTSMDDICVEEFGAN 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 202 EMCRCSTGCPGRGVKVKDCTPMSDIECVHRESGN 236

RESULT 6
US-08-883-036A-2
; Sequence 2, Application US/08883036A
; Patent No. 6072047
; GENERAL INFORMATION:
; APPLICANT: Rauch, Charles
; APPLICANT: Walczak, Henning
; TITLE OF INVENTION: Receptor That Binds TRAIL
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle,
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Macintosh 7.6
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/883,036A
FILING DATE: 26-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US --to be assigned--
FILING DATE: 04-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,536
FILING DATE: 28-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/815,255
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/799,861
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2625-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-883-036A-2
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Query Match          32.4%; Score 448; DB 3; Length 440;
Best Local Similarity 40.7%; Pred. No. 5,5e-28;
Matches 105; Conservative 23; Mismatches 68; Indels 62; Gaps 4;
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QY 3 RIPTLKRVVIVAVLLPVLAISATTAAROEVPQOTVAPQOQRHSFGEECPAGSHRSEH 62
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 33 RVPKTL--VLVVAIVALLVSASALITQODLAPQOQRAAPQOKRSSPSBGLCPGHHISED 90
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 63 TGACNPCTEGVDYTNASNEBSCFPCYCKSDQKHKSSCTMTRTDYVQCKEGTFRNENSP 122
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 91 GRDCISCKYGGDYSTHWNDLFLCLRCTRCDSGEVELSPTTTRNTVCCCEGTFRREDS 150
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 123 EMCRCRC-SRCPSEGVQVSNCTSMDDIOCVEEFGANATVETPAAEINTMTSPGPAPAAE 181
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 151 EMCRCRCRTGCRGMVKVGDCTPMSDIECVH----- 180
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 182 TMTNTPGTAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYL 241
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 -----KESGTRKHSQ-EADVAEETVTSPTSPGTPASSCSL 211
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 242 SCTVIGIIVLVLLIVPV 259
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 212 SGITIGVVAIVLVAV 229
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
US-09-333-593A-8
Sequence 8, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNEH, ALEMESEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
```

```
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 424
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-8
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```
Query Match          28.8%; Score 398.5; DB 4; Length 424;
Best Local Similarity 46.6%; Pred. No. 4.2e-24;
Matches 89; Conservative 23; Mismatches 64; Indels 15; Gaps 5;
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QY 3 RIPTLKRVVIVAVLLPVLAISATTAAROEVPQOTVAPQOQRHSFGEECPAGSHRSEH 62
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 33 RVPKTL--VLVVAIVALLVSASALITQODLAPQOQRAAPQOKRSSPSBGLCPGHHISED 90
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 63 TGACNPCTEGVDYTNASNEBSCFPCYCKSDQKHKSSCTMTRTDYVQCKEGTFRNENSP 122
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 91 GRDCISCKYGGDYSTHWNDLFLCLRCTRCDSGEVELSPTTTRNTVCCCEGTFRREDS 150
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 123 EMCRCRC-SRCPSEGVQVSNCTSMDDIOCVEEFGANATVETPAAEINTMTSPGPAPAAE 181
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 151 EMCRCRCRTGCRGMVKVGDCTPMSDIECVH-----ESGRSTEGKTEP---KSADK 199
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 182 TMTNTPGTAPAP 192
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 200 T-HTCPCPAP 209
      ||||| :|: ||| | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-09-333-593A-2
Sequence 2, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNEH, ALEMESEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 412
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-2
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Query Match          27.5%; Score 380.5; DB 4; Length 412;
Best Local Similarity 51.7%; Pred. No. 1.1e-22;
Matches 78; Conservative 17; Mismatches 53; Indels 3; Gaps 2;
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Db 33 RVPKTL -VLVVAVALLLVSMSLITQDLPQGRAAPQGRSSPSBGLCPREHTISED 90

QY 63 TGACNCPCHGEVDYTNASNNESCEPFCYVCKSDCKHKSCEFTPTCYOCCKEGFRRNNSP 122  
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

Db 91 GRDCISCKYGGDYISQWMDLLFLCRLCTRDSGSEVELSPCTTTNNYVCOCEEGGFREEDSP 150

QY 123 EMCKRC-SRCPSGEVOVSNCTSMDDIOCEE 152  
          |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

Db 151 EMCRRCRTGCPRGMYKVDCTPMWDIEICVHK 181

```

RESULT 9
US-09-329-633A-2
: Sequence 2, Application US/09329633A
: Patent No. 6252050
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Chuntarapal, Anan
: APPLICANT: Kim, K. Jin
: TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
: TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
: FILE REFERENCE: P14681 (REVISED)
: CURRENT APPLICATION NUMBER: US/09/329,633A
: CURRENT FILING DATE: 1999-06-10
: PRIOR APPLICATION NUMBER: US 60/089,253
: PRIOR FILING DATE: 1998-06-12
: NUMBER OF SEQ ID NOS: 2
: SEQ ID NO 2
: LENGTH: 411
: TYPE: PRT
: ORGANISM: human
: FEATURE:
: NAME/KEY: xaa
: LOCATION: 410
: OTHER INFORMATION: xaa = leu or met
US-09-329-633A-2

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Query Match	27.5%	Score 379.5	DB 4	Length 411
Best Local Similarity	51.7%	Pred. No. 1.3e-22		
Matches 78	Conservative 17	Mismatches 53	Indels 3	Gaps 2
QY	3	RIPKLKFEVYIVAVLLVLVAYATTAAROEVPQDTVAPOOORHSPKGECPAGHSRSEH	62	
Db	33	RVPKTL--VLVVAATLLVSAESALITQODLAPQORAAQOKRSSSEBLCPGHHSIED	90	
QY	63	TGACNPCTEGVDYINASNNBSPSCFPCYCKSDOKHKSSCTMTRDITYCQCKEGTFRNENSP	122	
Db	91	GRDCISCKYGGDYSTRHMNDLLFCILCTCRDSDGEVELSPCTTTRNRYCQCEEGTFREDSP	150	
QY	123	EMCRKC--SRCPBGEVQVSNCTSMDDIOCYEE	152	
Db	151	EMCRKCRTPGCPGMVAVGDCTPWSDIECVHK	181	

RESULT 10  
 US-09-072-029-1  
 : Sequence 1, Application US/09072029  
 : Patent No. 6340369  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Adams, Camilla W.  
 : APPLICANT: Ashkenazi, Avi J.  
 : APPLICANT: Chantcharapai, Anan  
 : APPLICANT: Kim, Kyung J.  
 : TITLE OF INVENTION: Apo-2 Receptor  
 : NUMBER OF SEQUENCES: 14  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Genentech, Inc.  
 : STREET: 1 DNA way  
 : CITY: South San Francisco  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinpatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079, 029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maischang, Diane L.  
REGISTRATION NUMBER: 35, 600  
REFERENCE/DOCKET NUMBER: P1101n2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEO ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

Query Match	27.5%	Score 379.5	DB 4	Length 411
Best Local Similarity	51.7%	Pred. No. 1.3e-22		
Matches	78	Conservative	17	Mismatches 53; Indels 3; Gaps 2
Qy	3	RIPKTLKEFWVVAVALPLPAYSATTTARQEEPPQOVAPQOORSHKSGEGCPAGSHSEH	62	
		:   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	33	RVPKTL-VLVVAVALLLVSASALITQODLAPQQAAPQOKRSSBELCPGHHISD	90	
Qy	63	TGACNPCTGEGVDYTNASNNPESCFPCYCKSPDQKHKSCTMTRDYVQCKEGTFRNENSP	122	
Db	91	GRDCISCKYGGDYSTRHMNDLFLCLETCTRCDSSEVELSPCTTTRNTVQCCEGTFREEDSP	150	
Qy	123	EMCRKC-SRCPSGEVOYNSCTSMDDIQCEE	152	
		:   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	151	EMCRKCRTCGCPRGMAVKGDCSTPMSIDCVHK	181	

```

RESULT 11
US-09-333-593A-4
; Sequence 4, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALESEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR
; TITLE OF INVENTION: tr6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 303
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-4

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Query Match 17.1%; Score 236.5; DB 4; Length 303;







GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: August 13, 2002, 08:31:29 ; Search time 51.8 Seconds  
(without alignments)  
40.741 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233

Perfect score: 100  
Sequence: 1 TSPGPAPAEETMTSPG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

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2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*  
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22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	100	100.0	249	22 AAB82182	FLAG-TRID clone w1
2	100	100.0	259	19 AAW64668	Human TRID protein
3	100	100.0	259	20 AAY05726	Tumour necrosis fa
4	100	100.0	259	20 AAN93578	Human hAP09 protei
5	100	100.0	259	20 AAW88408	Human Apo-2Dcr pro
6	100	100.0	259	22 AAU12321	Human PRO366 polyp
7	100	100.0	259	22 AAB20111	Human immunostimu
8	100	100.0	259	22 AAB36696	Human tumour necro
9	100	100.0	259	22 AAB53091	Human angiogenesis
10	100	100.0	268	22 AAB82181	FLAG-TRID clone w1
11	100	100.0	299	19 AAW76331	Human tumour necro

12	100	100.0	299	20 AAY29864	Human secreted pro
13	100	100.0	299	20 AAY05744	Tumour necrosis fa
14	100	100.0	299	20 AAY00933	Human TRAIL-R3 pro
15	100	100.0	299	20 AAW94671	Human TNF-related
16	100	100.0	299	20 AAN88409	Human Apo-2Dcr pro
17	100	100.0	299	21 AAB01343	Human TNF-related
18	54	54.0	350	20 AAY00934	Human DR5 protein
19	54	54.0	440	19 AAB99284	Human TRAIL recept
20	54	54.0	440	19 AAW79260	Tumour necrosis fa
21	54	54.0	440	20 AAY05725	Tumour necrosis fa
22	54	54.0	440	21 AAB01340	TNF-related apopto
23	54	54.0	801	22 AAB52850	Escherichia coli p
24	53	53.0	536	21 AAB53136	Macaca mulatta rha
25	52	52.0	221	22 AAY50369	Propionibacterium
26	51	51.0	219	22 AAU48350	Propionibacterium
27	51	51.0	2066	22 AAE10146	Streptomyces nours
28	49	49.0	167	22 AAU32618	Novel human secret
29	49	49.0	761	22 AAG02677	Novel human diagno
30	49	49.0	907	22 AAG01455	Novel human diagno
31	48.5	48.5	258	21 AAY93816	Human PRO1305 (UNG
32	48.5	48.5	258	22 AAU29165	Human PRO polypept
33	48.5	48.5	258	22 AAB66135	Protein of the inv
34	48.5	48.5	602	21 AAY95660	Human Zntf2 protei
35	48	48.0	152	22 AAU40239	Novel human diagno
36	48	48.0	189	22 AAG14657	Novel human diagno
37	48	48.0	238	22 AAG25281	Novel human diagno
38	48	48.0	259	22 AAG25407	Novel human diagno
39	48	48.0	1078	16 AAR71704	Collagen alpha 1 (
40	48	48.0	1078	13 AAY96125	Collagen type III
41	48	48.0	1196	21 AAR28916	Type III procollag
42	48	48.0	1466	22 AAB50291	Collagen type III
43	48	48.0	1469	22 AAB51591	Novel human diagno
44	47	47.0	191	22 AAB63572	Drosophila melanog
45	47	47.0	191	22 AAB67144	Drosophila melanog

## ALIGNMENTS

RESULT 1	
ID AAB82182	standard; Protein: 249 AA.
XX AAB82182;	
XX	
DT 23-JUL-2001	(first entry)
XX	
DE	FLAG-TRID clone without a transmembrane domain.
XX	
KW	FLAG-epitope tag; transmembrane domain; death domain; apoptosis;
KW	cell suicide; tissue homeostasis; cell proliferation;
KW	cell-cell signalling; Trail Receptor without intracellular Domain; TRID.
XX	
OS	Synthetic.
XX	
FH	
FT	Key
FT	Peptide
FT	Protein
FT	Peptide
FT	Misc-difference
FT	Label= FLAG-TRID
FT	/label= FLAG-epitope
FT	/note= "Insertion site for candidate sequences"
XX	
XX	W0200114542-A1.
XX	01-MAR-2001.
XX	
XX	23-AUG-2000; 2000WO-US23112.
XX	
XX	25-AUG-1999; 99US-0150747.
XX	

PA	(GENO-)GENOME THERAPEUTICS CORP
PI	Denome SA, Swain PM, Tzellas N;
XX	WI: 2001-374162/39.
DR	N-PSDB: AAH19326.
XX	
PT	Identifying a transmembrane domain of a membrane-spanning protein
PT	useful in defining processes in cell suicide and tissue homeostasis,
PT	comprises modifying the nucleic acid encoding a death domain-lacking
PT	membrane spanning protein
XX	
PS	Disclosure: Fig 2, 38pp: English.
XX	
CC	The present invention relates to methods for identifying a transmembrane
CC	domain (TM) of a membrane-spanning protein. The method comprises
CC	modifying a nucleic acid encoding a death domain (DD)-lacking membrane
CC	spanning protein (e.g. TRAIL receptor without intracellular Domain; TRID)
CC	by replacing the nucleic acid encoding the TM of the DD-lacking
CC	membrane-spanning protein with a candidate nucleic acid sequence to
CC	produce a nucleic acid encoding a modified DD-lacking membrane spanning
CC	protein. The modified nucleic acid is then transfected into a host cell,
CC	which expresses a DD-containing receptor. The absence of apoptosis of the
CC	host cell is determined following exposure of the transfected cell to an
CC	apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent
CC	apoptosis of the host cell. The modified nucleic acid encoding the
CC	modified death domain-lacking membrane-spanning protein can also include
CC	a nucleic acid sequence encoding an epitope tag. The present sequence is
CC	a FLAG-TRID clone, which was used in the method of the present invention.
CC	This sequence comprises human TRID protein and the FLAG-epitope tag. The
CC	FLAG-epitope is a useful marker to purify proteins encoded by the
CC	modified DD-lacking membrane-spanning protein. The identified TM and
CC	membrane-spanning proteins may be used in defining processes involved in
CC	cell suicide and tissue homeostasis, and to evaluate, interfere and treat
CC	events, such as cell proliferation and cell-cell signalling pathways.
XX	
SQ	Sequence 249 AA:
QY	1 TSPGTPAPAAETMTTSPG 19
DB	194 TSPGTPAPAAETMTTSPG 212
XX	
RESULT 2	
AAW64668	
ID	AAW64668 standard; Protein; 259 AA.
XX	
AC	AAW64668;
XX	
XX	23-OCF-1998 (first entry)
DT	
XX	
DE	Human TRID protein.
XX	
KW	TRAIL receptor without intracellular domain; TRID; TNFR-5; human;
KW	tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;
KW	haematopoietic tissue; immune system; ligand; apoptosis; treatment.
XX	
OS	Homo sapiens.
XX	
XX	
FH	Key
FT	Peptide
FT	1..27
FT	/label= signal
FT	27..259
FT	/label= TRID
FT	42..52
FT	/label= epitope
FT	58..66
FT	/label= epitope

FT	Region	68...76
FT	/label= epitope	
FT	Region	79...85
FT	/label= epitope	
FT	Region	91...102
FT	/label= epitope	
FT	Region	110...122
FT	/label= epitope	
FT	Region	126...136
FT	/label= epitope	
FT	Region	142...148
FT	/label= epitope	
PN	WO9830693-A2.	
PD	16-JUL-1998.	
XX		
XX	13-JAN-1998;	98WO-US00152.
XX	07-AUG-1997;	97US-0054885.
PR	14-JAN-1997;	97US-0035496.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Wei Y,	
PI	Yu G;	
XX		
DR	WPI: 1998-399141/34.	
DR	N-PSDB: AAV51348.	
XX		
PT	Human TRAIL receptor without an intracellular domain polypeptide -	
PT	used in the diagnosis of immune system-related disorder(s)	
PS	Claim 1b; Fig 1; 90pp; English.	
XX		
CC	This sequence represents a human TRID (TRAIL (TNF-related	
CC	apoptosis-inducing ligand) receptor without an intracellular domain).	
CC	TRID is a member of the tumour necrosis factor receptor (TNFR) family	
CC	also known as TNFR-5. TRID is expressed in haematopoietic tissues and	
CC	other normal human tissues. For a number of immune system-related	
CC	disorders, substantially altered (whether increased or decreased) levels	
CC	of TRID gene expression can be detected (whether increased or decreased) levels	
CC	of TRID gene expression can be detected (whether increased or decreased) levels	
CC	nucleic acids and antibodies are useful in the diagnosis of such immune	
CC	system related disorders. Mutations of the TRID gene can also be	
CC	detected. TRID can also be used to identify ligands which may be useful	
CC	in the treatment of apoptosis related disorders. TRID is administered to	
CC	humans at a parenteral dose of 0.01 to 1 mg/kg/day.	
XX		
SO	Sequence 259 AA;	
QY		
Query Match	100.0%; Score 100; DB 19; Length 259;	
Best Local Similarity	100.0%; Pred. No. 5.4e-05;	
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 TSPGPPAPAAEETWTSPG 19	
DB	185 tsgpfpapaaeetmtspg 203	
RESULT 3		
ID	AA05726	
AA05726	standard; Protein: 259 AA.	
AC	AA05726;	
XX		
DT	19-JUL-1999 (first entry)	
XX		
DE	Tumour necrosis factor receptor TRAIL-R3.	
XX		
TM	TRAIL-3; tumour necrosis factor receptor; apoptosis; cancer;	
XX	therapy.	

OS	Mammalia.	Location/Qualifiers
XX	Key	1..24
XX	Peptide	/note= "signal peptide"
FT	Protein	25..259
FT	Region	/note= "mature protein"
FT	Region	162..175
FT	Region	/note= "TAPB repeat"
FT	Region	176..191
FT	Region	/note= "TAPB repeat"
FT	Region	192..206
FT	Region	/note= "TAPB repeat"
FT	Region	207..221
FT	Region	/note= "TAPB repeat"
FT	Region	222..236
FT	Domain	/note= "TAPB repeat"
FT	Domain	238..259
FT	Domain	/note= "transmembrane domain"
PN	MO9912963-A2.	
XX	18-MAR-1999.	
PD	11-SEP-1998;	98WO-US19029.
PE	06-MAY-1998;	98US-0084422.
XX	12-SEP-1997;	97US-0058631.
PR	(BIOJ ) BIOGEN INC.	
XX	Tschopp J;	
PA	WPI; 1999-276942/23.	
XX	N-PSDB; AAX25349.	
XX	Novel tumor necrosis factor receptor proteins TRAIL-R2 and TRAIL-R3	
PT	Disclosure; Page 28; 28pp; English.	
XX	The present sequence represents TRAIL-R3, a novel mammalian	
XX	cysteine-rich receptor of the tumour necrosis factor receptor family	
CC	The invention is related to novel receptors for TRAIL, i.e. TRAIL-R2	
CC	(see AAY05725) and TRAIL-R3. TRAIL-R3 is highly glycosylated. It is	
CC	a putative glycosylphosphatidylinositol-anchored protein, which is	
CC	either cell-associated or processed and secreted. Secreted	
CC	TRAIL-R3 competes for the binding of TRAIL to TRAIL-R1 and/or	
CC	TRAIL-R2, thereby acting as an inhibitor of apoptosis. Expression	
CC	of TRAIL-R3 is restricted to peripheral blood lymphocytes and	
CC	skeletal muscle. It is likely that TRAIL-R3 acts as an important	
CC	regulator of TRAIL-R2 and -R3 induced cell death in vivo. A method	
CC	for preventing or reducing the advancement, severity or effects of	
CC	an immunological disease involves administering a TRAIL-R2 or	
CC	TRAIL-R3 blocking agent such as a soluble TRAIL-R (preferably	
CC	comprising a human immunoglobulin Fc domain) and an antibody. A	
CC	method of treating cancer involves administration of antibodies	
CC	against TRAIL-R3 or TRAIL-R2. A method of inducing cell death	
CC	involves administration of an agent capable of inhibiting the	
CC	binding of TRAIL-R2 or -R3 to its ligand.	
XX	Sequence 259 AA;	

AAW93578	
ID AAW93578 standard; Protein; 259 AA.	
XX	
AC AAW93578;	
XX	
DT 18-JUN-1999 (first entry)	
XX	
DE Human hAPO9 protein.	
XX	
KM Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormality; prostate cancer; APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; cytoplasmic domain; immunogen; antibody preparation; breast carcinoma; apoptosis; human.	
XX	
OS Homo sapiens.	
XX	
PN WO911791-A2.	
XX	
PD 11-MAR-1999.	
XX	
PF 04-SEP-1998; 98WO-US18393.	
XX	
PR 05-SEP-1997; 97US-0924634.	
XX	
PA (UNIT ) UNIT WASHINGTON.	
XX	
PI Chaudhary PM;	
XX	
DR WPt; 1999-205191/17.	
XX	
N-PSDB; AAX23412.	
PT New Tumor Necrosis Factor family receptor polypeptides and ligands - useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities	
XX	
Claim 24; Fig 6; 156pp; English.	
PS	
XX This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic molety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or expressed on the cell surface. The binding is preferably performed in vivo. APO4 polypeptides/active fragments are also useful for screening for agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transected to human breast carcinoma cell line MCF-7, and induced apoptosis.	
XX	
SQ Sequence 259 AA:	

AAW88408	standard: Protein; 259 AA.
ID	AAW88408
AC	AAW88408;
XX	
DT	26-APR-1999 (first entry)
XX	
DE	Human Apo-2Dcr protein (amino acids 1-259).
XX	
KM	Apo-2Dcr; human; apoptosis; tumour necrosis factor receptor;
KW	neurodegeneration; autoimmune disease; inflammation; cancer;
KW	therapy.
XX	
OS	Homo sapiens.
XX	
EH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..29
FT	/note= "predicted signal peptide"
FT	1..161
FT	/note= "extracellular domain, this domain is specifically claimed in Claim 5"
FT	Domain
FT	Domain
FT	/note= "cysteine-rich domain"
FT	110..149
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FT	162..176
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FT	/note= "N-glycosylation"
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XX	
PN	W09858062-A1.
XX	
PD	23-DEC-1998.
XX	
PE	12-JUN-1998; 98WO-US12455.
XX	
PR	18-JUN-1997; 97US-0878168.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;
PI	Kim KJ, Wood WI;
XX	
XX	WPI; 1999-095340/08.
DR	N-PSDB; AAV84347.
XX	
PT	New Apo-2Dcr polypeptide - used for modulation and diagnosis of
PT	apoptosis, e.g. in neurodegeneration
XX	
PS	Claim 1; Page 50-51; 88pp; English.
XX	
CC	This polypeptide comprises human Apo-2Dcr, a novel member of the
CC	tumour necrosis factor receptor family that binds to Apo-2 ligand. *
CC	Its amino acid sequence was deduced from the nucleotide sequence
CC	of an isolated cDNA clone (see AAV84347); an alternative translation

CC		initiation site in this clone will encode a polypeptide (see
CC	AAM68409)	comprising amino acid residues -40 to 269 of Apo-2DCR.
CC	Apo-2Dcr	shows more sequence identity to DR4 (60%) and Apo-2 (50%)
CC	than to other apoptosis-linked receptors. The polypeptide can be	
CC	obtained by expression in host cells using the vector deposited as	
CC	ATCC 209087. The invention provides vectors and host cells for	
CC	recombinant production of Apo-2Dcr polypeptides, antibodies, and	
CC	transgenic and knockout animals (useful e.g. for screening and	
CC	developing drugs that protect against excessive apoptosis).	
CC	Apo-2Dcr, or chimeras comprising Apo-2Dcr or its (claimed)	
CC	extracellular domain fused to a heterologous polypeptide are used	
CC	to modulate apoptosis of mammalian cells (claimed) and/or NF-kappaB	
CC	activation by Apo-2 ligand, and may be expressed in vivo or ex vivo	
CC	for gene therapy. They can be used in methods for the modulation	
CC	and diagnosis of apoptosis e.g. in cases of neurodegeneration,	
CC	autoimmune diseases and inflammation. Most human tumor cells do	
CC	not express Apo-2Dcr transcripts, but normal tissues do, suggesting	
CC	that Apo-2Dcr may permit selective killing of cancer cells by Apo-2	
CC	ligand, possibly by protecting normal, but not cancerous, cells.	
XX		
SC	Sequence	259 AA:
OY	1 TSPGTPAPAAEETMTTSPG 19 	Query Match 100.0%; Score 100; DB 20; Best Local Similarity 100.0%; Pred. No. 5,4e-05; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dd	185 TSPTCPAPAEEtmtltspg 203	
RESULT 6		
AAU12321		
ID	AAU12321 standard; Protein; 259 AA.	
XX	AAU12321;	
AC		
XX		
DT	24-OCT-2001 (first entry)	
XX		
DE	Human PRO366 polypeptide sequence.	
XX		
KM	Human secretory and transmembrane; PRO; mammalian; cancer; lung;	
KW	brest; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;	
KW	cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;	
KW	adipocyte; A-peptide; factor VIIA; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PM	WO200140466-A2.	
XX		
PD	07-JUN-2001.	
PF	01-DEC-2000; 2000WO-US32678.	
XX		
PR	01-DEC-1999; 99WO-US28301.	
PR	01-DEC-1999; 99WO-US28634.	
PR	02-DEC-1999; 99WO-US28551.	
PR	02-DEC-1999; 99WO-US28564.	
PR	02-DEC-1999; 99WO-US28565.	
PR	09-DEC-1999; 99US-0170262.	
PR	16-DEC-1999; 99WO-US30095.	
PR	20-DEC-1999; 99WO-US30911.	
PR	20-DEC-1999; 99WO-US30999.	
PR	30-DEC-1999; 99WO-US31243.	
PR	06-JAN-2000; 2000WO-US00277.	
PR	06-JAN-2000; 2000WO-US00376.	
PR	11-FEB-2000; 2000WO-US03565.	
PR	18-FEB-2000; 2000WO-US04341.	
PR	18-FEB-2000; 2000WO-US04342.	
PR	22-FEB-2000; 2000WO-US04414.	
PR	24-FEB-2000; 2000WO-US04914.	
PR	24-FEB-2000; 2000WO-US05004.	



PR 01-MAR-2000; 2000MO-US05601.  
 PR 20-MAR-2000; 2000MO-US07377.  
 PR 21-MAR-2000; 2000MO-US07532.  
 PR 30-MAR-2000; 2000MO-US08439.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 10-NOV-2000; 2000MO-US30873.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 DR N-PSDB; AAF21393.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 XX  
 PS Claim 12; Fig 300; 813pp; English.  
 XX  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 CC  
 XX  
 SQ Sequence 259 AA;

Query Match 100.0%; Score 100; DB 22; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAETMTTSPG 19  
 |||  
 Db 185 tsptgtpapaaeetmttspg 203

RESULT 7  
 AAB20111  
 ID AAB20111 standard; Protein; 259 AA.  
 XX

AC AAB20111;

XX 30-APR-2001 (first entry)

DE Human immunostimulant PRO366 (Apo-2DCR).

XX PRO366: UNQ321; human; immune disease; autoimmune disease;  
 KW antineumatic; antiarthritic; antiinflammatory; antianemic;  
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
 KW hepatotropic; virocidic; dermatological; antipsoriatic;

KW antistimatic; antiallergic; immunostimulant; Apo-2DCR;  
 KW tumour necrosis factor receptor; apoptosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..29  
 FT /label= signal\_peptide  
 FT Protein 30..259  
 FT /label= Mature-Protein  
 FT Domain 240..257  
 FT /note= "transmembrane domain"  
 FT Region 85..92  
 FT /note= "TNFR/NGFR family cysteine-rich region"  
 FT Modified-site 126..130  
 FT /note= "CAMP- and cGMP-dependent protein kinase  
 FT phosphorylation site"  
 FT Modified-site 56..62  
 FT /note= "N-myristoylation site"  
 FT Modified-site 72..78  
 FT /note= "N-myristoylation site"  
 FT Modified-site 114..120  
 FT /note= "N-myristoylation site"  
 FT Modified-site 154..160  
 FT /note= "N-myristoylation site"  
 FT Modified-site 233..239  
 FT /note= "N-myristoylation site"  
 XX  
 XX W0200105972-A1.  
 XX  
 XX 25-JAN-2001.  
 XX  
 XX 15-MAR-2000; 2000MO-US06884.  
 XX  
 XX 20-JUL-1999; 99US-0144758.  
 PR  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 PI Hillan KJ, Mark MR, Masters SB, Pitti RM, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 XX WPI; 2001-103149/11.  
 DR N-PSDB; AAF30053.  
 XX  
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes  
 PT  
 PS Claim 20; Fig 8; 127pp; English.  
 XX  
 CC The present sequence is that of PRO366 (UNQ321), also designated  
 CC Apo-2DCR, a novel human immunomodulator (27 KDa, PI 4.84), as  
 CC deduced from a human breast carcinoma cDNA clone (see AAF30053).  
 CC Apo-2DCR shows homology to apoptosis-linked receptors of the tumour  
 CC necrosis factor receptor family, such as DR4 and Apo-2. The invention  
 CC provides polynucleotides (see AAF30050-62) encoding novel human PRO  
 CC proteins (see AAB20108-20) including PRO366. Claimed compositions  
 CC comprising these proteins or their agonists are useful for increasing  
 CC infiltration of inflammatory cells into a tissue of a mammal,  
 CC stimulating or enhancing an immune response, or increasing the  
 CC proliferation of T-lymphocytes in a mammal in response to an antigen.  
 CC Claimed compositions comprising a PRO polypeptide or its antagonist  
 CC have the opposite effect. A claimed method for treating an immune  
 CC related disorder, such as a T cell disorder, involves administering  
 CC a PRO polypeptide, an agonist antibody or an antagonist antibody.  
 CC The disorder is selected from systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,  
 CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory  
 CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia,  
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,  
 CC demyelinated diseases (such as multiple sclerosis), autoimmune

CC chronic active hepatitis, primary biliary cirrhosis, granulomatous  
CC hepatitis, sclerosing cholangitis, inflammatory bowel disease  
CC (ulcerative colitis and Crohn's disease), gluten-sensitive  
CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
CC (such as bullous skin disease, erythema multiforme and psoriasis),  
CC allergic diseases (such as asthma, allergic rhinitis, atopic  
CC dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
CC and a method of stimulating an immune response in a mammal using  
CC PRO366.  
XX  
SQ Sequence 259 AA:

Query Match 100.0%; Score 100; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTSPG 19  
|||  
Db 185 tsptpapaeeetmtspg 203

RESULT 8  
AAB36696  
ID AAB36696 standard; Protein: 259 AA.  
XX  
AC AAB36696;  
XX  
DT 15-MAR-2001 (first entry)  
XX  
DE Human tumour necrosis factor receptor 5 (TR5) protein SEQ ID NO:2.  
XX  
XX Human; tumour necrosis factor receptor 5; TR5; TNFR-5; TR5; nototropic;  
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
KW apoptotic cell death related disease; autoimmune disorder;  
KW cardiovascular disorder; viral infection.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200071150-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 18-MAY-2000; 2000WO-US13515.  
XX  
PR 20-MAY-1999; 99US-0135164.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Wei Y, Ruben SM, Gentz RL, Ni J;  
XX  
DR WPI; 2001-041051/05.  
XX  
DR N-PSDB; AAC90774.  
XX  
XX Nucleic acid encoding a TR5 polypeptide, also referred to as tumor  
PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
PT prevention of cancer, autoimmune disorders and viral infection -  
XX  
XX  
XX Claim 15; Fig 1; 285pp; English.  
XX  
XX The present sequence represents the human TR5 protein (tumour necrosis  
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
CC intracellular domain, also referred to as tumour necrosis factor

CC receptor 5 (TNFR-5 or TR5)). TR5 has cytostatic, immunosuppressive,  
CC nototropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
CC activities, and can be used in gene therapy. The TR5 polynucleotides  
CC are useful for detecting complementary polynucleotides. TR5 proteins and  
CC polynucleotides are useful in the treatment of tumours, resistance to  
CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
CC They are also useful for inducing proliferation of T-cells, endothelial  
CC cells and certain haematopoietic cells, to regulate antiviral responses  
CC and to prevent certain autoimmune diseases after stimulation of TR5 by  
CC an agonist or TRAIL binding facilitator. The antibodies which bind TR5  
CC polypeptides are useful for treating and/or preventing diseases  
CC associated with increased or decreased apoptotic cell death. The TR5  
CC polynucleotides, proteins, antibodies, agonists and antagonists are  
CC useful in the diagnosis, treatment or prevention of: (a) cancer;  
CC (b) autoimmune disorders; (c) diseases associated with increased  
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection.  
XX  
SQ Sequence 259 AA:

Query Match 100.0%; Score 100; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTSPG 19  
|||  
Db 185 tsptpapaeeetmtspg 203

RESULT 9  
AAB53091  
ID AAB53091 standard; Protein: 259 AA.  
XX  
AC AAB53091;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO366, SEQ ID NO:152.  
XX  
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX

PA (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WT;  
XX WPI: 2001-090793/10.  
DR N-PSDB: AAC97488.  
XX  
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
XX Claim 69; Fig 56; 293pp; English.  
XX  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
CC invention.  
XX  
XX Sequence 259 AA;  
SO

Query Match 100.0%; Score 100; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTTSPG 19  
|||||  
Db 185 tsptgtpapaaeetmttspg 203

RESULT 10  
AAB82181  
ID AAB82181 standard; Protein; 268 AA.  
XX  
XX AAB82181;  
XX  
XX 23-JUL-2001 (first entry)  
XX  
XX FLAG-TRID clone with a transmembrane domain.  
XX  
XX FLAG-epitope tag; transmembrane domain; death domain; apoptosis;  
KW cell suicide; tissue homeostasis; cell proliferation;  
KW cell-cell signalling; Trail Receptor without Intracellular Domain; TRID.  
XX

OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..23  
FT /label= Signal\_peptide  
FT Protein 24..268  
FT /label= FLAG-TRID\_protein  
FT Peptide 27..34  
FT /label= FLAG-epitope\_TAG  
FT Region 250..268  
FT /label= Transmembrane\_region  
XX  
XX WO200114542-A1.  
XX  
XX 01-MAR-2001.  
XX  
XX 23-AUG-2000; 2000WO-US23112.  
XX  
XX 25-AUG-1999; 99US-0150747.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Denome SA, Swain PM, Tzellas N;  
PI WPI: 2001-374162/39.  
DR N-PSDB: AAH19325.  
XX  
XX  
XX Identifying a transmembrane domain of a membrane-spanning protein  
PT useful in defining processes in cell suicide and tissue homeostasis,  
PT comprises modifying the nucleic acid encoding a death domain-lacking  
PT membrane spanning protein -  
XX  
XX  
XX Disclosure; Fig 1; 38pp; English.  
XX  
XX The present invention relates to methods for identifying a transmembrane  
CC domain (TM) of a membrane-spanning protein. The method comprises  
CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane  
CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID)  
CC by replacing the nucleic acid encoding the TM of the DD-lacking  
CC membrane-spanning protein with a candidate nucleic acid sequence to  
CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
CC protein. The modified nucleic acid is then transfected into a host cell,  
CC which expresses a DD-containing receptor. The absence of apoptosis of the  
CC host cell is determined following exposure of the transfected cell to an  
CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
CC apoptosis of the host cell. The modified nucleic acid encoding the  
CC modified death domain-lacking membrane-spanning protein can also include  
CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
CC a FLAG-TRID clone, which was used in the method of the present invention.  
CC This sequence comprises human TRID protein and the FLAG-epitope tag. The  
CC FLAG-epitope is a useful marker to purify proteins encoded by the  
CC modified DD-lacking membrane-spanning protein. The identified TM and  
CC membrane-spanning proteins may be used in defining processes involved in  
CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat  
CC events, such as cell proliferation and cell-cell signalling pathways.  
XX  
XX Sequence 268 AA;  
SQ

Query Match 100.0%; Score 100; DB 22; Length 268;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTTSPG 19  
|||||  
Db 194 tsptgtpapaaeetmttspg 212

RESULT 11  
AAW76331  
ID AAW76331 standard; Protein; 299 AA.  
XX  
XX AAW76331;  
AC

XX 11-JAN-1999 (first entry)  
 DT Human tumour necrosis related receptor TR5.  
 DE  
 XX  
 KW Tumour necrosis related receptor; TR5; human; inflammation;  
 KW arthritis; septicaemia; transplant rejection; autoimmune disease;  
 KW inflammatory bowel disease; graft versus host disease; infection;  
 KW stroke; ischaemia; acute respiratory disease syndrome; psoriasis;  
 KW stenosis; brain injury; AIDS; bone disease; cancer;  
 KW atherosclerosis; Alzheimer's disease; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..165  
 FT /label= Sig\_peptide  
 FT 66..299  
 FT /label= Mat\_protein  
 FT  
 XX  
 PN EP867509-A2.  
 XX  
 PD 30-SEP-1998.  
 XX  
 PF 04-FEB-1998; 98EP-0300827.  
 XX  
 PR 28-JUL-1997; 97US-0901469.  
 PR 05-FEB-1997; 97US-0795910.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PI Lyn SDP, Tan KB, Truneh A, Young PR;  
 XX  
 DR WP1: 1998-497862/43.  
 DR N-PSDB; AAV56990.  
 XX  
 XX New polynucleotide encoding TR5 polypeptide - used to diagnose,  
 PT prevent and treat e.g. Inflammation, arthritis, septicaemia,  
 PT autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis,  
 PT restenosis, brain injury, AIDS and bone diseases  
 XX  
 PS Claim 5; Fig 1; 22pp; English.  
 CC This is the amino acid sequence of human tumour necrosis related  
 CC receptor TR5, as deduced from the sequence of an isolated cDNA  
 CC clone (see AAV56990). The protein is characterised as a GPI-linked  
 CC protein that has a membrane proximal O-glycosylation region. The  
 CC invention provides methods for the recombinant production of TR5  
 CC and its use in diagnostic and therapeutic methods. Treatment of a  
 CC subject in need of enhanced TR5 activity comprises administering an  
 CC agonist to the polypeptide and/or providing TR5 polynucleotide in a  
 CC form so as to effect production of the polypeptide activity in vivo.  
 CC Treatment of a subject with the need to inhibit TR5 polypeptide  
 CC activity comprises administering an antagonist to the polypeptide,  
 CC administering a nucleic acid that inhibits the expression of the  
 CC nucleotide sequence encoding the polypeptide and/or administering a  
 CC polypeptide that competes with the polypeptide for its ligand,  
 CC substrate or receptor. Diagnosing a disease or a susceptibility  
 CC to a disease related to expression or activity of TR5 polypeptide,  
 CC comprises determining the presence or absence of mutation in the  
 CC nucleotide sequence encoding the TR5 polypeptide in the genome of  
 CC the subject and/or analysing for the presence or amount of TR5  
 CC polypeptide expression in a sample. Identification of compounds  
 CC which bind to TR5 comprises contacting host cells with a candidate  
 CC compound and assessing the ability of it to bind to the cells. The  
 CC active agents can be used for the treatment of chronic and acute  
 CC inflammation, arthritis, septicaemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis), transplant rejection,  
 CC graft vs host disease, infection, stroke, ischaemia, acute  
 CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone  
 CC diseases, cancer (e.g. lymphoproliferative disorders),  
 CC atherosclerosis and Alzheimer's disease.  
 CC  
 XX

SQL Sequence 299 AA;  
 Query Match 100.0%; Score 100; DB 19; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TSPGPAPAAEETMTSPG 19  
 ||||||||||||||||  
 DB 225 tsqgpapaaetmtspg 243  
 RESULT 12  
 AAY29864  
 ID AAY29864 standard; Protein; 299 AA.  
 XX  
 AC AAY29864;  
 XX  
 DT 17-NOV-1999 (first entry)  
 XX  
 DE Human secreted protein clone j1442\_1.  
 XX  
 KW Human; secreted protein; biological activity; nutritional; cytokine;  
 KW cell proliferation; differentiation; immune stimulating; vaccine;  
 KW haematopoiesis regulation; tissue growth; haemostatic; thrombolytic;  
 KW anti-inflammatory; tumour inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9346287-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 11-MAR-1999; 99WO-US05243.  
 XX  
 PR 11-MAR-1998; 98US-0077521.  
 PR 14-MAR-1998; 98US-0079124.  
 PR 10-MAR-1999; 99US-0266105.  
 XX  
 PA (GENY ) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MO, Steininger RJ;  
 XX  
 DR WP1: 1999-551362/46.  
 DR N-PSDB; AA221096.  
 XX  
 XX Polynucleotides encoding secreted human proteins, derived from human  
 PT fetal brain, human adult blood, human adult bladder, or human adult  
 PT neural tissue cDNA libraries.  
 XX  
 PS Claim 17; Page 104; 118pp; English.  
 CC AA221093 to AA221102 encode new human secreted proteins and AAY29861 to  
 CC AAY29873 represent the secreted proteins encoded by the polynucleotide  
 CC sequences. AA221103 to AA221112 represent probes for the secreted  
 CC proteins. The polynucleotides and proteins are predicted to have  
 CC biological activities which would make them suitable for treating,  
 CC preventing or ameliorating medical conditions in humans and animals,  
 CC although no supporting data is given. Suggested activities include  
 CC nutritional activity, cytokine and cell proliferation/differentiation  
 CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cadherin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity. The polynucleotides and proteins can also be used  
 CC as nutritional sources or supplements. Such uses include use as a protein  
 CC or amino acid supplement, use as a carbon source, use as a nitrogen  
 CC source and use as a source of carbohydrate. They may also have utility  
 CC in compositions used for bone, cartilage, tendon, ligament, and/or nerve  
 CC tissue growth or regeneration, as well as for wound healing and tissue  
 CC repair and replacement, and in the treatment of burns, incisions and

CC ulcers. The proteins which induce cartilage and/or bone growth in  
 CC circumstances where bone is not normally formed, have application in  
 CC the healing of bone fractures and cartilage damage or defects in humans  
 CC and other animals.

XX Sequence 299 AA;

Query Match 100.0%; Score 100; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAETMTSPG 19  
 |||||  
 Db 225 tsptpapaeeetmtspg 243

#### RESULT 13

AA05744  
 ID AAY05744 standard; Protein: 299 AA.

XX AAY05744;

XX 19-JUL-1999 (first entry)

DE Tumour necrosis factor receptor TR5.

XX Tumour necrosis factor receptor: TR5; TRID: DCRL; agonist;  
 KW antagonist; screening; human; cancer; AIDS; Alzheimer's disease;  
 KW inflammation; arthritis; septicemia; autoimmune disease;  
 KW psoriasis; inflammatory bowel disease; transplant rejection;  
 KW graft versus host disease; infection; stroke; ischaemia;  
 KW acute respiratory disease syndrome; restenosis; brain injury;  
 KW bone disease; atherosclerosis; therapy.

XX Homo sapiens.

PN EP911633-A1.

PD 28-APR-1999.

PF 02-OCT-1998; 98EP-0203332.

PR 08-OCT-1997; 97US-0061334.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PI McDonnell PC, Young PR, Zou J;

XX WPI; 1999-246560/21.

PT Identifying agonists and antagonists of tumor necrosis factor  
 PT related receptors TR1, TR3 and TR5, and of ligand TL3, useful for  
 PT treatment of cancer, AIDS, Alzheimer's disease, bone disease etc  
 PS Disclosure; Page 13-14; 23pp; English.

XX The present sequence represents tumor necrosis factor receptor  
 CC (TNFR) TR5, also known as TRID or DCRL. The invention relates  
 CC to TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and  
 CC their ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in  
 CC claimed methods of identifying agonists and antagonists, i.e.  
 CC compounds that bind to the receptors or ligand, and which activate  
 CC (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or  
 CC TR3. A screening kit for identifying agonists, antagonists,  
 CC ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or  
 CC TL3 polypeptides is provided. The agonists and antagonists are  
 CC useful for treatment of chronic and acute inflammation, arthritis,  
 CC septicemia, autoimmune disease e.g. inflammatory bowel disease,  
 CC psoriasis, transplant rejection, graft versus host disease,  
 CC infection, stroke, ischaemia, acute respiratory disease syndrome,  
 CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.  
 CC lymphoproliferative disorders), atherosclerosis and Alzheimer's

CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.

XX Sequence 299 AA;

Query Match 100.0%; Score 100; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAETMTSPG 19  
 |||||  
 Db 225 tsptpapaeeetmtspg 243

#### RESULT 14

AA00933  
 ID AAY00933 standard; Protein: 299 AA.

XX AAY00933;

XX 02-JUN-1999 (first entry)

DE Human TRAIL-R3 protein sequence.

XX Human; DR5; TRAIL-R3; apoptosis related condition; cancer; therapy;  
 KW autoimmune disease; viral infection; degenerative disorder;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischaemic injury;  
 KW cerebellar degeneration; myelodysplastic syndrome.

XX Homo sapiens.

PN WO9909165-A1.

PD 25-FEB-1999.

PF 14-AUG-1998; 98WO-US16945.

PR 15-AUG-1997; 97US-0055906.

XX (IDUN-) IDUN PHARM INC.

PI Alnemri ES;

XX WPI; 1999-181035/15.

DR N-PSDB; AAX27280.

PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
 PT protein - useful in for screening for (antagonists that modulate  
 PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
 PS Claim 16; Page 62-63; 71pp; English.

XX This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An  
 CC antibody against the TRAIL receptors is useful for detecting mammalian  
 CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
 CC bioassays for screening for (antagonists of DR5 or TRAIL-R3 proteins.  
 CC (Anti)agonists identified by the assay are useful for modulating the  
 CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
 CC related conditions which are treated in this way, include cancer  
 CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
 CC erythematosus and immune-mediated glomerulonephritis), viral infections  
 CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
 CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
 CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
 CC syndromes (e.g. aplastic anaemia) and ischemic injury (e.g. myocardial  
 CC infarction and stroke). The polynucleotides can also be used to treat  
 CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
 CC used to form a composition that is useful for inhibiting expression of a  
 CC human DR5 or TRAIL-R3 protein.

XX Sequence 299 AA;

Query Match 100.0%; Score 100; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETWTSPG 19  
 |||||  
 DB 225 tsptgtpapaaeetmtltspg 243

## RESULT 15

AAM94671  
 ID AAM94671 standard; Protein: 299 AA.

XX  
 AC AAM94671;

XX  
 DT 04-MAY-1999 (first entry)

XX  
 DE Human TNF-related apoptosis-inducing ligand binding protein.

XX  
 KW Human; TNF-related apoptosis-inducing ligand binding protein; clotting;

KW TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy;

KW thrombotic microangiopathy; thrombotic thrombocytopenic purpura;

XX  
 KW haemolytic-uraemic syndrome; systemic lupus erythematosus.

OS Homo sapiens.

XX  
 PN WO9900423-A1.

XX  
 PD 07-JAN-1999.

XX  
 PP 25-JUN-1998; 98WO-US13491.

XX  
 PR 26-JUN-1997; 97US-0883529.

XX  
 PA (IMMUNEX ) IMMUNEX CORP.

XX  
 PI Smith CA, Walczak H;

XX  
 DR WPI; 1999-095685/08.

XX  
 DR N-PSDB; AAX16692.

XX  
 PT New isolated TRAIL binding protein - which binds to a tumour

XX  
 PT necrosis factor-related apoptosis inducing ligand, used in the

XX  
 PT diagnosis and treatment of TRAIL-mediated disorders

XX  
 PS Claim 1: Fig 1; 47pp; English.

XX  
 CC The present sequence is human tumour necrosis factor (TNF)-related

XX  
 CC apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be

XX  
 CC used for inhibiting the biological activities of TRAIL or for purifying

XX  
 CC TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated

XX  
 CC disorder such as T cell death in HIV-infected patients. They can be used

XX  
 CC for treating thrombotic microangiopathies such as thrombotic

XX  
 CC thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small

XX  
 CC blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic

XX  
 CC acids can also be used for gene therapy. They can also be used as

XX  
 CC carriers for delivering attached agents to cells bearing TRAIL.

XX  
 SQ Sequence 299 AA;

Query Match 100.0%; Score 100; DB 20; Length 299;

Best Local Similarity 100.0%; Pred. No. 6.1e-05;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETWTSPG 19  
 |||||  
 DB 225 tsptgtpapaaeetmtltspg 243

Search completed: August 13, 2002, 08:31:30  
 Job time: 124 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 13, 2002, 08:30:04 ; Search time 28.27 Seconds  
(without alignments)  
64.581 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233  
Perfect score: 100  
Sequence: 1 TSPCTPAPAAEETMTTSPG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.0	801	2	T29018	hypothetical prote
2	52.0	878	2	T21621	hypothetical prote
3	51.0	2938	2	T30249	cell proliferation
4	50.0	292	2	S24189	mucin - rat
5	49.5	49.5	1	NDBE61	exonuclease (EC 3.
6	48.0	427	2	G71272	iron-sulfur cofact
7	48.0	433	2	S20963	homeotic protein H
8	48.0	650	2	T22002	hypothetical prote
9	48.0	846	2	T21700	hypothetical prote
10	48.0	1323	2	T30253	spalt protein - mo
11	48.0	1466	1	CGH07L	collagen alpha 1(I
12	47.0	284	2	S60743	secreted antigen P
13	47.0	284	2	F70888	probable p1ng prot
14	47.0	375	2	F75467	probable lipoprote
15	47.0	413	2	S76200	ferredoxin-NADP+
16	47.0	488	2	A27353	collagen alpha 1(I
17	47.0	495	2	AD2275	hypothetical prote
18	47.0	504	2	T13475	hypothetical prote
19	47.0	833	2	T22139	hypothetical prote
20	47.0	1049	1	CG807S	hypothetical prote
21	47.0	1464	2	SS9856	collagen alpha 1(I
22	46.5	228	2	T10507	ribulose-phosphate
23	46.0	107	2	A72701	hypothetical prote
24	46.0	285	2	H70594	hypothetical prote
25	46.0	347	2	T14313	hypothetical prote
26	46.0	424	2	T33663	hypothetical prote
27	46.0	514	2	A31643	cell adhesion 80K
28	46.0	905	1	RGBY55	regulatory protein
29	46.0	998	2	T35745	probable ATP-bind1

30	46	46.0	2440	2	S39162	transcription coac
31	46	46.0	7463	2	T36248	CDA peptide synthe
32	45.5	45.5	223	1	MEVNSV	matrix protein - s
33	45.5	45.5	583	2	F69153	conserved hypotet
34	45.5	45.5	651	2	T15624	hypothetical prote
35	45.5	45.5	2105	2	T18968	hypothetical prote
36	45	45.0	340	2	C70743	probable serine-ty
37	45	45.0	348	2	I49262	cyclin cdk inhibit
38	45	45.0	429	2	A48377	glutamate-1-semial
39	45	45.0	454	2	A56954	yes-associated pro
40	45	45.0	478	2	A32555	major mezoicote su
41	45	45.0	348	2	T27542	hypothetical prote
42	45	45.0	632	2	S42731	collagen alpha 1 c
43	45	45.0	736	2	T25447	hypothetical prote
44	45	45.0	896	2	I56563	interleukin-3 rece
45	45	45.0	1176	2	A49848	nitrite reductase

## ALIGNMENTS

## RESULT 1

T29018  
hypothetical protein ZK84.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000

C:Accession: T29018

R:Kirsten, J.

Submitted to the EMBL Data Library, April 1995  
A:Description: The sequence of C. elegans cosmid ZK84.

A:Reference number: 220553

A:Accession: T29018

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-801 <KIR>

A:Cross-references: EMBL:U23181; PIDN:MAC48204.1; GSPDB:GN00020; CESP:ZK84.1

A:Experimental source: strain Bristol N2; clone ZK84

C:Genetics:

A:Gene: CESP:ZK84.1

A:Map position: 2

A:Introns: 22/2; 45/3; 108/1

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 52.0% Score 52; DB 2; Length 801;  
Best Local Similarity 76.9% Pred. No. 26;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PAPAETMTTSP 18

Db 585 PAPAETMTTSP 597

RESULT 2  
T21621  
hypothetical protein F32A7.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T21621

R:Kershaw, J.

Submitted to the EMBL Data Library, November 1996

A:Reference number: Z19451

A:Accession: T21621

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-878 <WIL>

A:Cross-references: EMBL:Z83107; PIDN:CAR05498.1; GSPDB:GN00019; CESP:F32A7.5

A:Experimental source: clone F32A7

C:Genetics:

A:Gene: CESP:F32A7.5

A:Map position: 1

A:Introns: 74/3; 380/3; 439/3; 567/3; 728/3; 818/1

Query Match 52.0%; Score 52; DB 2; Length 878;  
Best Local Similarity 55.6%; Pred. No. 29;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETMTSP 18  
|:| | | | | | | | | |  
Db 354 TAPSKPAPAPASAAATSP 371

## RESULT 3

cell proliferation antigen Ki-67 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T30249  
R:Starborg, M.; Gell, K.; Brundell, E.; Hoog, C.  
J. Cell Sci. 109, 143-153, 1996  
A:Title: The murine Ki-67 cell proliferation antigen accumulates in the nucleolar and he  
1 for cell cycle progression.  
A:Reference number: 220787; MUID:96431717  
A:Accession: T30249  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2938 <SRA>  
A:Cross-references: EMBL:X82786; NID:g1177527; PIDN:CAA58026.1; PID:g1177528  
A:Experimental source: strain CBA; testis  
C:Genetics:  
A:Gene: Ki-67  
C:Keywords: cell cycle control; nucleus; tandem repeat

Query Match 51.0%; Score 51; DB 2; Length 2938;  
Best Local Similarity 62.5%; Pred. No. 1,4e+02;  
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 SPCGTPAPAAEETMTS 17  
| | | | | | | | | |  
Db 1863 SPGTPAPQENNDCTA 1878

## RESULT 4

mucin - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C:Accession: S24169  
R:Huan, L.J.; Xu, G.; Forstner, G.; Forstner, J.  
Biochim. Biophys. Acta 1132, 79-82, 1992  
A:Title: A serine, threonine and proline-rich region near the carboxyl-terminus of a rat  
A:Reference number: S24169; MUID:92379096  
A:Accession: S24169  
A:Molecule type: mRNA  
A:Residues: 1-292 <HUA>

Query Match 50.0%; Score 50; DB 2; Length 292;  
Best Local Similarity 36.4%; Pred. No. 17;  
Matches 12; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

OY 1 TSPGTPAPAAEETMTSPG 19  
| | | | | | | | | |  
Db 116 TSPSPSPPESTTLSTPTTTATSTSTSSPG 148

## RESULT 5

NDBE61  
exonuclease (EC 3.1.11.-) - human herpesvirus 1 (strain 17)  
N:Alternate names: gene UL12 protein (deoxyribonuclease)  
C:Species: human herpesvirus 1  
A:Note: host Homo sapiens (man)  
C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 16-Jun-2000  
C:Accession: A00781; C30083

R:McGeoch, D.J.; Dolan, A.; Frame, M.C.  
Nucleic Acids Res. 14, 3435-3448, 1986  
A:Title: DNA sequence of the region in the genome of herpes simplex virus type 1 cont  
A:Reference number: A93620; MUID:86205244  
A:Accession: A00781

A:Molecule type: DNA  
A:Residues: 1-626 <MCG>  
A:Cross-references: GB:X03839; NID:g959841; PIDN:CAA27453.1; PID:g959844  
R:McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P  
J. Gen. Virol. 69, 1531-1574, 1988  
A:Title: The complete DNA sequence of the long unique region in the genome of herpes  
A:Reference number: A30083; MUID:86274327  
A:Accession: C30083  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-626 <MCG>  
A:Cross-references: GB:X14112; NID:g1944536; PIDN:CAA3325.1; PID:g959513; GB:BD0317  
C:Genetics:  
A:Gene: UL12  
A:Map position: 0.16-0.20  
C:Superfamily: herpesvirus exonuclease  
C:Keywords: exonuclease; hydrolase

Query Match 49.5%; Score 49.5; DB 1; Length 626;  
Best Local Similarity 64.7%; Pred. No. 44;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 2 SPCGTPAPAAEETMTSP 18  
| | | | | | | | | |  
Db 604 SPG-PGPAAEETSSSP 619

## RESULT 6

iron-sulfur cofactor synthesis protein nifs2 TP0863 [similarity] - syphilis spirochet  
G71272  
N:Contains: L-cysteine sulfurtransferase (EC 2.8.1.-)  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: G71272  
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; M  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770  
A:Accession: G71272  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-427 <COL>  
A:Cross-references: GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AC65826.1; PID:g332  
A:Experimental source: strain Nichols  
C:Genetics:  
A:Gene: TP0863  
C:Superfamily: nitrogen fixation protein nifs  
C:Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase  
F:23/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted  
F:374/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 48.0%; Score 48; DB 2; Length 427;  
Best Local Similarity 52.9%; Pred. No. 47;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETMTS 17  
| | | | | | | | | |  
Db 209 TPCTPAPTAQRAALYS 225

## RESULT 7

S20963  
homeotic protein Hox B3 - mouse  
N:Alternate names: homeotic protein Hox 2.7

C:Species: Mus musculus (house mouse)  
 C:Date: 22-Nov-1993 #sequence\_revision 21-Jul-1995 #text\_change 20-Aug-1999  
 C:Accession: S20963; D42694  
 R:Sham, M.H.; Hunt, P.; Nonchev, S.; Papalopulu, N.; Graham, A.; Boncinelli, E.; Krumlauf  
 EMOJ. 11, 1825-1836, 1992  
 A:Title: Analysis of the murine Hox-2.7 gene: conserved alternative transcripts with dif  
 A:Reference number: S20963; MUID:92258392  
 A:Accession: S20963  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-433 <SHA>  
 A:Cross-references: GB:X66177; GB:S35629; GB:S35738; NID:g312229; PIDN:CAA46951.1; PID:g  
 R:Nazarelli, A.; Kim, Y.; Nirenberg, M.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2883-2887, 1992  
 A:Title: Hox-1.11 and Hox-4.9 homeobox genes.  
 A:Reference number: A42694; MUID:92212934  
 A:Accession: D42694  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 213-238 <NAZ>  
 A:Note: sequence extracted from NCBI backbone (NCBIN:92310, NCBI:P:92316)  
 C:Superfamily: homeotic protein Hox B3; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:192-248/Domain: homeobox homology <HOX>

Query Match 48.0%; Score 48; DB 2; Length 433;  
 Best Local Similarity 60.0%; Pred. No. 48;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 PGTPAPAAEETMTTS 17  
 ||:|:|:|:|:|:|  
 Db 87 PGSPPPSAAPTSTTS 101

RESULT 8  
 T22002  
 hypothetical protein F39H11.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T22002  
 R:White, S.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19500  
 A:Accession: T22002  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-650 <NIL>  
 A:Cross-references: EMBL:Z81079; PIDN:CAH03084.1; GSPDB:GN00019; CESP:F39H11.4  
 A:Experimental source: clone F39H11  
 C:Genetics:  
 A:Gene: CESP:F39H11.4  
 A:Map position: 1  
 A:Introns: 109/3; 154/1; 357/1; 420/3; 464/3; 566/2; 594/1; 628/3

Query Match 48.0%; Score 48; DB 2; Length 650;  
 Best Local Similarity 60.0%; Pred. No. 73;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 SPCTPAPAAEETMTT 16  
 :||:|:|:|:|:|:|  
 Db 346 AFGAPAPAYGTTLT 360

RESULT 9  
 T21700  
 hypothetical protein F33E2.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T21700  
 R:Lennard, N.  
 submitted to the EMBL Data Library, January 1997

A:Reference number: Z19461  
 A:Accession: T21700  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-846 <NIL>  
 A:Cross-references: EMBL:Z84574; PIDN:CAH06541.1; GSPDB:GN00019; CESP:F33E2.6  
 A:Experimental source: clone F33E2  
 C:Genetics:  
 A:Gene: CESP:F33E2.6  
 A:Map position: 1  
 A:Introns: 99/3; 213/3; 332/3; 525/3

Query Match 48.0%; Score 48; DB 2; Length 846;  
 Best Local Similarity 56.2%; Pred. No. 95;  
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 3 PGTPAPAAEETMTTSP 18  
 ||:|:|:|:|:|:|  
 Db 796 PGTEAPPTTEAPMTTTP 811

RESULT 10  
 T30253  
 spalt protein - mouse (fragment)  
 N:Alternate names: zinc finger protein msal  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
 C:Accession: T30253  
 R:Ott, T.; Kaestner, K.H.; Monaghan, A.P.; Schutz, G.  
 Mech. Dev. 56, 117-128, 1996  
 A:Title: The mouse homolog of the region specific homeotic gene spalt of Drosophila  
 A:Reference number: Z20791; MUID:96391179  
 A:Accession: T30253  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: mRNA  
 A:Residues: 1-1323 <OTT>  
 A:Cross-references: EMBL:X97581; NID:g1296844; PIDN:CAA66196.1; PID:g1296845  
 C:Genetics:  
 A:Gene: msal  
 C:Function:  
 A:Description: may play an important role in the development of the nervous system

Query Match 48.0%; Score 48; DB 2; Length 1323;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 SPCTPAPAAEETMTTSPG 19  
 ||:|:|:|:|:|:|  
 Db 530 SPQRPPASSECTSLSPG 547

RESULT 11  
 CGH07L  
 collagen alpha 1(III) chain precursor - human  
 N:Alternate names: procollagen alpha 1(III) chain  
 C:Species: Homo sapiens (hmn)  
 C:Date: 24-Apr-1984 #sequence\_revision 01-Sep-1995 #text\_change 21-Jul-2000  
 C:Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868; S59511;  
 R:Prockop, D.J.  
 submitted to the EMBL Data Library, February 1989  
 A:Reference number: S05272  
 A:Accession: S05272  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1240, 'V', 1242-1466 <PRC>  
 A:Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058  
 R:Ala-Kokko, L.; Kontusari, S.; Baldwin, C.T.; Kulvanliem, H.; Prockop, D.J.  
 Biochem. J. 260, 509-516, 1989  
 A:Title: Structure of cDNA clones coding for the entire prepro-alpha1(III) chain of h  
 erences.  
 A:Reference number: S04642; MUID:89350838

A:Accession: S04642  
A:Molecule type: mRNA  
A:Residues: 1-1196 <ALA>  
A:Cross-references: EMBL:X14420; NID:930057; PIDD:CAA32583.1; PID:930058  
A:Note: the complete sequence is not shown  
R:Benson-Chanda, V.; Su, M.W.; Well, D.; Chu, M.L.; Ramirez, F.  
Gene 78, 253-265, 1989  
A:Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene  
A:Reference number: PE0011; MUID:93378752  
A:Accession: PE0011  
A:Molecule type: DNA  
A:Residues: 1-176 <BEN>  
A:Cross-references: GB:M2639; NID:9180813; PIDD:AAA52040.1; PID:9180814  
R:Toman, P.D.; Ricca, G.A.; de Crombrughe, B.  
Nucleic Acids Res. 16, 7201, 1988  
A:Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pre  
A:Reference number: S01726; MUID:88303360  
A:Accession: S01726  
A:Molecule type: mRNA  
A:Residues: 1-170 <TOM>  
A:Cross-references: EMBL:X07240; NID:930060; PIDD:CAA30229.1; PID:930061  
A:Note: the authors translated the codon CAG for residue 154 as His  
R:Janeczko, R.A.; Ramirez, F.  
Nucleic Acids Res. 17, 6742, 1989  
A:Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.  
A:Reference number: S04887; MUID:89386015  
A:Accession: S04887  
A:Molecule type: mRNA  
A:Residues: 149-163, 'G', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634,  
A:Cross-references: EMBL:X15333; NID:929645; PIDD:CAA33387.1; PID:930045  
A:Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide  
R:Sejer, J.M.; Kang, A.H.  
Biochemistry 16, 1158-1164, 1977  
A:Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide  
A:Reference number: A90399; MUID:77134724  
A:Accession: A90399  
A:Molecule type: protein  
A:Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SEY1>  
A:Experimental source: liver  
A:Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact  
R:Sejer, J.M.  
submitted to the Atlas, December 1977  
A:Reference number: A94562  
A:Accession: A94562  
A:Molecule type: protein  
A:Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SEY2>  
A:Experimental source: liver  
A:Note: author submitted corrections to A90399  
R:Milewicz, D.M.; Wiltz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.  
Am. J. Hum. Genet. 53, 62-70, 1993  
A:Title: Parental somatic and germ-line mosaicism for a multexon deletion with unusual  
ispring.  
A:Reference number: I51868; MUID:93304430  
A:Accession: I51868  
A>Status: preliminary: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 186-194 <MIL>  
A:Cross-references: GB:S62925; NID:9386425; PIDD:AA13937.1; PID:94261637  
R:Chiodo, A.A.; Silience, D.O.; Cole, W.G.; Bateman, J.F.  
Biochem. J. 311, 939-943, 1995  
A:Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3  
A:Reference number: S59511; MUID:96067614  
A:Accession: S59511  
A:Molecule type: mRNA  
A:Residues: 302-423 <CHR>  
A:Cross-references: GB:S79877; NID:91195576; PIDD:AA35615.1; PID:91195577  
R:Sejer, J.M.; Kang, A.H.  
Biochemistry 17, 3404-3411, 1978  
A:Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe  
A:Reference number: A90414; MUID:79000343  
A:Accession: A90414  
A:Molecule type: protein  
A:Residues: 399-675, 'N', 677-727 <SEY3>

A:Experimental source: liver  
R:Lee, B.; Vitale, E.; Superli-Furga, A.; Steinmann, B.; Ramirez, F.  
J. Biol. Chem. 266, 5256-5259, 1991  
A:Title: G to T transversion at position +5 of a splice donor site causes skipping of  
A:Reference number: I55349; MUID:91161621  
A:Accession: I55349  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 537-605 <LEE>  
A:Cross-references: GB:M59312; NID:9180815; PIDD:AAA52041.1; PID:9180816  
R:Sejer, J.M.; Mainardi, C.; Kang, A.H.  
Biochemistry 19, 1583-1589, 1980  
A:Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from  
A:Reference number: A90438; MUID:80198282  
A:Accession: A90438  
A:Molecule type: protein  
A:Residues: 728-895, 'A', 897-964 <SEY4>  
A:Experimental source: liver  
R:Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; C  
J. Biol. Chem. 265, 17070-17077, 1990  
A:Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping  
A:Reference number: A38303; MUID:91009133  
A:Accession: A38303  
A:Molecule type: mRNA  
A:Residues: 861-1015 <COL>  
A:Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:9180878; PIDD:AA59383.1; PI  
A:Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos  
R:Mankoo, B.S.; Dalgleish, R.  
Nucleic Acids Res. 16, 2337, 1988  
A:Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.  
A:Reference number: S02119; MUID:88189827  
A:Accession: S02119  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>  
A:Cross-references: EMBL:X06700; NID:930053; PIDD:CAA29886.1; PID:930054  
R:Sejer, J.M.; Kang, A.H.  
Biochemistry 20, 2621-2627, 1981  
A:Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from  
A:Reference number: A90446; MUID:81208139  
A:Accession: A90446  
A:Molecule type: protein  
A:Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 11  
A:Experimental source: liver  
R:Loide, H.R.; Brinker, J.M.; May, M.; Pihlajantemi, T.; Morrow, S.; Rosenbloom, J.  
Nucleic Acids Res. 12, 9383-9394, 1984  
A:Title: Molecular cloning and carboxyl-propeptide analysis of human type III procoll  
A:Reference number: A93551; MUID:85087944  
A:Accession: A93551  
A:Molecule type: mRNA  
A:Residues: 1065-1155, 'P', 1157-1466 <LOI>  
A:Cross-references: EMBL:X01655; EMBL:X01742; NID:929584; PIDD:CAA25821.1  
R:Miskulin, M.; Dalgleish, R.; Kluge-Beckerman, B.; Renhard, S.I.; Tolstoshev, P.; Br  
Biochemistry 25, 1408-1413, 1986  
A:Title: Human type III collagen gene expression is coordinately modulated with the c  
A:Reference number: I52393; MUID:86187804  
A:Accession: I52393  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1161-1200 <MIS>  
A:Cross-references: GB:M13146; NID:9180415; PIDD:AAA52003.1; PID:9180416  
R:Emmanuel, B.S.; Cammizzaro, L.A.; Sejer, J.M.; Myers, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985  
A:Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long  
A:Reference number: I59025; MUID:85216505  
A:Accession: I59025  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1165-1196 <EMA>  
A:Cross-references: GB:M11134; NID:9180417; PIDD:AAA52004.1; PID:9180418  
R:Chu, M.L.; Well, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.  
J. Biol. Chem. 260, 4357-4363, 1985  
A:Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(III) collagen

A:Reference number: A92516; MUID:85157600  
A:Accession: A92516  
A:Molecule type: DNA  
A:Residues: 1176-1240, 'V', 1242-1356, 'P', 1358-1466 <CHUD>  
A:Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB:M10798  
A:Experimental source: liver  
A>Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given for the other residues are as shown  
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit of collagen are 3-hydroxylated. About 15% of the lysines are 3-hydroxylated and some are subsequently modified.  
C:Genetics:  
A:Gene: GDB:COL3A1  
A:Cross-references: GDB:118729; OMIM:120180  
A:Map position: 2q31-2q31  
A:Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3  
A>Note: the 11st of introns is incomplete; defects in this gene can result in Ehlers-Danlos syndrome  
C:Complex: type III collagen is a homotrimer of monomers initially linked by disulfide bonds. The length of the chain is formed with desmosine cross-links made from lysine and allysine  
C:Function:  
A:Description: structural component of extracellular fibrous polymer that maintains integrity of connective tissue  
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C:Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hydroxyproline; signal sequence; status predicted <STG>  
F:1-23/Domain: signal sequence; status predicted <STG>  
F:24-153/Domain: amino-terminal propeptide; status predicted <PRO>  
F:31-91/Domain: von Willebrand factor type C repeat homology <VWC>  
F:154-1221/Product: collagen alpha 1(I) chain; status predicted <MAT>  
F:154-167/Region: amino-terminal nonhelical telopeptide  
F:168-1196/Region: helical  
F:1091-1093/Region: cell attachment (R-G-D) motif  
F:1197-1221/Region: carboxyl-terminal nonhelical telopeptide  
F:1222-1466/Domain: carboxyl-terminal propeptide; status predicted <CPR>  
F:1338-1466/Domain: fibrillar collagen carboxyl-terminal homology <CC>  
F:24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:153-154/Cleavage site: pro-Gln (procollagen N-endopeptidase) #status predicted  
F:154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:161,1212/Modified site: allysine (Lys) #status predicted  
F:263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental  
F:263/Binding site: carboxylate (Lys) (covalent) #status experimental  
F:584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental  
F:948-949/Cleavage site: Gly-Ile (collagenase) #status experimental  
F:1106/Binding site: carboxylate (Lys) (covalent) #status predicted

Query Match 48.0%; Score 48; DB 1; Length 1466;  
Best Local Similarity 44.4%; Pred. No. 1.7e+02;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SPGTPAPAAEETMTSPG 19  
Db 1117 APGSPGAGGAGGAGSPG 1134  
:|||||::|

RESULT 12  
S60743  
secreted antigen P36/P34 precursor - Mycobacterium bovis  
C:Species: Mycobacterium bovis  
C>Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S60743  
R:Bigli, F.; Alitto, A.; Fisanotti, J.C.; Romano, M.I.; Cataldi, A.  
Infect. Immun. 63, 2581-2586, 1995  
A:Title: Characterization of a novel Mycobacterium bovis secreted antigen containing PG  
A:Reference number: S60743; MUID:95310015  
A:Accession: S60743  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-284 <BIG>  
A:Cross-references: EMBL:Z48749  
C:Genetics:  
A:Start codon: GTG

Qy 1 TSPGTPAPAAEETMTSPG 19  
Db 100 TSPGTPGGLTDPALTSFG 118  
:|||||:|

RESULT 13  
F70888  
probable pirc protein - Mycobacterium tuberculosis (strain H37Rv)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: F70888  
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, R.; Johnson, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellern, S.; Squares, S.; Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987  
A:Accession: F70888  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-284 <COL>  
A:Cross-references: GB:AL022076; GB:AL123456; NID:93256026; PIDN:CAA17874.1; PID:el25  
A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: pirc

Query Match 47.0%; Score 47; DB 2; Length 284;  
Best Local Similarity 47.4%; Pred. No. 42;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TSPGTPAPAAEETMTSPG 19  
Db 100 TSPGTPGGLTDPALTSFG 118  
:|||||:|

RESULT 14  
F75467  
probable lipoprotein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C:Accession: F75467  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1  
A:Reference number: A75250; MUID:20036896  
A:Accession: F75467  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-375 <WHT>  
A:Cross-references: GB:AE001939; GB:AE000513; NID:96458563; PIDN:AAE10427.1; PID:9645  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR0848  
A:Map position: 1

Query Match 47.0%; Score 47; DB 2; Length 375;  
Best Local Similarity 52.9%; Pred. No. 56;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SPGTPAPAAEETMTSPG 18  
Db 67 TPATPAPAPATPAP 83  
:|||||:|

RESULT 15  
S76200  
ferredoxin-NADP+ reductase (EC 1.18.1.2) precursor - Synechocystis sp. (strain PCC 6

C:Species: *Synechocystis* sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C:Accession: S76200  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
 DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
 S.  
 A:Reference number: S74322; MUID:97061201  
 A:Accession: S76200  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-413 <KAN>  
 A:Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18459.1; PID:g165354  
 A:Experimental source: PCC 6803  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C:Genetics:  
 A:Gene: petH  
 C:Complex: monomer  
 C:Function:  
 A:Description: catalyzes electron transfer from reduced ferredoxin to NADP  
 A:Pathway: photosynthesis  
 A:Note: FAD cofactor  
 C:Superfamily: ferredoxin-NADP+ reductase; cytochrome-b5 reductase homology  
 C:Keywords: electron transfer; FAD; flavoprotein; NADP; oxidoreductase; photosynthesis  
 F:1-112/Domain: signal sequence #status predicted <SIG>  
 F:113-413/Product: ferredoxin-NADP+ reductase #status predicted <MAT>  
 F:121-260/Domain: FAD binding #status predicted <FAD>  
 F:143-398/Domain: cytochrome-b5 reductase homology <CBR>  
 F:261-413/Domain: NADP binding #status predicted <NADP>

Query Match 47.0%; Score 47; DB 2; Length 413;  
 Best Local Similarity 61.5%; Pred. No. 62;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 PAPAETMTTSP 18  
 ||| : ||||:|  
 Db 105 PAPSNTMTTTP 117

Search completed: August 13, 2002, 08:30:05  
 Job time: 39 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:36:16 ; Search time 15.81 Seconds

(without alignments)  
46.532 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233

Perfect score: 100

Sequence: 1 TSPGTPAPAAETMTTSPG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	259	1 T10C_HUMAN	O14798 h tumor nec
2	54	54.0	440	1 T10B_HUMAN	O14763 homo sapien
3	49.5	49.5	626	1 EXON_HSV11	P04294 herpes simp
4	48	48.0	433	1 HXB3_MOUSE	P09026 mus musculu
5	48	48.0	559	1 FZD1_XENLA	Q919m5 xenopus lae
6	48	48.0	984	1 SX13_MOUSE	O04891 mus musculu
7	48	48.0	1466	1 CA13_MOUSE	P02461 homo sapien
8	47	47.0	284	1 ERP_MYCTU	Q50793 mycobacteri
9	47	47.0	413	1 FENR_STNY3	Q35318 synchocyst
10	47	47.0	1049	1 CA13_BOVIN	P04258 bos taurus
11	47	47.0	1464	1 CA13_MOUSE	P08121 mus musculu
12	47	47.0	2261	1 ABC1_HUMAN	Q95477 homo sapien
13	46.5	46.5	228	1 RPE_RHOCA	P51012 rhodobacter
14	46	46.0	514	1 CSA_DICT1	P08796 dictyosteli
15	46	46.0	706	1 Z131_CHICK	Q90623 gallus gall
16	46	46.0	905	1 SNF5_YEAST	P18480 saccharomyc
17	46	46.0	2442	1 CBP_HUMAN	Q92793 homo sapien
18	45.5	45.5	223	1 VMAP_SVCV	P04888 spring viro
19	45	45.0	275	1 TFE2D_ARPSF	O17488 artemia san
20	45	45.0	340	1 Y480_MYCTU	Q11146 mycobacteri
21	45	45.0	348	1 CDNC_MOUSE	P49919 mus musculu
22	45	45.0	429	1 GSA_XANCH	Q06741 xanthomonas
23	45	45.0	454	1 YAG5_HUMAN	P46937 homo sapien
24	45	45.0	652	1 YD84_HUMAN	Q92923 homo sapien
25	45	45.0	1176	1 NIR_NEURC	P38681 neurospora
26	44.5	44.5	398	1 CIW4_MOUSE	O88434 mus musculu
27	44	44.0	252	1 BTE4_HUMAN	Q08656 ratu
28	44	44.0	333	1 HXAI_RAT	Q14242 homo sapie
29	44	44.0	412	1 SEPL_HUMAN	P11557 escherichia
30	44	44.0	427	1 DAMX_ECOLI	O83500 treponema p
31	44	44.0	525	1 Y487_TREPA	P07359 homo sapie
32	44	44.0	626	1 GPBA_HUMAN	P46557 caenorhabdi
33	44	44.0	781	1 YK67_CAEEL	

34	44	44.0	889	1 ENV_STVSP	P19503 simian immu
35	44	44.0	1670	1 CA34_HUMAN	O01955 homo sapien
36	43.5	43.5	839	1 APB1_RAT	O35430 rattus norv
37	43	43.0	137	1 GILZ_MOUSE	O92857 mus musculu
38	43	43.0	205	1 YJ11_MYCTU	O07722 mycobacteri
39	43	43.0	261	1 LPRF_MYCTU	P71798 mycobacteri
40	43	43.0	331	1 HXAI_MOUSE	P09022 mus musculu
41	43	43.0	351	1 OPSP_CHICK	P51475 gallus gall
42	43	43.0	384	1 VASP_CANFA	P50551 canis fami
43	43	43.0	427	1 GSA_PASMU	Q9C99 pasteurella
44	43	43.0	431	1 HXB3_HUMAN	P14651 homo sapien
45	43	43.0	432	1 GSA_VIBCH	O9ku97 vibrio chol

## ALIGNMENTS

RESULT 1  
T10C\_HUMAN STANDARD; PRT; 259 AA.  
AC 014798: 014755:  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10C precursor (Decoy receptor 1) (DCR1) (Decoy TRAIL receptor without death domain) (TNF-related apoptosis-inducing ligand receptor 3) (TRAIL receptor-3) (TRAIL-R3) (TRAIL receptor without an intracellular domain) (Lymphocyte inhibitor of TRAIL) (Antagonist decoy receptor for TRAIL/Apo-2L).  
GN TNFRSF10C OR DCR1 OR TRAILR3 OR TRID OR LIT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=97467318; PubMed=9325248;  
RA MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;  
RT "Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";  
J. Biol. Chem. 272:25417-25420(1997).  
RN [2]  
RP MEDLINE=97461602; PubMed=9314565;  
RA Degli-Esposti M.A., Smolak P.J., Walczak H., Waugh J., Huang C.-P., Dubose R.E., Goodwin R.G., Smith C.A.;  
RT "Cloning and characterization of TRAIL-R3, a novel member of the emerging TRAIL receptor family.";  
J. Exp. Med. 186:1165-1170(1997).  
RN [3]  
RP MEDLINE=97390508; PubMed=9242610;  
RA Pan G., Ni J., Wei Y.-F., Yu G.-L., Gentz R., Dixit V.M.;  
RT "An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";  
Science 277:815-818(1997).  
RN [4]  
RP MEDLINE=97390509; PubMed=9242611;  
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M., Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I., Goddard A.D., Godowski P., Ashkenazi A.;  
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy receptors.";  
Science 277:818-821(1997).  
RN [5]  
RP MEDLINE=98039016; PubMed=9373179;  
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,

	Query Match Similarity	100.0%;	Score 100;	DB 1;	Length 259;	
	Best Local Similarity	100.0%;	Pred. NO. 3.2e-06;			
	Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1 TSPGTPAPAAEETMTTSPG 19					
Db	185 TSPGTPAPAAEETMTTSPG 203					
RESULT#	2					
ID	T10B_HUMAN	STANDARD:	PRT: 440 AA.			
AC	Q15763; Q15531; O15508; O15517; O14720; Q9BYE0;					
DT	16-OCT-2001 (Rel. 40, Created)					
DI	16-OCT-2001 (Rel. 40, Last sequence update)					
DE	01-MAR-2002 (Rel. 41, Last annotation update)					
DE	Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL receptor-2) (TRAIL-R2).					
GN	TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
NCBI_TaxID=9606;	[1]					
RP	SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF N-TERMINUS.					
KC	TISSUE=Foreskin fibroblast;					
RX	MEDLINE=97453925; PubMed=9311998;					
RX	Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y., Bojani N.B., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Goodwin R.G., Rauch C.T.;					
RA	"TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";					
RT	EMBO J. 16:5386-5397(1997).					
RL	[2]					
RN	SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE SPLICING.					
RP	MEDLINE=97431692; PubMed=9285725;					
RX	Screation G.R., Mongkolkeha J., Xu X.-N., Cowper A.E., McMichael A.J., Bell J.I.,					
RA	"TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL.";					
RT	Curr. Biol. 7:693-696(1997).					
RL	[3]					
RN	SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.					
RP	TISSUE=Liver and Spleen;					
RC	TISSUE=Ovary;					
RX	MEDLINE=97467719; PubMed=9326928;					
RA	Wu G.-S., Burns T.F., McDonald E.R. II, Jiang W., Meng R., Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R., Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;					
RT	"KILLER/DIF5 Is a DNA damage-inducible p53-regulated death receptor gene.";					
RL	Nat. Genet. 17:141-143(1997).					
RN	[5]					
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).					
RX	MEDLINE=97390508; PubMed=9242610;					
RA	Pan G., Ni J., Wei Y.-F., Yu G.-T., Gentz R., Dixit V.M.;					
RT	"An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";					
RL	Science 277:815-818(1997).					
RN	[6]					
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).					
RX	MEDLINE=97467316; PubMed=9325248;					
RA	MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;					



RT "Identification and molecular cloning of two novel receptors for the  
RT cytotoxic ligand TRAIL.";  
RT J. Biol. Chem. 272:25417-25420(1997).  
RN [7]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=98090092; PubMed=9430227;  
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
RT Immunity 7:821-830(1997).  
RN [8]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=97390509; PubMed=9242611;  
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,  
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,  
RA Goddard A.D., Godowski P., Ashkenazi A.;  
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy  
RT receptors.";  
RT Science 277:818-821(1997).  
RN [9]  
RP SEQUENCE FROM N.A. (LONG ISOFORM).  
RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;  
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2  
RT gene in colorectal carcinoma.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RA Cao X., Zhang W., Man T.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RA Parish T., Vu T., Gilbert T., Gross J., O'Hara P.;  
RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A. (LONG ISOFORM).  
RA Strausberg R.;  
RC TISSUE=Cervix;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
RX MEDLINE=20017034; PubMed=10549288;  
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M.,  
RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
RT "Triggering cell death: the crystal structure of ApozL/TRAIL in a  
RT complex with death receptor 5.";  
RL Mol. Cell 4:563-571(1999).  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
RX PubMed=10542098;  
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
RT Jones E.Y., Screaton G.R.;  
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
RT specificity in apoptotic initiation.";  
RL Nat. Struct. Biol. 6:1048-1053(1999).  
CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates  
CC apoptosis in a caspase-dependent manner. Can trigger the nuclear  
CC factor kappaB-pathway and can bind the cytoplasmic adapter  
CC molecule FADD/MORT1 which engages initiator caspases such as  
CC caspase 8 leading to subsequent activation of effector caspases  
CC that execute apoptotic death of the cell.  
CC -1- SUBUNIT: Homotrimer (Potential). Can interact with TRADD and RIP.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS. A LONG FORM/TRICK2B (SHOWN HERE)  
CC AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
CC very highly expressed in tumor cell lines such as HeLa S3, K562,  
CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral  
CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
CC the intestinal tract; not detectable in brain.  
CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.  
CC -1- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell

CC carcinoma of the head and neck.  
CC -1- SIMILARITY: CONTAINS 1 IA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
CC -----  
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CC -----  
DR EMBL: AF016849; AAC51778.1; -  
DR EMBL: AF018657; AAB70577.1; -  
DR EMBL: AF018658; AAB70578.1; -  
DR EMBL: AF016266; AAB81180.1; -  
DR EMBL: AF022386; AAB71949.1; -  
DR EMBL: AF012628; AAB67109.1; -  
DR EMBL: AF020501; AAB71412.1; -  
DR EMBL: AF016268; AAC01565.1; -  
DR EMBL: AF012535; AAB67103.1; -  
DR EMBL: AB014718; BAA33723.1; -  
DR EMBL: AB014710; BAA33723.1; JOINED.  
DR EMBL: AB014711; BAA33723.1; JOINED.  
DR EMBL: AB014712; BAA33723.1; JOINED.  
DR EMBL: AB014713; BAA33723.1; JOINED.  
DR EMBL: AB014714; BAA33723.1; JOINED.  
DR EMBL: AB014715; BAA33723.1; JOINED.  
DR EMBL: AB014716; BAA33723.1; JOINED.  
DR EMBL: AB014717; BAA33723.1; JOINED.  
DR EMBL: AF153687; AAF75587.1; -  
DR EMBL: AF192548; AAF07175.1; -  
DR EMBL: BC001281; AAH01281.1; -  
DR MIM: 603612; -  
DR MIM: 601400; -  
DR PDB: 1D0G; 22-OCT-99.  
DR PDB: 1D4V; 01-NOV-99.  
DR InterPro: IPR000488; Death.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00531; death; 1.  
DR Pfam: PF00020; TNFR\_c6; 2.  
DR SMART: SM00005; DEATH; 1.  
DR SMART: SM00208; TNFR; 2.  
DR PROSITE: PS50017; DEATH DOMAIN; 1.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
DR Receptor: Apoptosis; Transmembrane; Repeat; Signal;  
KW Alternative splicing; 3D-structure.  
FT SIGNAL 1 55  
FT CHAIN 56 440  
FT DOMAIN 56 210 TUMOR NECROSIS FACTOR RECEPTOR  
FT TRANSMEM 231 SUPERFAMILY MEMBER 10B  
FT DOMAIN 211 231 EXTRACELLULAR (POTENTIAL).  
FT REPEAT 232 440 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 97 137 TNFR-CYS 1.  
FT REPEAT 138 178 TNFR-CYS 2.  
FT REPEAT 192 206 TAPE.  
FT DOMAIN 339 422 DEATH.  
FT DOMAIN 250 253 POLY-GLY.  
FT DISULFID 81 94  
FT DISULFID 97 113  
FT DISULFID 116 129  
FT DISULFID 119 137  
FT DISULFID 139 153  
FT DISULFID 156 170  
FT DISULFID 160 178  
Query Match 54.0%; Score 54; DB 1; Length 440;  
Best Local Similarity 76.9%; Pred. No. 4.4;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 7 APAAEETMTTSPG 19  
||| |||:|:|

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Db      191 APAVEETVSSPG 203

RESULT 3
EXON_HSV11
ID      EXON_HSV11      STANDARD:      PRT:      626 AA.
AC      P04294;
DT      20-MAR-1987 (Rel. 04, Created)
DT      20-MAR-1987 (Rel. 04, Last sequence update)
DT      01-MAR-1992 (Rel. 22, Last annotation update)
DE      Alkaline exonuclease (EC 3.1.11.-).
CN      U12.
OS      Herpes simplex virus (type 1 / strain 17).
OC      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Alphaherpesvirinae; Simplexvirus.
OX      NCBI_TaxID=10299;

RN      RP
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88274327; PubMed=2839594;
RA      McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA      McNab D., Perry L.J., Scott J.E., Taylor P.;
RT      "The complete DNA sequence of the long unique region in the genome of
RT      herpes simplex virus type 1".
RL      J. Gen. Virol. 69:1531-1574(1988).
RN      RP
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86205244; PubMed=3010237;
RA      McGeoch D.J., Dolan A., Frame M.C.;
RT      "DNA sequence of the region in the genome of herpes simplex virus
RT      type 1 containing the exonuclease gene and neighbouring genes.";
RL      Nucleic Acids Res. 14:3435-3448(1986).
CC      -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES ALKALINE EXONUCLEASE
CC      FAMILY.
-----
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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-----
DR      EMBL; D10879; BAA01658.1; -;
DR      EMBL; X14112; CAA32325.1; -;
DR      EMBL; X03839; CAA27453.1; -;
DR      PIR; A00781; NDBE61.
DR      PIR; C30083; C30083.
DR      InterPro: IPR001616; Herpes_alk_exo.
DR      Pfam: PF01771; Herpes_alk_exo.
DR      PRINTS; PR00924; ALKEXNUCLASE.
DR      Hydrolase; Nuclease; Exonuclease.
SQ      SEQUENCE 626 AA; 67508 MW; 7B86C941A0105035 CRC64;

Query Match      49.5%; Score 49.5; DB 1; Length 626;
Best Local Similarity 64.7%; Pred. No. 24;
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      2 SPGTPAPAAEETMTSP 18
      111 11111111111
Db      604 SPG-PCPAAAEETSSSP 619

RESULT 4
HXB3_MOUSE
ID      HXB3_MOUSE      STANDARD:      PRT:      433 AA.
AC      P09026; P10285; Q61680;
DT      01-NOV-1988 (Rel. 09, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Homeobox protein Hox-B3 (Hox-2.7) (MH-23).
GN      HOXB3 OR HOXB-3 OR Hox-2.7.
OS      Mus musculus (Mouse).

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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;

RN      RP
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92258392; PubMed=1582411;
RA      Sham M.H., Hunt P., Nonchev S., Papalopulu N., Graham A.,
RA      Boncinelli E., Krumlauf R.;
RT      "Analysis of the murine Hox-2.7 gene: conserved alternative
RT      transcripts with differential distributions in the nervous system and
RT      the potential for shared regulatory regions.";
RL      EMBO J. 11:1825-1836(1992).
RN      RP
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95196953; PubMed=7890121;
RA      Brown W.M., Taylor G.R.;
RT      "The 5'-sequence of the murine Hox-b3 (Hox-2.7) gene and its intron
RT      contain multiple transcription-regulatory elements.";
RL      Int. J. Biochem. 26:1403-1409(1994).
RN      RP
RP      SEQUENCE OF 152-361 FROM N.A.
RX      MEDLINE=88054465; PubMed=2890503;
RA      Lonai P., Arman E., Czosnek H., Ruddle F.H., Blatt C.;
RT      "New murine homeoboxes: structure, chromosomal assignment, and
RT      differential expression in adult erythropoiesis.";
RL      DNA 6:409-418(1987).
RN      RP
RP      SEQUENCE OF 181-265 FROM N.A.
RX      MEDLINE=89091992; PubMed=2463210;
RA      Graham A., Papalopulu N., Lorimer J., Mcvey J.H., Tuddenham E.G.D.,
RA      Krumlauf R.;
RT      "Characterization of a murine homeo box gene, Hox-2.6, related to the
RT      Drosophila Deformed gene.";
RL      Genes Dev. 2:1424-1438(1988).
CC      -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC      A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC      SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
-----
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-----
DR      EMBL; X66177; CAA46951.1; -;
DR      EMBL; U02278; AAB60496.1; -;
DR      EMBL; M18168; AAA37840.1; -;
DR      PIR; S20963; S20963.
DR      PIR; C29585; C29585.
DR      HSSP; P02833; ISAN.
DR      TRANSFAC; T01724; -.
DR      MGD; MGI:96184; Hoxb3.
DR      InterPro: IPR001827; Antennapedia.
DR      InterPro: IPR001356; Homeobox.
DR      Pfam: PF00046; homeobox.1.
DR      PRINTS; PR00025; ANTENNAPEDIA.
DR      PRINTS; PR00024; HOMEOBOX.
DR      SMART; SM00389; HOX; 1.
DR      PROSITE; PS00027; HOMEOBOX_1; 1.
DR      PROSITE; PS00032; ANTENNAPEDIA; 1.
DR      PROSITE; PS00071; HOMEOBOX_2; 1.
KW      Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW      transcription regulation.
FT      DOMAIN 129 134      ANTP-TYPE HEXAPEPTIDE.
FT      DOMAIN 154 181      GLY-RICH.
FT      DNA_BIND 191 250      HOMEOBOX.
FT      CONFLICT 113 113      G -> C (IN REF. 1).
FT      CONFLICT 119 119      A -> S (IN REF. 1).
FT      CONFLICT 152 169      GCGGGGGGGGGGGGGG -> RLMMRPAAVVAAAAAARG

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RX MEDLINE=98201614; PubMed=9524265;
RA Kido S., Hirooka Y., Ogawa M., Sakai Y., Yoshimura Y., Aiso S.;
RT "Cloning and characterization of mouse mSox13 cDNA.";
RL Gene 208:201-206(1998).
RN [3]
RP SEQUENCE OF 405-460 FROM N.A.
RX MEDLINE=93181275; PubMed=844186;
RA Wright E.M., Snopce B., Koopman P.;
RT "Seven new members of the Sox gene family expressed during mouse
development.";
RL Nucleic Acids Res. 21:744-744(1993).
CC -1- FUNCTION: BINDS TO THE SEQUENCE 5'-AACAT-3'.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, HIGH LEVELS OF EXPRESSION ARE
CC FOUND IN THE ARTERIAL WALLS AT 13.5 DAYS POST COITUM (DPC). LOW
CC LEVELS ARE FOUND IN THE INNER EAR AT 13.5 DPC AND IN SOME CELLS IN
CC THE THYMUS AT 16.5 DPC. EXPRESSED IN THE TRACHEAL EPITHELIUM BELOW
CC THE VOCAL CORD AND IN THE HAIR FOLLICLES AT 18 DPC.
CC -1- SIMILARITY: CONTAINS 1 HMG BOX.
CC -----
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CC -----
DR EMBL; AJ000740; CAA04278.1; -
DR EMBL; AB006329; BAA25786.1; -
DR EMBL; Z18962; CAA79487.1; -
DR PIR; S30241; S30241.
DR HSSP; O05066; IHRV.
DR MGD; MGI:98361; Sox13.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR SMART; SM00398; HMG; 1.
DR DNASIS; SMO0398; HMG; 1.
KW DNA-binding; Nuclear protein; Alternative splicing.
FT DOMAIN 159 195 GLN-RICH.
FT DNASIS 397 465 HMG BOX.
FT VARSPIC 495 519 PGCSPKHHPRSPSLVARGGLML -> OGAROSYITP
FT (IN ISOFORM 2).
FT VARSPIC 603 609 SWSYSQT -> ELVVLND (IN ISOFORM 2).
FT VARSPIC 610 984 MISSING (IN ISOFORM 2).
FT CONFLICT 35 35 P -> L (IN REF. 2).
FT CONFLICT 41 42 AT -> TN (IN REF. 2).
FT CONFLICT 195 195 O -> QQ (IN REF. 2).
SQ SEQUENCE 984 AA; 108897 MW; 7F5506EDADEB98C5 CRC64;

Query Match 48.0%; Score 48; DB 1; Length 984;
Best Local Similarity 53.3%; Pred. No. 59;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TSPGTPAPAEETMT 15
DB 28 TOPGDPAPASODAAAT 42

RESULT 7
CA13_HUMAN
AC P02461; O15112; STANDARD; PRT; 1466 AA.
DT 01-JUN-1986 (Rel. 01, Created)
DT 01-JUN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Collagen alpha 1(III) chain precursor.
GN COL3A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Skin fibroblast;
RX MEDLINE=89350838; PubMed=2764886;
RA Ala-Kokko L., Kontusaari S., Balowin C.T., Kuivaniemi H.,
RT Prockop D.J.;
RT "Structure of cDNA clones coding for the entire prepro alpha 1 (III)
RT chain of human type III procollagen. Differences in protein structure
RT from type I procollagen and conservation of codon preferences.";
RL Biochem. J. 260:509-516(1989).
RN [2]
RP SEQUENCE OF 149-1225 FROM N.A.
RX MEDLINE=89386015; PubMed=2780304;
RA Janeczko R.A., Ramirez F.;
RT "Nucleotide and amino acid sequences of the entire human alpha 1
RT (III) collagen.";
RL Nucleic Acids Res. 17:6742-6742(1989).
RN [3]
RP SEQUENCE OF 168-398.
RX MEDLINE=77134724; PubMed=557335;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of cyanogen
RT bromide peptides from the amino-terminal segment of type III collagen
RT of human liver.";
RL Biochemistry 16:1158-1164(1977).
RN [4]
RP REVISIONS.
RA Seyer J.M.;
RL Submitted (DEC-1977) to the PIR data bank.
RN [5]
RP SEQUENCE OF 399-727.
RX MEDLINE=79000343; PubMed=687591;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of five
RT consecutive CNBr peptides from type III collagen of human liver.";
RL Biochemistry 17:3404-3411(1978).
RN [6]
RP SEQUENCE OF 728-964.
RX MEDLINE=80198282; PubMed=6246925;
RA Seyer J.M., Mairhardt C., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of alpha 1
RT (III)-CB5 from type III collagen of human liver.";
RL Biochemistry 19:1583-1589(1980).
RN [7]
RP SEQUENCE OF 950-1466 FROM N.A.
RX MEDLINE=88189827; PubMed=3357782;
RA Markoo B.S., Dalgleish R.;
RT "Human pro alpha 1(III) collagen: cDNA sequence for the 3' end.";
RL Nucleic Acids Res. 16:2337-2337(1988).
RN [8]
RP REVISION TO 1184.
RX MEDLINE=89098346; PubMed=3211760;
RA Molyneux K., Dalgleish R.;
RT "Human type III collagen 'variant' is a cDNA cloning artefact.";
RL Nucleic Acids Res. 16:11833-11833(1988).
RN [9]
RP SEQUENCE OF 1065-1466 FROM N.A.
RX MEDLINE=85087944; PubMed=6096827;
RA Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morrow S.,
RT Rosenbloom J., Myers J.C.;
RT "Molecular cloning and carboxyl-propeptide analysis of human type III
RT procollagen.";
RL Nucleic Acids Res. 12:9383-9394(1984).
RN [10]
RP SEQUENCE OF 965-1200.
RX MEDLINE=81208139; PubMed=7016180;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of alpha
RT 1(III)-CB9 from type III collagen of human liver.";
RL Biochemistry 20:2621-2627(1981).
RN [11]
RP SEQUENCE OF 1176-1466 FROM N.A.

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RX MEDLINE=85157600; PubMed=2579949;  
 RA Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sipola M., Ramirez F.;  
 RT "Isolation of cDNA and genomic clones encoding human pro-alpha 1  
 (III) collagen. Partial characterization of the 3' end region of the  
 RT gene.";  
 RL J. Biol. Chem. 260:4357-4363(1985).  
 RN [12]  
 RP SEQUENCE OF 1161-1200 FROM N.A.  
 RX MEDLINE=86187804; PubMed=3754462;  
 RA Miskulin M., Dalgleish R., Klueve-Beckerman B., Rennard S.I.,  
 RA Tolstoshev P., Brantly M., Crystal R.G.;  
 RT "Human type III collagen gene expression is coordinately modulated  
 RT with the type I collagen genes during fibroblast growth.";  
 RL Biochemistry 25:1408-1413(1986).  
 RN [13]  
 RP SEQUENCE OF 1-170 FROM N.A.  
 RX TISSUE-Placenta;  
 RA Tomlin D., Ricca G., de Crombrughe B.;  
 RT "Nucleotide sequence of a cDNA coding for the amino-terminal region  
 RT of human prepro alpha 1(III) collagen.";  
 RL Nucleic Acids Res. 16:7201-7201(1988).  
 RN [14]  
 RP SEQUENCE OF 1-176 FROM N.A.  
 RX MEDLINE=89378752; PubMed=2777083;  
 RA Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;  
 RT "Cloning and analysis of the 5' portion of the human type-III  
 RT procollagen gene (COL3A1).";  
 RL Gene 78:255-265(1989).  
 RN [15]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=97255959; PubMed=9101290;  
 RA Kuivaniemi H., Tromp G., Prockop D.J.;  
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
 RT associated collagen (type IX), and network-forming collagen (type X)  
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
 RL Hum. Mutat. 9:300-315(1997).  
 RN [16]  
 RP VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668.  
 RX MEDLINE=93293988; PubMed=8514866;  
 RA Tromp G., Wu Y., Prockop D.J., Madhathri S.L., Kleinert C.,  
 RA Barley J.J., Zhang J., Noerregaard O., Darling R.C., Abbott W.M.,  
 RA Cole C.W., Jaakola P., Rynanen M., Pearce W.H., Yao J.S.T.,  
 RA Majamaa K., Smulens S.N., Gatalica Z., Ferrell R.E., Jimenez S.A.,  
 RA Jackson C.E., Michels V.V., Kaye M., Kuivaniemi H.;  
 RT "Sequencing of cDNA from 50 unrelated patients reveals that mutations  
 RT in the triple-helical domain of type III procollagen are an  
 RT infrequent cause of aortic aneurysms.";  
 RL J. Clin. Invest. 91:2539-2545(1993).  
 RN [17]  
 RP VARIANT THR-698.  
 RX MEDLINE=91045136; PubMed=2235526;  
 RA Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S.,  
 RA Wu Y., Ganguly A., Prockop D.J.;  
 RT "G to A polymorphism in exon 31 of the COL3A1 gene.";  
 RL Nucleic Acids Res. 18:6180-6180(1990).  
 RN [18]  
 RP VARIANT AORTIC ANEURYSM ARG-786.  
 RX MEDLINE=91056145; PubMed=2243125;  
 RA Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;  
 RT "A mutation in the gene for type III procollagen (COL3A1) in a family  
 RT with aortic aneurysms.";  
 RL J. Clin. Invest. 86:1465-1473(1990).  
 RN [19]  
 RP VARIANT EDS-IV ARG-828.  
 RX MEDLINE=94016385; PubMed=8411057;  
 RA Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;  
 RT "The substitution of glycine 661 by arginine in type III collagen  
 RT produces mutant molecules with different thermal stabilities and  
 RT causes Ehlers-Danlos syndrome type IV.";  
 RL J. Med. Genet. 30:690-693(1993).  
 RN [20]  
 RP VARIANT EDS-IV SER-957.

RX MEDLINE=89109135; PubMed=2492273;  
 RA Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;  
 RT "A single base mutation that substitutes serine for glycine 790 of  
 RT the alpha 1 (III) chain of type III procollagen exposes an arginine  
 RT and causes Ehlers-Danlos syndrome IV.";  
 RL J. Biol. Chem. 264:1349-1352(1989).  
 RN [21]  
 RP VARIANT EDS-IV VAL-960.  
 RX MEDLINE=95268429; PubMed=7749417;  
 RA Tromp G., de Paape A., Nuytink L., Madhathri S.L., Kuivaniemi H.;  
 RT "Substitution of valine for glycine 793 in type III procollagen in  
 RT Ehlers-Danlos syndrome type IV.";  
 RL Hum. Mutat. 5:179-181(1995).  
 RN [22]  
 RP VARIANT EDS-IV GLU-1014.  
 RX MEDLINE=92316511; PubMed=1352273;  
 RA Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,  
 RA Pope F.M.;  
 RT "A single base mutation in the gene for type III collagen (COL3A1)  
 RT converts glycine 847 to glutamic acid in a family with Ehlers-Danlos  
 RT syndrome type IV. An unaffected family member is mosaic for the  
 RT mutation.";  
 RL Hum. Genet. 89:414-418(1992).  
 RN [23]  
 RP VARIANT EDS-IV ASP-1050.  
 RX MEDLINE=90037070; PubMed=2808425;  
 RA Tromp G., Kuivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;  
 RT "Single base mutation in the type III procollagen gene that converts  
 RT the codon for glycine 883 to aspartate in a mild variant of  
 RT Ehlers-Danlos syndrome IV.";  
 RL J. Biol. Chem. 264:19313-19317(1989).  
 RN [24]  
 RP VARIANT EDS-IV VAL-1077.  
 RX MEDLINE=91374480; PubMed=1895316;  
 RA Richards A.J., Lloyd J.C., Ward P.N., de Paape A., Narcisi P.,  
 RA Pope F.M.;  
 RT "Characterisation of a glycine to valine substitution at amino acid  
 RT position 910 of the triple helical region of type III collagen in a  
 RT patient with Ehlers-Danlos syndrome type IV.";  
 RL J. Med. Genet. 28:458-463(1991).  
 RN [25]  
 RP VARIANT EDS-IV GLU-1173.  
 RX MEDLINE=93022543; PubMed=1357232;  
 RA Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;  
 RT "Query Match 48.0%; Score 48; DB 1; Length 1466;  
 RT Best Local Similarity 44.4%; Pred. No. 89;  
 RT Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 SPGTPAPAEETMTSPG 19  
 Db 1117 APGSPGAPGCGAIGSPG 1134  
 ID ERP MYCTU STANDARD: PRT: 284 AA.  
 AC 050793: 053586: 053468:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Exported repetitive protein precursor (Cell surface protein plrg)  
 DE (EXP53).  
 GN ERP OR PIRG OR RV3810 OR MT3917 OR MTV026.15.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MT103;  
 RX MEDLINE=96118692; PubMed=7496523;  
 RA Berthet F.-X., Raugier J., Lim E.M., Philipp W., Clocquel B.,

RA Portnoi D.;  
 RT "Characterization of the Mycobacterium tuberculosis erp gene encoding  
 a potential cell surface protein with repetitive structures."; *Microbiology* 141:2123-2130(1995).  
 RL [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 Davies R., Devlin K., Feltham A., Galloway S., Hamlin N., Holroyd S.,  
 Hornsby T., Jagels K., Kirogh A., McLean J., Moule S., Murphy L.,  
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultison J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence."; *Nature* 393:537-544(1998).  
 RL [3]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Feldman J., Khouri H., Gill J., Mikula A.,  
 Bishal W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 laboratory strains."; *Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.*  
 RL [4]  
 RN  
 RP SEQUENCE OF 1-24 FROM N.A.  
 RC STRAIN=MT103;  
 RX MEDLINE=95095987; PubMed=7798150;  
 RA Lim E.M., Raubzier J., Timm J., Torrea G., Murray A., Gicquel B.,  
 Portnoi D.;  
 RT "Identification of Mycobacterium tuberculosis DNA sequences encoding  
 exported proteins by using phoA gene fusions."; *J. Bacteriol.* 177:59-65(1995).  
 RL [5]  
 RN  
 RP CHARACTERIZATION;  
 RX MEDLINE=9900810; PubMed=9784137;  
 RA Berthel F.-X., Lagranderie M., Gounon P., Laurent-Winter C.,  
 Enseignel D., Chavaret P., Thouron F., Maranghi E., Pellicic V.,  
 RT Portnoi D., Marchal G., Gicquel B.;  
 RT "Attenuation of virulence by disruption of the Mycobacterium  
 tuberculosis erp gene."; *Science* 282:759-762(1998).  
 RL  
 CC -1- FUNCTION: SURFACE-EXPOSED PROTEIN REQUIRED FOR MULTIPLICATION AND  
 INTRACELLULAR GROWTH.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- SIMILARITY: TO M.LEPRAE 28 KDA ANTIGEN.  
 CC  
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 CC  
 CC EMBL: L38851; AAA96136.1; -;  
 DR EMBL: AL022076; CA11874.1; -;  
 DR EMBL: AE007185; AAK48283.1; -;  
 DR EMBL: S74657; AAB32855.1; -;  
 DR TIGR: MT3917; -;  
 DR TubercuList: RV3810; -;  
 KW Antigen; Transmembrane; Repeat; Signal; Complete proteome.  
 FT SIGNAL 1 22  
 FT CHAIN 23 284  
 FT DOMAIN 23 252  
 FT TRANSMEM 253 273  
 FT DOMAIN 274 284  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 92 121 6 x 5 AA TANDEM REPEATS OF P-[GA]-L-T-S.  
 FT REPEAT 92 96 1-1.  
 FT REPEAT 97 101 1-2.  
 FT REPEAT 102 106 1-3.  
 FT REPEAT 107 111 1-4.  
 FT REPEAT 112 116 1-5.  
 FT REPEAT 117 121 1-6.  
 FT DOMAIN 144 173 6 x 5 AA APPROXIMATE TANDEM REPEATS OF  
 P-[ATG]-[LG]-X-X.  
 FT REPEAT 144 148 2-1.  
 FT REPEAT 149 153 2-2.  
 FT REPEAT 154 158 2-3.  
 FT REPEAT 159 163 2-4.  
 FT REPEAT 164 168 2-5.  
 FT REPEAT 169 173 2-6.  
 FT VARIANT 256 256 A -> V (IN ISOLATE MT103).  
 FT CONFLICT 5 5 R -> S (IN REF. 4).  
 FT CONFLICT 7 7 R -> S (IN REF. 4).  
 FT SEQUENCE 284 AA; 27700 MM; 1164C7FE3E7ADE42 CRC64;  
 SQ  
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 Best Local Similarity 47.4%; Pred. NO. 22;  
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 TSPGPAPAEETMTSPG 19  
 Db 100 TSPGLTSPGLDPAATSPG 118  
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 RESULT 9  
 FENR\_SYNV3  
 ID FENR\_SYNV3 STANDARD; PRT; 413 AA.  
 AC 055318; P74364;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ferredoxin-NADP reductase (EC 1.18.1.2) (FNR).  
 GN FNR OR SLR1643.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Thor J.J.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K.,  
 RA Okumura S., Shimo S., Takeuchi C., Wada T., Matsunabe A.,  
 RA Yanada M., Yasuda M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions."; *DNA Res.* 3:109-136(1996).  
 RL  
 CC -1- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) - oxidized  
 ferredoxin + NADPH.  
 CC  
 CC -1- COFACTOR: FAD.  
 CC -1- SUBCELLULAR LOCATION: MAY BE BOUND TO THE THYLAKOID MEMBRANE OR  
 ANCHORED TO THE THYLAKOID-BOUND PHCOBLISOMES.  
 CC -1- SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBLISOME LINKER  
 PROTEIN CPD.  
 CC  
 CC -1- SIMILARITY: WITH OTHER SPECIES FNR.  
 CC  
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CC -----
DR EMBL; X94297; CA63961.1; -.
DR EMBL; D90914; BAA18459.1; -.
DR HSSP; P21890; 1BJK.
DR InterPro; IPR001685; Cpcd.
DR InterPro; IPR001709; Flavyrid_cyt_redctse.
DR Pfam; PF01383; Cpcd; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00371; PNCRC.
DR ProDom; PD002828; Cpcd; 1.
DR Oxidoreductase; Flavoprotein; NADP; FAD; Thylakoid; Membrane;
KW Phycobilisome; Complete proteome.
FT DOMAIN 1 82 Cpcd-LIKE.
FT DISULFID 231 236 BY SIMILARITY.
FT NE_BIND 265 283 NADP (RIBOSE PART) (BY SIMILARITY).
FT CONFLICT 182 182 E -> K (IN REF. 1).
FT CONFLICT 243 243 D -> S (IN REF. 1).
FT CONFLICT 347 350 QHRV -> STGL (IN REF. 1).
SQ SEQUENCE 413 AA; 46359 MW; FF33709639FCAA8 CRC64;

Query Match 47.0%; Score 47; DB 1; Length 413;
Best Local Similarity 61.3%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PAPAEEETMTSP 18
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Db 105 PAPESNKTMTTTP 117

RESULT 10
CAL3_BOVIN STANDARD; PRT; 1049 AA.
AC P04256;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Collagen alpha 1(III) chain.
GN COL3A1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN 11
RP SEQUENCE OF 1-242.
RX MEDLINE=80026026; Pubmed=488906;
RA Fietzek P.P., Allmann H., Rautenberg J., Henkel W., Wachter E.,
RA Kuhn K.;
RT "The covalent structure of calf skin type III collagen. I. The amino
RT acid sequence of the amino terminal region of the alpha 1(III) chain
RT (positions 1-222).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:809-820(1979).
[2]
RP SEQUENCE OF 243-422.
RX MEDLINE=80026027; Pubmed=488907;
RA Dewes H., Fietzek P.P., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. II. The amino
RT acid sequence of the cyanogen bromide peptide alpha 1(III)CH1,8,10,2
RT (positions 223-402).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:821-832(1979).
[3]
RP SEQUENCE OF 423-571.
RX MEDLINE=80026028; Pubmed=488908;
RA Beltz H., Fietzek P.P., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. III. The
RT amino acid sequence of the cyanogen bromide peptide alpha 1(III)CH4
RT (positions 403-551).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:833-840(1979).
[4]
RP SEQUENCE OF 572-808.

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RX MEDLINE=80026029; Pubmed=488909;
RA Lang H., Glanville R.W., Fietzek P.P., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. IV. The amino
RT acid sequence of the cyanogen bromide peptide alpha 1(III)CB5
RT (positions 552-788).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:841-850(1979).
[5]
RP SEQUENCE OF 809-947.
RX MEDLINE=80026030; Pubmed=488910;
RA Dewes H., Fietzek P.P., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. V. The amino
RT acid sequence of the cyanogen bromide peptide alpha 1(III)CB9A
RT (position 789-927).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:851-860(1979).
[6]
RP SEQUENCE OF 948-1049.
RX MEDLINE=80026031; Pubmed=488911;
RA Allmann H., Fietzek P.P., Glanville R.W., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. VI. The amino
RT acid sequence of the carboxyterminal cyanogen bromide peptide alpha
RT 1(III)CB9B (positions 928-1028).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:861-868(1979).
CC -1 FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONNECTIVE TISSUES
CC ALONG WITH TYPE I COLLAGEN.
CC -1 SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS ARE
CC LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE
CC ALSO CROSS-LINKED VIA HYDROXYLISINES.
CC -1 PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
DR PIR; A02862; CGB07S.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR001007; WMFC.
DR Pfam; PF01391; Collagen; 17.
DR PROSITE; PS01208; WMFC; PARTIAL.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen.
FT DOMAIN 1 14 NONHELICAL REGION (N-TERMINAL).
FT DOMAIN 15 1040 TRIPLE-HELICAL REGION.
FT DOMAIN 1041 1049 NONHELICAL REGION (C-TERMINAL).
FT MOD_RES 95 95 HYDROXYLATION.
FT MOD_RES 107 107 HYDROXYLATION.
FT MOD_RES 119 119 HYDROXYLATION.
FT MOD_RES 938 938 HYDROXYLATION.
FT MOD_RES 950 950 HYDROXYLATION.
FT CARBOHYD 107 107 O-LINKED (GAL. . .).
FT CARBOHYD 950 950 O-LINKED (GAL. . .).
FT DISULFID 1040 1040 INTERCHAIN.
FT DISULFID 1041 1041 INTERCHAIN.
SQ SEQUENCE 1049 AA; 93651 MW; 8EEC33D1C66EC9A3 CRC64;

Query Match 47.0%; Score 47; DB 1; Length 1049;
Best Local Similarity 44.4%; Pred. No. 85;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 SPGTPAPAEEETMTSPG 19
   111 : 111
Db 961 APGSPGPGHCGAVGSPG 978

RESULT 11
CAL3_MOUSE STANDARD; PRT; 1464 AA.
AC P08121; O61429; Q9CRN7;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Collagen alpha 1(III) chain precursor.
GN COL3A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL X DBA; TISSUE=Embryo;
RA MEDLINE=95011609; PubMed=7926795;
RT Toman D., de Crombrughe B.;
RT "The mouse type-III procollagen-encoding gene: genomic cloning and
RT complete DNA sequence."
RL Gene 147:161-168(1994).
RN [2]
RP SEQUENCE OF 1-488 FROM N.A.
RX MEDLINE=88167858; PubMed=3443309;
RA Wood L., Theriault N., Vogel G.;
RT "Complete nucleotide sequence of the N-terminal domains of the murine
RT alpha-1 type-III collagen chain."
RL Gene 61:225-230(1987).
RN [3]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=85131189; PubMed=3972847;
RA Liu G., Mudryj M., de Crombrughe B.;
RT "Identification of the promoter and first exon of the mouse alpha 1
RT (III) collagen gene."
RL J. Biol. Chem. 260:3773-3777(1985).
RN [4]
RP SEQUENCE OF 810-1464 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RA MEDLINE=21085660; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Akawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE OF 1442-1464 FROM N.A.
RC STRAIN=C57BL;
RA MEDLINE=91274355; PubMed=2054384;
RA Metcarranta M., Toman D., de Crombrughe B., Vuorio E.;
RT "Specific hybridization probes for mouse type I, II, III and IX
RT collagen mRNAs."
RL Biochim. Biophys. Acta 1089:241-243(1991).
CC -1- FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SORT CONNECTIVE TISSUES
CC ALONG WITH TYPE I COLLAGEN.
CC -1- SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS ARE
CC LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE
CC ALSO CROSS-LINKED VIA HYDROXYLYSINES.
CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC O-LINKED GLYCAN CONSISTS OF GLC-GAL DISACCHARIDE (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
CC -----
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CC -----
DR EMBL, X52046; CAA36279.1; -

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DR EMBL, M18933; AAA37338.1; -
DR EMBL, K03037; -; NOT_ANNOTATED_CDS.
DR EMBL, AK019448; BAB31724.1; -
DR EMBL, X57983; CAA1048.1; -
DR PIR, A22287; A22287.
DR PIR, A27353; A27353.
DR PIR, S16373; S16373.
DR MGI, 88453; Col3a1.
DR InterPro: IPR000087; Collagen.
DR InterPro: IPR000885; Fib_collagen_C.
DR InterPro: IPR001007; VWFC.
DR Pfam: PF01410; COLF1; 1.
DR Pfam: PF01391; Collagen; 17.
DR ProDom: PD002078; Fib_collagen_C; 1.
DR SMART: SM00038; COLF1; 1.
DR SMART: SM00214; VWFC; 1.
DR PROSITE: PS01208; VWFC; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Signal.
FT SIGNAL 1 23
FT PROPEP 24 154
FT CHAIN 155 1203
FT PROPEP 1204 1464
FT DOMAIN 31 90
FT DOMAIN 155 169
FT CARBOHD 262 262
FT MOD_RES 262 262
FT MOD_RES 283 283
FT MOD_RES 859 859
FT MOD_RES 976 976
FT MOD_RES 1093 1093
FT MOD_RES 1105 1105
FT DISULFD 1196 1195
FT SEQUENCE 1464 AA; 138944 MW; 2104EC27A886090B CRC64;
SQ
Query Match 47.0%; Score 47; DB 1; Length 1464;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
OY 2 SPGTPAPAAEETMTTSPG 19
Db 453 SPGTPGPKGDEGDKGSPG 470
RESULT 12
ID ABC1_HUMAN STANDARD; PRT; 2261 AA.
AC O95477; O9UN08; O9UN07; O9UN06; O9NOV4; O9UN09; O96785; O96556;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE transporter 1) (ATP-binding cassette 1) (Cholesterol efflux
DE regulatory protein).
GN ABCA1 OR ABC1 OR CERP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20345099; PubMed=10884428;
RA Santamarina-Li Pojo S., Peterson K.M., Knapper C.L., Qiu Y.,
RA Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P.,
RA Handenchild C.C., Prades C., Chimini G., Blackmon E.E.,
RA Francis T.L., Duverger N., Rubin E.M., Rosier M., Denefle P.,
RA Fredrickson D.S., Brewer H.B. Jr.;
RT "Complete genomic sequence of the human ABCA1 gene: analysis of the
RT human and mouse ATP-binding cassette A promoter."

```



Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SKIN;  
 RA Schwartz K., Lawn R.M., Wade D.P.;  
 RT "ABCA1 gene expression and apoA-I-mediated cholesterol efflux are  
 regulated by LXR.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21251004; PubMed=11352567;  
 RA Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;  
 RT "Human and mouse ABCA1 comparative sequencing and transgenesis  
 studies revealing novel regulatory sequences.";  
 RL Genomics 73:66-76(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A.,  
 RA Kioka N., Amachi T., Yokoyama S., Ueda K.;  
 RT "A new topological model of functional human ABCA1-signal peptide  
 cleavage and glycosylation of a large extracellular domain.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 21-2261 FROM N.A.  
 RX MEDLINE=99194549; PubMed=10092505;  
 RA Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F.,  
 RA Chmial G., Kaminski W.E., Schmitz G.;  
 RT "Molecular cloning of the human ATP-binding cassette transporter 1  
 (ABCA1): evidence for sterol-dependent regulation in macrophages.";  
 RL Biochem. Biophys. Res. Commun. 257:29-33(1999).  
 RN [6]  
 RP SEQUENCE OF 21-2261 FROM N.A.  
 RX MEDLINE=99364413; PubMed=10431238;  
 RA Rust S., Rosier M., Funke H., Reil J., Amoura Z., Piette J.-C.,  
 RA Delzenne J.-F., Brewer H.B., Duverger N., Denefle P., Assmann G.;  
 RT "Tangier disease is caused by mutations in the gene encoding  
 ATP-binding cassette transporter 1.";  
 RL Nat. Genet. 22:352-355(1999).  
 RN [7]  
 RP VARIANTS FHA THR-1091 AND 1893-GLU-ASP-1894 DEL.  
 RX MEDLINE=20001430; PubMed=10533863;  
 RA Marci M., Brooks-Wilson A., Clee S.M., Roomp K., Zhang L.-H., Yu L.,  
 RA Collins J.A., van Dam M., Molhuizen H.O.F., Loubser O.,  
 RA Ouellette B.F.F., Senses C.W., Fichter K., Mott S., Denis M.,  
 RA Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.;  
 RT "Mutations in the ABC1 gene in familial HDL deficiency with defective  
 cholesterol efflux.";  
 RL Lancet 354:1341-1346(1999).  
 RN [8]  
 RP VARIANTS TD ARG-597 AND ARG-1477, AND VARIANT FHA LEU-693 DEL.  
 RX MEDLINE=99364411; PubMed=10431236;  
 RA Brooks-Wilson A., Marci M., Clee S.M., Zhang L.-H., Roomp K.,  
 RA van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,  
 RA Loubser O., Ouellette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,  
 RA Senses C.W., Scherer S., Mott S., Denis M., Martindale D.,  
 RA Frohlich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,  
 RA Hayden M.R.;  
 RT "Mutations in ABC1 in Tangier disease and familial high-density  
 lipoprotein deficiency.";  
 RL Nat. Genet. 22:336-345(1999).  
 RN [9]  
 RP VARIANTS TD SER-590; SER-935 AND VAL-937, AND VARIANTS ALA-399 AND  
 MEV-883.  
 RX MEDLINE=99364412; PubMed=10431237;  
 RA Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,  
 RA Diedrich W., Drobnik W., Barlage S., Buechler C.,  
 RA Porsch-Oeschuerst M., Kaminski J.W.E., Hahnemann H.W., Oette K.,  
 RA Rothe G., Aslanidis C., Lackner K.J., Schmitz G.;  
 RT "The gene encoding ATP-binding cassette transporter 1 is mutated in  
 Tangier disease.";  
 RL Nat. Genet. 22:347-351(1999).  
 RN [10]  
 RP VARIANTS TD ILE-929; ARG-597 AND ARG-1477, AND VARIANTS FHA LEU-693  
 DEL; THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.  
 RX MEDLINE=20540002; PubMed=11086027;  
 RA Clee S.M., Kastelein J.J.P., van Dam M., Marci M., Roomp K.,  
 RA Zwarts K.Y., Collins J.A., Roelants R., Tamasawa N., Stlic T.,  
 RA Suda T., Geska R., Boucher B., Rondeau C., Desouch C.,  
 RA Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,  
 RA Hayden M.R.;  
 RT "Age and residual cholesterol efflux affect HDL cholesterol levels and  
 coronary artery disease in ABCA1 heterozygotes.";  
 RL J. Clin. Invest. 106:1263-1270(2000).  
 RN [11]  
 RP VARIANTS TD ASN-1289 AND HIS-1800.  
 RX MEDLINE=20171564; PubMed=10706591;  
 RA Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,  
 RA Van Berendse P., Goldkamp A.L., Thurston L.M., Fitzgerald M.G.,  
 RA Vasek-McKenna D., O'Neill G., Eberhart G.P., Weffenbach B.,  
 RA Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z.;  
 RT "Novel mutations in the gene encoding ATP-binding cassette 1 in four  
 Tangier disease kindreds.";  
 RL J. Lipid Res. 41:433-441(2000).  
 RN [12]  
 RP VARIANT TD ASP-1046, VARIANT FHA CYS-230, AND VARIANTS LYS-219;  
 ILE-825; MET-883 AND LYS-1587.  
 RX MEDLINE=20396633; PubMed=10938021;  
 RA Wang J., Burnett J.R., Near S., Young K., Zimman B., Hanley A.J.G.,  
 RA Connelly P.W., Harris S.B., Hegele R.A.;  
 RT "Common and rare ABCA1 variants affecting plasma HDL cholesterol.";  
 RL Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).  
 RN [13]  
 RP VARIANT TD TRP-587, AND VARIANT LEU-2168.  
 RX MEDLINE=21157002; PubMed=11257260;  
 RA Bertolini S., Pisciotto L., Serl M., Cusano R., Cantafora A.,  
 RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;  
 RT "A point mutation in ABC1 gene in a patient with severe premature  
 coronary heart disease and mild clinical phenotype of Tangier  
 disease.";  
 RL Atherosclerosis 154:599-605(2001).  
 RN [14]  
 RP VARIANTS LYS-219; MET-883 AND ASP-1172.  
 RX MEDLINE=21157003; PubMed=11257261;  
 RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kiehl D.,  
 RA Probst N., Ordovas J.M., Aslanidis C., Lackner K.J.,  
 RA Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,  
 RA Schmitz G.;  
 RT "Common variants in the gene encoding ATP-binding cassette transporter  
 1 in men with low HDL cholesterol levels and coronary heart disease.";  
 RL Atherosclerosis 154:607-611(2001).  
 RN [15]  
 RP VARIANT TD LEU-1506.  
 RX MEDLINE=21369429; PubMed=11476961;  
 RA Lapicka-Bodzioch K., Bodzioch M., Krnell M., Kiehl D., Probst M.,  
 RA Kiehl B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,  
 RA Sutrop N., Schmitz G.;  
 RT "Homogeneous assay based on 52 primer sets to scan for mutations of  
 the ABCA1 gene and its application in genetic analysis of a new  
 patient with familial high-density lipoprotein deficiency syndrome.";  
 RL Biochim. Biophys. Acta 1537:42-48(2001).  
 RN [16]  
 RP VARIANTS TD ASN-1289 AND TRP-2081, AND VARIANT LYS-219.  
 RX MEDLINE=21369433; PubMed=11476965;  
 RA Huang W., Moriyama K., Koga T., Hua H., Ageta M., Kawabata S.,  
 RA Mawatari K., Imamura T., Eto T., Kawamura M., Teramachi T., Sasaki J.;  
 RT "Novel mutations in ABCA1 gene in Japanese patients with Tangier  
 disease and familial high density lipoprotein deficiency with  
 coronary heart disease.";  
 RL Biochim. Biophys. Acta 1537:71-78(2001).  
 RN [17]  
 RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;  
 MEV-883; ASP-1172; LYS-1587 AND CYS-1731.  
 RX MEDLINE=21198379; PubMed=11238261;  
 RA Clee S.M., Zwinderman A.H., Engert J.C., Zwarts K.Y.,  
 RA Molhuizen H.O.F., Roomp K., Jukema J.W., van Wiltland M., van Dam M.,  
 RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,

RA Hayden M.R.;  
RT "Common genetic variation in ABCA1 is associated with altered  
RT lipoprotein levels and a modified risk for coronary artery disease.";  
RL Circulation 103:1198-1205(2001).  
RN [18]  
RP VARIANT TD THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611.  
RX MEDLINE-21645894; PubMed-11785958;  
RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,  
RA Ishihara M., Sakane N., Zhang Z., Tsuji K., Matsuyama A., Ohama T.,  
RA Matsura F., Ishigami M., Sakai N., Hiroka H., Hattori H.,  
RA Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T.,  
RA Yamashita S., Matsuzawa Y.;  
RT "Expression and functional analyses of novel mutations of ATP-binding  
RT cassette transporter-1 in Japanese patients with high-density  
RT lipoprotein deficiency.";  
RL Biochem. Biophys. Res. Commun. 290:713-721(2002).  
CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION  
CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL  
CC TRANSPORT.  
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN  
CC MACROPHAGES.  
CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,  
CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN  
CC ATP BINDING CASSETTE (ABC) DOMAIN.  
CC -1- DISEASE: DEFECTS IN ABCA1 ARE A CAUSE OF HIGH DENSITY LIPOPROTEIN  
CC DEFICIENCY TYPE I (HDLI), ALSO KNOWN AS TANGIER DISEASE (TD). TD  
CC IS A RECESSIVE DISORDER CHARACTERIZED BY ABSENCE OF HIGH DENSITY  
CC LIPOPROTEIN (HDL) CHOLESTEROL FROM PLASMA, HEPATOSPLENOMEGALY,  
CC PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY  
CC DISEASE (CAD).  
CC -1- DISEASE: Defects in ABCA1 are a cause of high density lipoprotein

Query Match 47.0%; Score 47; DB 1; Length 2261;  
Best Local Similarity 56.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 3 PGTPAPAAEEMTTPSP 18  
Db 1425 PDTPQAGEEMTTPAP 1440

RESULT 13  
RPE\_RHOCA STANDARD; PRT; 228 AA.  
ID RPE\_RHOCA  
AC P51012;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (Pentose-5-phosphate 3-  
DE epimerase) (PPE) (RSP3E).  
GN CBEE.  
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
OC Rhodobacter.  
OX NCBI\_TaxID=1061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 11166;  
RA Latimer F.W., Lu T.-Y.S., Buley D.M.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: D-ribulose 5-phosphate = D-xylulose 5-  
CC phosphate.  
CC -1- PATHWAY: CALVIN CYCLE.  
CC -1- SIMILARITY: BELONGS TO THE RIBULOSE-PHOSPHATE 3-EPIMERASE FAMILY.  
CC -----  
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DR EMBL: U23145; AAB82049.1; -.  
DR HSSP; Q43843; IRPX.  
DR InterPro: IPR000056; Ribul\_P\_3\_epim.  
DR Pfam: PF00834; Ribul\_P\_3\_epim; 1  
DR PROSITE; PS01085; RIBUL\_P\_3\_EPIMER\_1; 1.  
DR PROSITE; PS01086; RIBUL\_P\_3\_EPIMER\_2; FALSE\_NEG.  
KW Isomerase; Carbohydrate metabolism; Calvin cycle.  
SQ SEQUENCE 228 AA; 23878 MW; FCD392695BCD396B CRC64;

Query Match 46.5%; Score 46.5; DB 1; Length 228;  
Best Local Similarity 40.7%; Pred. No. 21;  
Matches 11; Conservative 2; Mismatches 5; Indels 9; Gaps 1;

Oy 2 SPGPAPAAE-----TMTTSPG 19  
Db 120 NPGTPAAEIEHVLDIADVVCWTVNPG 146

RESULT 14  
CSA\_DICDI STANDARD; PRT; 514 AA.  
ID CSA\_DICDI  
AC P08796; P19408;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Contact site A protein precursor (CSA) (Membrane-associated  
DE glycoprotein gp80) (Cell adhesion molecule gp80).  
GN CSAA.  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Eukaryozoa; Dictyostelida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Noegel A., Gerisch G., Stadler J., Westphal M.;  
RT "Complete sequence and transcript regulation of a cell adhesion  
RT protein from aggregating Dictyostelium cells.";  
RL EMBO J. 5:1473-1476(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-69105362; PubMed-3063296;  
RA Siu C.-H., Wong L.M., Lam T.Y., Kamboj R.K., Choi A., Cho A.;  
RT "Molecular mechanisms of cell-cell interaction in Dictyostelium  
RT discoideum.";  
RL Biochem. Cell Biol. 66:1089-1099(1988).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX2;  
RX MEDLINE-92406924; PubMed-1326559;  
RA Desbarats L., Lam T.Y., Wong L.M., Siu C.H.;  
RT "Identification of a unique CAMP-response element in the gene  
RT encoding the cell adhesion molecule gp80 in Dictyostelium  
RT discoideum.";  
RL J. Biol. Chem. 267:19655-19664(1992).  
RN [4]  
RP SEQUENCE OF 20-49.  
RA Wong L.M., Siu C.-H.;  
RT "Cloning of cDNA for the contact site A glycoprotein of Dictyostelium  
RT discoideum";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:4248-4252(1986).  
RN [5]  
RP CELL-BINDING DOMAIN.  
RX MEDLINE-69034443; PubMed-3182938;  
RA Kamboj R.K., Wong L.M., Lam T.Y., Siu C.H.;  
RT "Mapping of a cell-binding domain in the cell adhesion molecule gp80  
RT of Dictyostelium discoideum.";  
RL J. Cell Biol. 107:1835-1843(1988).  
RN [6]  
RP GPI-ANCHOR.  
RX MEDLINE-69251561; PubMed-2721485;  
RA Stadler J., Keenan T.W., Bauer G., Gerisch G.;  
RT "The contact site A glycoprotein of Dictyostelium discoideum carries  
RT a phospholipid anchor of a novel type";

RL EMBL J. 8:371-377(1989).  
CC -1- FUNCTION: THIS CELL-SURFACE GLYCOPROTEIN MEDIATES CELL-CELL  
CC BINDING VIA HOMOPHILIC INTERACTION.  
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR  
CC THAT CONTAINS A PHOSPHOCERAMIDE MOIETY. SUCH ANCHOR MEDIATES A  
CC FAST AND LONG PERSISTENCE CELL ADHESION OF THE PROTEIN.  
CC -1- DEVELOPMENTAL STAGE: RESTRICTED TO THE AGGREGATION STAGE OF  
CC DEVELOPMENT OF D.DISCOIDEUM.  
CC -1- PTM: ACETYLATED, PHOSPHORYLATED ON SERINE AND N-GLYCOSYLATED WITH  
CC TWO TYPES OF OLIGOSACCHARIDE CHAINS.  
CC -1- MISCELLANEOUS: THE EXPRESSION OF THIS STRINGENTLY REGULATED  
CC PROTEIN DURING CELL DEVELOPMENT IS MEDIATED THROUGH CELL-SURFACE  
CC CAMP RECEPTORS.  
CC -1- SIMILARITY: THE C-TERMINAL REGION CONTAINS CLUSTERS OF PROLINE  
CC REGULARLY ALTERNATING WITH A HYDROXYAMINO ACID AND SHOWS  
CC SIMILARITY TO THE HINGE REGION OF IMMUNOGLOBULINS. THIS DOMAIN  
CC MIGHT ACT AS A SPACER TO ELEVATE SITES ACTIVE IN CELL CONTACT  
CC INTO THE EXTRACELLULAR SPACE.  
CC -----  
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CC -----  
DR EMBL; X04004; CAA27634.1; -;  
DR EMBL; M36545; AAA33212.1; -;  
DR EMBL; X66483; CAA47110.1; -;  
DR PIR; A23951; A23951.  
DR PIR; A26310; A26310.  
DR PIR; A31643; A31643.  
DR PIR; S22066; S22066.  
DR PIR; A44100; A44100.  
DR Dictydb; DD02005; csaa.  
DR InterPro; IPR002909; IPT\_TIG.  
DR Pfam; PF01833; TIG. 3.  
KW Cell adhesion; Glycoprotein; Membrane; Phosphorylation; Repeat;  
KW GPI-anchor; Lipoprotein; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 492 CONTACT SITE A PROTEIN.  
FT PROPEP 493 514 REMOVED IN MATURE FORM (POTENTIAL).  
FT DOMAIN 20 453 GLOBULAR (POTENTIAL).  
FT DOMAIN 454 485 PRO-RICH (HINGE STRUCTURE).  
FT DOMAIN 462 479 2 X 8 AA REPEATS, PRO-RICH.  
FT REPEAT 462 469 1.  
FT REPEAT 472 479 2.  
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT LIPID 492 492 GPI-ANCHOR (POTENTIAL).  
FT CONFLICT 216 216 V -> G (IN REF. 1).  
SQ SEQUENCE 514 AA; 53696 MW; 96A1C7CF42FEC096 CRC64;  
  
Query Match 46.0%; Score 46; DB 1; Length 514;  
Best Local Similarity 50.0%; Pred. No. 55;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 TSPGTPAPAAEETMTSP 18  
| | | | | | | | | |  
Db 460 TDTATPSPPTPETATPSP 477  
  
RESULT 15  
ID 2151\_CHICK STANDARD; PRT; 706 AA.  
AC 090625;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Zinc finger protein 151 (Zinc finger protein 213) (Fragment).  
OS Gallus gallus (Chicken).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Artiosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
CC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96003919; PubMed=7575457;  
RA Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;  
RT "An unusual arrangement of 13 zinc fingers in the vertebrate gene  
RT 213.";  
RL Biochem. J. 311:219-224(1995).  
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).  
CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
CC FINGER PROTEINS.  
CC -1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U14555; AAA21556.1; -;  
DR HSSP; P08047; ISP2.  
DR InterPro; IPR000210; BTB\_POZ.  
DR InterPro; IPR000822; Znf-C2H2.  
DR Pfam; PF00096; Zf-C2H2. 13.  
DR SMART; SM00355; Znf\_C2H2. 13.  
DR PROSITE; PS50097; BTB, PARTIAL.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 12.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 13.  
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
KW Nuclear protein; Repeat.  
FT NON\_TER 1 1  
FT DOMAIN <1 12 BTB.  
FT DOMAIN 205 640 ZINC FINGERS.  
FT ZN\_FING 205 227 C2H2-TYPE.  
FT ZN\_FING 233 255 C2H2-TYPE.  
FT ZN\_FING 261 283 C2H2-TYPE.  
FT ZN\_FING 289 311 C2H2-TYPE.  
FT ZN\_FING 317 339 C2H2-TYPE.  
FT ZN\_FING 345 367 C2H2-TYPE.  
FT ZN\_FING 373 395 C2H2-TYPE.  
FT ZN\_FING 401 423 C2H2-TYPE.  
FT ZN\_FING 427 450 C2H2-TYPE.  
FT ZN\_FING 457 479 C2H2-TYPE.  
FT ZN\_FING 485 507 C2H2-TYPE.  
FT ZN\_FING 513 536 C2H2-TYPE.  
FT ZN\_FING 618 640 C2H2-TYPE.  
SQ SEQUENCE 706 AA; 76820 MW; 4BDAC680808F1136 CRC64;  
  
Query Match 46.0%; Score 46; DB 1; Length 706;  
Best Local Similarity 50.0%; Pred. No. 76;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
  
QY 2 SPGTPAPAAEETMTSPG 19  
| | | | | | | | | |  
Db 99 SPSRPQPAESEVGNSSPG 116  
  
Search completed: August 13, 2002, 08:36:17  
Job time: 366 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:37:06 ; Search time 43.32 seconds  
(without alignments)  
75.875 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233  
Perfect score: 100  
Sequence: 1 TSPGPAPAEETMTSPG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp.\_archaea:\*  
2: sp.\_bacteria:\*  
3: sp.\_fungi:\*  
4: sp.\_human:\*  
5: sp.\_invertebrate:\*  
6: sp.\_mammal:\*  
7: sp.\_mhc:\*  
8: sp.\_organelle:\*  
9: sp.\_phage:\*  
10: sp.\_plant:\*  
11: sp.\_rodent:\*  
12: sp.\_virus:\*  
13: sp.\_vertebrate:\*  
14: sp.\_unclassified:\*  
15: sp.\_virus:\*  
16: sp.\_bacteriap:\*  
17: sp.\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.0	956	10	Q9LJ64	Q9LJ64 arabidopsis
2	53.0	536	12	Q9WR75	Q9WR75 macaca mulatta
3	53.0	536	12	Q9J2L9	Q9J2L9 macaca mulatta
4	52.0	801	5	Q23635	Q23635 caenorhabditis
5	52.0	874	2	Q9K4C4	Q9K4C4 streptomyces
6	52.0	878	5	P91859	P91859 caenorhabditis
7	51.0	379	11	O88852	O88852 mus musculus
8	51.0	989	5	O9GY99	O9GY99 leishmania
9	51.0	2066	2	Q9LAX1	Q9LAX1 streptomyces
10	51.0	2938	11	Q61769	Q61769 mus musculus
11	49.5	49.5	500	12	Q68979 human herpes
12	49.5	49.5	626	12	Q68978 human herpes
13	49.5	49.5	626	12	Q9QNF5 human herpes
14	49.5	49.5	626	12	Q9QNF4 human herpes
15	49.0	139	2	Q9AKS1	Q9AKS1 pseudomonas
16	49.0	282	13	Q9DF19	Q9DF19 gallus gallus

17	49.0	575	11	O88339	O88339 rattus norvegicus
18	48.0	132	4	P78429	P78429 homo sapiens
19	48.0	253	12	Q99CW8	Q99CW8 bovine herpes
20	48.0	424	11	Q99N63	Q99N63 mesocricetus
21	48.0	427	16	O83835	O83835 leoponema p
22	48.0	490	3	Q96V97	Q96V97 oriplomycetes
23	48.0	497	4	Q9H6L5	Q9H6L5 homo sapiens
24	48.0	595	11	O922L3	O922L3 mus musculus
25	48.0	606	4	Q9Y2D9	Q9Y2D9 homo sapiens
26	48.0	650	5	O17866	O17866 caenorhabditis
27	48.0	778	5	Q9U9K6	Q9U9K6 caenorhabditis
28	48.0	846	5	O01699	O01699 caenorhabditis
29	48.0	862	11	O9JIK1	O9JIK1 rattus norvegicus
30	48.0	864	5	Q93336	Q93336 caenorhabditis
31	48.0	1117	5	Q9U9K7	Q9U9K7 caenorhabditis
32	48.0	1272	4	Q9UGH1	Q9UGH1 homo sapiens
33	48.0	1300	4	Q9BXA9	Q9BXA9 homo sapiens
34	48.0	1323	11	O62255	O62255 mus musculus
35	48.0	3940	3	Q9HE19	Q9HE19 neurospora
36	47.5	2635	12	P88955	P88955 mus musculus
37	47.5	2635	12	O40942	O40942 kaposis sarcoma
38	47.0	191	5	O9VE7	O9VE7 drosophila
39	47.0	275	10	O9LIX7	O9LIX7 oryza sativa
40	47.0	375	16	Q9RW21	Q9RW21 delnococtus
41	47.0	405	4	Q9BU21	Q9BU21 homo sapiens
42	47.0	408	2	Q9Z4V4	Q9Z4V4 streptomyces
43	47.0	539	4	Q9NM45	Q9NM45 homo sapiens
44	47.0	551	4	Q9F613	Q9F613 homo sapiens
45	47.0	576	4	Q9HA18	Q9HA18 homo sapiens

#### ALIGNMENTS

RESULT 1  
Q9LJ64 PRELIMINARY; PRT; 956 AA.  
ID Q9LJ64  
AC Q9LJ64;  
DT 01-OCR-2000 (TREMREL. 15, Created)  
DT 01-OCR-2000 (TREMREL. 15, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE EXTENSIN PROTEIN-LIKE.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;  
OC eumids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=20363099; Pubmed=10907853;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, TAC and BAC clones."  
RT DNA Res. 7:217-221(2000).  
DR EMBL: AP000735; BAB01698.1;  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003882; Pistil\_extensin.  
DR InterPro: IPR002965; P-rich\_extensin.  
DR PRINTS: PR01217; PRICHEXTENSIN.  
DR SMART: SM00370; LRR\_5.  
DR PROSITE: PS00201; FLAVODOXIN; UNKNOWN 1.  
SQ SEQUENCE 956 AA; 102822 MW; E34E1B5E63BBA7C3 CRC64;









Query Match 49.5%; Score 49.5; DB 12; Length 500;  
Best Local Similarity 64.7%; Pred. No. 46;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 SPGPAPAAEETMTTSP 18  
||| | ||| | :||  
Db 478 SPG-PGPAAEETSSSP 493

## RESULT 12

Q68978 PRELIMINARY; PRT; 626 AA.  
AC Q68978;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DE ALKALINE EXONUCLEASE.  
GN AE.  
OS human herpesvirus 1.  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10298;

RN [1]  
RP SEQUENCE OF 1-189 FROM N.A.  
RX MEDLINE=84036396; PubMed=6313961;  
RA Costa R.H., Draper K.G., Banks L., Powell K.L., Cohen G.,  
RA Eisenberg R., Wagner E.K.;  
RT "High-resolution characterization of herpes simplex virus type 1  
transcripts encoding alkaline exonuclease and a 50,000-dalton protein  
tentatively identified as a capsid protein.";  
RL J. Virol. 48:591-603(1983).  
RN [2]  
RP SEQUENCE FROM N.A.

RX MEDLINE=86144016; PubMed=3005609;  
RA Draper K.G., Devi-Rao G., Costa R.H., Blair E.D., Thompson R.L.,  
RA Wagner E.K.;  
RT "Characterization of the genes encoding herpes simplex virus type 1  
RT and type 2 alkaline exonucleases and overlapping proteins.";  
RL J. Virol. 57:1023-1036(1986).  
DR EMBL\_K02022; AAA45771.1; -;  
DR InterPro: IPR001616; Herpes\_alk\_exo.  
DR Pfam: PF01771; Herpes\_alk\_exo; 1.  
DR PRINTS: PR00924; ALKEXNUCLASE.  
KM Exonuclease.  
SQ SEQUENCE 626 AA; 67469 MW; A651D03A29C70260 CRC64;

Query Match 49.5%; Score 49.5; DB 12; Length 626;  
Best Local Similarity 64.7%; Pred. No. 58;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 SPGPAPAAEETMTTSP 18  
||| | ||| | :||  
Db 604 SPG-PGPAAEETSSSP 619

## RESULT 13

O9QNF5 PRELIMINARY; PRT; 626 AA.  
AC O9QNF5;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE ALKALINE DEOXYRIBONUCLEASE.  
GN U112.  
OS human herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10298;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WT51;

RX MEDLINE=99286799; PubMed=10358747;  
RA Chiba A., Suzutani T., Saijo M., Koyano S., Azuma M.;  
RT "Analysis of nucleotide sequence variations in herpes simplex virus  
RT types 1 and 2, and varicella-zoster virus.";  
RL Acta Virol. 42:401-407(1998).  
DR EMBL; AB009265; BAA84004.2; -;  
DR InterPro: IPR001616; Herpes\_alk\_exo.  
DR Pfam: PF01771; Herpes\_alk\_exo; 1.  
DR PRINTS: PR00924; ALKEXNUCLASE.  
SQ SEQUENCE 626 AA; 67492 MW; F5F92710E50A54A2 CRC64;

QY 2 SPGPAPAAEETMTTSP 18  
||| | ||| | :||  
Db 604 SPG-PGPAAEETSSSP 619

Query Match 49.5%; Score 49.5; DB 12; Length 626;  
Best Local Similarity 64.7%; Pred. No. 58;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 SPGPAPAAEETMTTSP 18  
||| | ||| | :||  
Db 604 SPG-PGPAAEETSSSP 619

## RESULT 14

O9QNF4 PRELIMINARY; PRT; 626 AA.  
AC O9QNF4;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE ALKALINE DEOXYRIBONUCLEASE.  
GN U112.  
OS human herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10298;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KH169;  
RX MEDLINE=99286799; PubMed=10358747;  
RA Chiba A., Suzutani T., Saijo M., Koyano S., Azuma M.;  
RT "Analysis of nucleotide sequence variations in herpes simplex virus  
RT types 1 and 2, and varicella-zoster virus.";  
RL Acta Virol. 42:401-407(1998).  
DR EMBL; AB009266; BAA84005.2; -;  
DR InterPro: IPR001616; Herpes\_alk\_exo.  
DR Pfam: PF01771; Herpes\_alk\_exo; 1.  
DR PRINTS: PR00924; ALKEXNUCLASE.  
SQ SEQUENCE 626 AA; 67484 MW; 88183DEAB9B0DA71 CRC64;

Query Match 49.5%; Score 49.5; DB 12; Length 626;  
Best Local Similarity 64.7%; Pred. No. 58;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 SPGPAPAAEETMTTSP 18  
||| | ||| | :||  
Db 604 SPG-PGPAAEETSSSP 619

## RESULT 15

O9AKS1 PRELIMINARY; PRT; 139 AA.  
AC O9AKS1;  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)  
DE TATB PROTEIN.  
GN TATB.  
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=316;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-ZOBELL ATCC14405;  
RX MEDLINE=21101859; PubMed=11160097;  
RA Heikilla M.P.; Honisch U.; Wunsch W.G.;  
RT "Role of the Tat transport system in nitrous oxide reductase  
translocation and cytochrome cdi biosynthesis in Pseudomonas  
stutzeri.";  
RL J. Bacteriol. 183:1663-1671(2001).  
DR EMBL: AJ299712; CAC29148.1; -.  
DR InterPro: IPR003998; TatB.  
DR PRINTS: PR01506; TATBPROTEIN.  
SO SEQUENCE 139 AA; 14772 MW; 5F82C4A9F09195AF CRC64;

Query Match 49.0%; Score 49; DB 2; Length 139;  
Best Local Similarity 58.8%; Pred. No. 15;  
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 SPCTPAPAAEETMTSP 18  
|| ||||| |  
Db 117 SPAVPAPAAEPAPTPRP 133

Search completed: August 13, 2002, 08:37:08  
Job time: 392 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:30:31 : Search time 20.64 Seconds  
(Without alignments)  
22.485 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233  
Perfect score: 100  
Sequence: 1 TSPGTPAPAAETMTTSPG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfilltest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	%	Match length	DB	ID	Description
No.	Score					
1	100	100.0	259	4	US-09-006-353A-2	Sequence 2, Appl1
2	100	100.0	299	4	US-09-153-927-3	Sequence 3, Appl1
3	54	54.0	440	3	US-08-883-036A-2	Sequence 2, Appl1
4	48	48.0	1057	3	US-08-931-820-4	Sequence 4, Appl1
5	48	48.0	1078	3	US-08-963-825-21	Sequence 21, Appl1
6	48	48.0	1078	4	US-09-570-573-21	Sequence 21, Appl1
7	48	48.0	1078	4	US-09-548-608-21	Sequence 21, Appl1
8	47	47.0	284	4	US-08-793-701-39	Sequence 39, Appl1
9	47	47.0	284	4	US-08-793-701-41	Sequence 41, Appl1
10	47	47.0	284	4	US-08-793-701-57	Sequence 57, Appl1
11	45	45.0	348	3	US-08-415-655-5	Sequence 5, Appl1
12	45	45.0	348	3	US-08-415-655-13	Sequence 13, Appl1
13	45	45.0	348	3	US-08-415-655-15	Sequence 15, Appl1
14	45	45.0	454	3	US-08-348-518C-4	Sequence 4, Appl1
15	45	45.0	454	3	US-08-476-509B-4	Sequence 4, Appl1
16	44	44.0	402	2	US-08-477-254A-2	Sequence 2, Appl1
17	44	44.0	402	2	US-08-477-254B-2	Sequence 2, Appl1
18	44	44.0	402	2	US-08-428-734B-2	Sequence 2, Appl1
19	44	44.0	402	3	US-09-063-237-1	Sequence 1, Appl1
20	44	44.0	402	3	US-08-713-356F-2	Sequence 2, Appl1
21	44	44.0	412	2	US-08-477-254A-4	Sequence 4, Appl1
22	44	44.0	412	2	US-08-477-254B-4	Sequence 4, Appl1
23	44	44.0	412	2	US-08-428-734B-4	Sequence 4, Appl1
24	44	44.0	412	4	US-08-713-556F-4	Sequence 4, Appl1
25	44	44.0	610	1	US-07-821-717B-6	Sequence 6, Appl1
26	44	44.0	610	1	US-08-119-262B-6	Sequence 6, Appl1
27	44	44.0	610	1	US-08-135-929A-11	Sequence 11, Appl1

28	44	44.0	610	1	US-08-234-265A-11	Sequence 11, Appl1
29	43	43.0	471	2	US-08-399-889-24	Sequence 24, Appl1
30	43	43.0	471	3	US-09-167-364-24	Sequence 2, Appl1
31	43	43.0	471	4	US-09-439-897-2	Sequence 2, Appl1
32	43	43.0	557	4	US-08-979-608A-5	Sequence 5, Appl1
33	43	43.0	659	4	US-09-189-462-4	Sequence 4, Appl1
34	43	43.0	4472	2	US-08-804-227C-2	Sequence 2, Appl1
35	42	42.0	207	2	US-08-609-443B-15	Sequence 15, Appl1
36	42	42.0	207	2	US-08-569-063C-15	Sequence 15, Appl1
37	42	42.0	247	3	US-09-129-888-2	Sequence 2, Appl1
38	42	42.0	366	4	US-09-086-483A-2	Sequence 2, Appl1
39	42	42.0	786	4	US-09-103-429A-3	Sequence 3, Appl1
40	42	42.0	805	4	US-09-103-429A-4	Sequence 4, Appl1
41	42	42.0	880	2	US-08-916-917-12	Sequence 12, Appl1
42	42	42.0	880	3	US-09-225-170-12	Sequence 12, Appl1
43	42	42.0	880	4	US-09-378-255-6	Sequence 6, Appl1
44	42	42.0	880	4	US-09-141-212-2	Sequence 2, Appl1
45	42	42.0	880	4	US-09-141-212-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-09-006-353A-2  
: Sequence 2, Application US/0906353A  
: Patent No. 6261801  
: GENERAL INFORMATION:  
: APPLICANT: WEI, YING-FEI  
: APPLICANT: YU, GUO-LING  
: APPLICANT: GENTZ, REINER  
: APPLICANT: RUBEN, STEVEN  
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
: NUMBER OF SEQUENCES: 26  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
: STREET: 9410 KEY WEST AVENUE  
: CITY: ROCKVILLE  
: STATE: MD  
: COUNTRY: US  
: ZIP: 20850  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/006,353A  
: FILING DATE:  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: BROOKS, ANDERS A  
: REFERENCE/DOCKET NUMBER: P3341  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (301) 309-8504  
: TELEFAX: (301) 309-8512  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 259 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-09-006-353A-2

Query Match 100.0%; Score 100; DB 4; Length 259;  
Best Local Similarity 100.0%; Pred. No. 8.4e-06;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAETMTTSPG 19  
Db 185 TSPGTPAPAAETMTTSPG 203

RESULT 2  
US-09-153-927-3  
Sequence 3, Application US/09153927A  
Patent No. 6297022  
GENERAL INFORMATION:  
APPLICANT: McDONNELL, Peter C.  
APPLICANT: Young, Peter R.  
APPLICANT: Zou, Jun  
TITLE OF INVENTION: A Method of Identifying Agonists and  
TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3  
TITLE OF INVENTION: and TR5  
FILE REFERENCE: GH50031  
CURRENT APPLICATION NUMBER: US/09/153,927A  
CURRENT FILING DATE: 1998-09-16  
EARLIER APPLICATION NUMBER: 60/061,334  
EARLIER FILING DATE: 1997-10-08  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Human  
US-09-153-927-3

Query Match 100.0%; Score 100; DB 4; Length 299;  
Best Local Similarity 100.0%; Pred. No. 9.8e-06;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETMTTSPG 19  
|||||  
DB 225 TSPGTPAPAAEETMTTSPG 243

RESULT 3  
US-08-883-036A-2  
Sequence 2, Application US/08883036A  
Patent No. 6072047  
GENERAL INFORMATION:  
APPLICANT: Rauch, Charles  
APPLICANT: Walczak, Hennig  
TITLE OF INVENTION: Receptor That Binds TRAIL  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle,  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Macintosh 7.6  
SOFTWARE: Microsoft Word, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/883,036A  
FILING DATE: 26-JUN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US --to be assigned--  
FILING DATE: 04-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/829,536  
FILING DATE: 28-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/815,255  
FILING DATE: 12-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/799,861  
FILING DATE: 13-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2625-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-883-036A-2

Query Match 54.0%; Score 54; DB 3; Length 440;  
Best Local Similarity 76.9%; Pred. No. 9.6;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 APAEETMTTSPG 19  
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DB 191 APAEETMTTSPG 203

RESULT 4  
US-08-931-820-4  
Sequence 4, Application US/08931820  
Patent No. 6010863  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Assay for collagen degradation  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,820  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 96202596.1  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1057 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Collagen type III  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1055  
OTHER INFORMATION: /label=Modified  
OTHER INFORMATION: /note="Ala may be Pro"  
US-08-931-820-4

Query Match 48.0%; Score 48; DB 3; Length 1057;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 SPTGTPAPAAEETMTTSPG 19  
||| : ||| : |||  
DB 969 APTGTPAPAAEETMTTSPG 986

```
RESULT 5
US-08-963-825-21
; Sequence 21, Application US/08963825
; Patent No. 6110689
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,825
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN ALPHA 1 (III)
; US-08-963-825-21

Query Match 48.0%; Score 48; DB 3; Length 1078;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 SPCGPAPAEFTMTSPG 19
Db 970 APGSPGAGGGAIGSPG 987

RESULT 6
US-09-570-573-21
; Sequence 21, Application US/09570573
; Patent No. 6342361
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
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; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/570,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/187,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN ALPHA 1 (III)
; US-09-570-573-21

Query Match 48.0%; Score 48; DB 4; Length 1078;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 SPCGPAPAEFTMTSPG 19
Db 970 APGSPGAGGGAIGSPG 987

RESULT 7
US-09-548-608-21
; Sequence 21, Application US/09548608
; Patent No. 6353442
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.05  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/548,608  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/187,319  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: GOGORTIS, ADDA C  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 4305/08701  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1078 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: COLLAGEN ALPHA 1 (III)  
US-09-548-608-21

Query Match 48.0%; Score 48; DB 4; Length 1078;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SPCTPAPAEETMTSPG 19  
:||:||||: |||  
Db 970 APGSPRAGCGGATGSPG 987

RESULT 8  
US-08-793-701-39  
Sequence 39, Application US/08793701  
Patent No. 6248581  
GENERAL INFORMATION:  
APPLICANT: GICQUEL, Brigitte  
APPLICANT: LIM, Eng Mong  
APPLICANT: PORTNOI, Denis  
APPLICANT: BERTHER, Francois-Xavier  
APPLICANT: TIMM, Juliano  
TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
NUMBER OF INVENTION: EXPRESSION VECTORS  
TITLE OF INVENTION: EXPRESSION VECTORS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
ADDRESS: DUNNER, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,701  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR9501133  
FILING DATE: 30-AUG-1995  
PRIOR APPLICATION DATA: FR 94/10585

FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McDONELL, Leslie A.  
REGISTRATION NUMBER: 34,872  
REFERENCE/DOCKET NUMBER: 02356.0075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4132  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 284 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-701-39

Query Match 47.0%; Score 47; DB 4; Length 284;  
Best Local Similarity 47.4%; Pred. No. 47;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TSPGTPAPAEETMTSPG 19  
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Db 100 TSPGLTSPGLTDPALISPG 118

RESULT 9  
US-08-793-701-41  
Sequence 41, Application US/08793701  
Patent No. 6248581  
GENERAL INFORMATION:  
APPLICANT: GICQUEL, Brigitte  
APPLICANT: LIM, Eng Mong  
APPLICANT: PORTNOI, Denis  
APPLICANT: BERTHER, Francois-Xavier  
APPLICANT: TIMM, Juliano  
TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
NUMBER OF INVENTION: EXPRESSION VECTORS  
TITLE OF INVENTION: EXPRESSION VECTORS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
ADDRESS: DUNNER, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,701  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR9501133  
FILING DATE: 30-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10585  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McDONELL, Leslie A.  
REGISTRATION NUMBER: 34,872  
REFERENCE/DOCKET NUMBER: 02356.0075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4132  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 284 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-701-41

Query Match 47.0%; Score 47; DB 4; Length 284;  
Best Local Similarity 47.4%; Pred. No. 47;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAETMTSPG 19  
||||| : : : : :  
Db 100 TSPGLTSPGLTDPALTSFG 118

RESULT 10  
US-08-793-701-57  
Sequence 57, Application US/08793701  
Patent No. 6248581  
GENERAL INFORMATION:  
APPLICANT: GICQUEL, Brigitte  
APPLICANT: LIM, Eng Mong  
APPLICANT: BERTHOI, Denis  
APPLICANT: BERTHET, Francois-Xavier  
APPLICANT: TIMM, Juliano  
TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
EXPRESSION VECTORS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESS: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
ADDRESSEE: DUNNER, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793.701  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR9501133  
FILING DATE: 30-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10585  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, Leslie A.  
REGISTRATION NUMBER: 34,872  
REFERENCE/DOCKET NUMBER: 02356.0075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4132  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 284 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-793-701-57

Query Match 47.0%; Score 47; DB 4; Length 284;  
Best Local Similarity 47.4%; Pred. No. 47;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
OY 1 TSPGTPAPAAETMTSPG 19  
||||| : : : : :  
Db 100 TSPGLTSPGLTDPALTSFG 118

Db 100 TSPGLTSPGLTDPALTSFG 118

RESULT 11  
US-08-415-655-5  
Sequence 5, Application US/08415655  
Patent No. 6025480  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Lee, Mong-hong  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: P75K1P2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
TITLE OF INVENTION: SAME  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESS: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/415.655  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/47418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-415-655-5

Query Match 45.0%; Score 45; DB 3; Length 348;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

OY 1 TSPGTPAPAAETMTSP 18  
||||| : : : : :  
Db 152 TSPATPAPASD-LTSDP 167

RESULT 12  
US-08-415-655-13  
Sequence 13, Application US/08415655  
Patent No. 6025480  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Lee, Mong-hong  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: P75K1P2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
TITLE OF INVENTION: SAME  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESS: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/415,655  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/47418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-415-655-13

Query Match 45.0%; Score 45; DB 3; Length 348;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 1 TSPGTPAPAAEETMTSP 18  
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Db 152 TTPATPAPASD--LTS DP 167

RESULT 13  
US-08-415-655-15  
Sequence 15, Application US/08415655  
Patent No. 6025480  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Lee, Mong-hong  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
TITLE OF INVENTION: SAME  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/415,655  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/47418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-415-655-15

Query Match 45.0%; Score 45; DB 3; Length 348;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 1 TSPGTPAPAAEETMTSP 18  
| | | | | : : : : :  
Db 152 TTPATPAPASD--LTS DP 167

RESULT 14  
US-08-348-518C-4  
Sequence 4, Application US/08348518C  
Patent No. 6022740  
GENERAL INFORMATION:  
APPLICANT: SUDOL, MARIUS  
APPLICANT: PEER, BORK  
APPLICANT: HENRY, CHEN  
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A  
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,518C  
FILING DATE: 01-DEC-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 454 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-348-518C-4

Query Match 45.0%; Score 45; DB 3; Length 454;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTSP 18  
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Db 31 SGPQPAPAPATOAPOAP 48



RESULT 15  
US-08-476-509B-4  
; Sequence 4, Application US/08476509B  
; Patent No. 6034212  
; GENERAL INFORMATION:  
; APPLICANT: SUDOL, MARIUS  
; APPLICANT: PEER, BORK  
; APPLICANT: HENRY, CHEN  
; TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A  
; TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICS  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,509B  
; FILING DATE: 01-DEC-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-101 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 343-1684  
; TELEFAX: 201 487-5800  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 454 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-476-509B-4

Query Match 45.0%; Score 45; DB 3; Length 454;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEFTMTSP 18  
: || || || || :  
DB 31 SGGQPPAPATQAAPQAP 48

Search completed: August 13, 2002, 08:30:32  
Job time: 66 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:31:31 ; Search time 29.73 Seconds  
(without alignments)  
870.508 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_27\_259  
Perfect score: 233  
Sequence: 1 TTARQEEYPOQTVAPOQORH.....YLSCTIVGIVLVLLIVFV 233

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 5

Total number of hits satisfying chosen parameters: 10957

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	233	100.0	259	19	AAW64668 Human TRID protein
2	233	100.0	259	20	AAW88408 Human Apo-2Dcr pro
3	233	100.0	259	22	AAU12321 Human PRO366 poly
4	233	100.0	259	22	AAW20111 Human immunostimul
5	233	100.0	259	22	AAW36696 Human tumour necro
6	233	100.0	259	22	AAW53091 Human anglogenesis
7	233	100.0	268	12	AAW82181 FLAG-TRID clone w1
8	233	100.0	299	19	AAW76331 Human tumour necro
9	233	100.0	299	20	AAW29864 Human secreted pro
10	233	100.0	299	20	AAW05744 Tumour necrosis fa
11	233	100.0	299	20	AAW09333 Human TRAIL-R3 pro

12	233	100.0	299	20	AAW94671 Human TNF-related
13	233	100.0	299	20	AAW88409 Human Apo-2Dcr pro
14	233	100.0	299	21	AAW01343 Death receptor, H
15	214	91.8	249	22	AAW82182 FLAG-TRID clone w1
16	185	79.4	259	20	AAW93578 Human hsp90 protei
17	140	60.1	259	20	AAW05726 Tumour necrosis fa
18	48	20.6	366	20	AAW88450 Human Apo-2Dcr pep
19	14	6.0	386	20	AAW98200 RTD, inhibitor of
20	14	6.0	386	20	AAW04144 Human Targo-74 pro
21	14	6.0	386	20	AAW99018 Human TRAIL recept
22	14	6.0	386	20	AAW99019 Human TRAIL recept
23	14	6.0	386	20	AAW92792 Human TNF receptor
24	14	6.0	386	21	AAW01341 TNF-related apopto
25	14	6.0	386	21	AAW69991 Human receptor-ass
26	14	6.0	386	22	AAU12341 Human PRO288 poly
27	14	6.0	386	22	AAW31187 Amino acid sequenc
28	14	6.0	386	22	AAW50892 Human TR10 recepto
29	14	6.0	109	22	AAW68231 Drosophila melanog
30	8	3.4	217	22	AAW93909 Human protein sequ
31	8	3.4	272	22	AAW41810 Human polypeptide
32	8	3.4	272	22	AAW41811 Human TR6 partial
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34	8	3.4	303	22	AAW48349 Partial amino acid
35	8	3.4	350	20	AAW00934 Human DR5 protein
36	8	3.4	411	19	AAW79261 Tumour necrosis fa
37	8	3.4	411	19	AAW76827 Human TR6 protein.
38	8	3.4	411	19	AAW79083 Human death domain
39	8	3.4	411	20	AAW93608 Human killer adria
40	8	3.4	411	20	AAW93576 Human hsp90 protei
41	8	3.4	411	20	AAW00932 Human DR5 protein
42	8	3.4	411	20	AAW88410 Human Apo-2 ligand
43	8	3.4	411	20	AAW83321 Human Apo-2 protei
44	8	3.4	411	21	AAW29790 Human death domain
45	8	3.4	411	21	AAW55805 Human Apo-2 polype
46	8	3.4	411	22	AAW04038 Human Apoptotic pr
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48	8	3.4	411	22	AAW73443 Human Apo-2 recept
49	8	3.4	411	22	AAW48348 Human tumour necro
50	8	3.4	424	22	AAW48352 TR6-Ig fusion prot
51	8	3.4	440	19	AAW99284 Human TRAIL recept
52	8	3.4	440	19	AAW79260 Tumour necrosis fa
53	8	3.4	440	20	AAW05725 Tumour necrosis fa
54	8	3.4	440	21	AAW01340 TNF-related apopto
55	8	3.4	444	20	AAW35231 Protein involved i
56	8	3.0	24	18	AAW33935 Beta1-adrenergic r
57	7	3.0	29	18	AAW10929 Polyclonal anti-fe
58	7	3.0	54	21	AAW52674 Arabidopsis thalia
59	7	3.0	61	20	AAW30434 Mature nematode ex
60	7	3.0	61	21	AAW15319 N. americanum nemat
61	7	3.0	71	21	AAW10929 Arabidopsis thalia
62	7	3.0	74	21	AAW10928 Arabidopsis thalia
63	7	3.0	75	21	AAW10927 Arabidopsis thalia
64	7	3.0	76	22	AAW75966 Human colon cancer
65	7	3.0	79	17	AAW91704 Namfap. Necator a
66	7	3.0	79	20	AAW30412 Nematode extracted
67	7	3.0	85	21	AAW52673 Arabidopsis thalia
68	7	3.0	93	15	AAW50794 G-protein coupled
69	7	3.0	93	17	AAW02986 Arabidopsis thalia
70	7	3.0	98	21	AAW52672 Arabidopsis thalia
71	7	3.0	100	22	AAW67913 Drosophila melanog
72	7	3.0	112	21	AAW38574 Arabidopsis thalia
73	7	3.0	122	21	AAW09814 Arabidopsis thalia
74	7	3.0	124	21	AAW09813 Arabidopsis thalia
75	7	3.0	136	21	AAW32125 Arabidopsis thalia
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77	7	3.0	138	21	AAW32124 Arabidopsis thalia
78	7	3.0	138	21	AAW47701 Arabidopsis thalia
79	7	3.0	153	21	AAW38573 Arabidopsis thalia
80	7	3.0	155	21	AAW38572 Arabidopsis thalia
81	7	3.0	215	22	ABG10788 Novel human diagno
82	7	3.0	235	22	ABG17696 Novel human diagno
83	7	3.0	235	22	ABG18326 Novel human diagno
84	7	3.0	240	19	AAW5914 S. pneumoniae deri

85	7	3.0	244	21	AGC09812	Arabidopsis thalia	158	6	2.6	44	22	ABB32242	Peptide #4893 enco
86	7	3.0	256	22	ABB60500	Drosophila melanog	159	6	2.6	44	22	ABB37490	Peptide #4996 enco
87	7	3.0	258	21	AGC47700	Arabidopsis thalia	160	6	2.6	44	22	ABB22791	Protein #4790 enco
88	7	3.0	262	21	AGC32123	Arabidopsis thalia	161	6	2.6	44	22	AAW70610	Human bone marrow
89	7	3.0	267	19	AAW81726	M. tuberculosis im	162	6	2.6	44	22	AAW18450	Peptide #4884 enco
90	7	3.0	267	19	AAW64359	Mycobacterium tube	163	6	2.6	44	22	AAW30925	Peptide #4962 enco
91	7	3.0	267	20	AAW39156	M. tuberculosis an	164	6	2.6	44	22	AAW06040	Peptide #4728 enco
92	7	3.0	289	22	ABG17560	Novel human diagno	165	6	2.6	48	20	AAW60201	Human colon cancer
93	7	3.0	292	18	AAW18809	Dihydrocolonic a	166	6	2.6	49	22	AAW94998	Human endometrium
94	7	3.0	325	22	AAW93734	Human protein sequ	167	6	2.6	50	22	AAW04078	Human polypeptide
95	7	3.0	330	22	AAW94001	Human stomach can	168	6	2.6	51	22	AAW62748	Propionibacterium
96	7	3.0	330	22	AAW94271	Human protein sequ	169	6	2.6	52	21	AAW34661	Arabidopsis thalia
97	7	3.0	332	21	AAW41611	Human ORFX ORF1375	170	6	2.6	52	21	AAW02891	Human secreted pro
98	7	3.0	332	21	AAW40024	Human polypeptide	171	6	2.6	54	21	AAW19541	Arabidopsis thalia
99	7	3.0	345	19	AAW80643	S. pneumoniae prot	172	6	2.6	54	22	AAW01144	Human polypeptide
100	7	3.0	360	20	AAW40025	Human polypeptide	173	6	2.6	57	22	AAW05225	Human polypeptide
101	7	3.0	365	22	AAW13737	Murine beta-1 adre	174	6	2.6	58	22	AAW45956	Propionibacterium
102	7	3.0	377	15	AAW48693	G-protein coupled	175	6	2.6	58	22	AAW65301	Propionibacterium
103	7	3.0	377	15	AAW02665	Drosophila melanog	176	6	2.6	62	22	AAW44360	Propionibacterium
104	7	3.0	390	22	ABW65316	Propionibacterium	177	6	2.6	63	22	AAW55914	Propionibacterium
105	7	3.0	397	22	AAW46161	Propionibacterium	178	6	2.6	63	22	AAW86245	Human immune/haema
106	7	3.0	401	18	AAW11802	Onchocerca volvulu	179	6	2.6	64	21	AAW76162	Human secreted pro
107	7	3.0	407	18	AAW11800	Onchocerca volvulu	180	6	2.6	64	21	AAW76162	PTDOL APF-encode
108	7	3.0	410	20	AAW93577	Human APORP protei	181	6	2.6	64	22	AAW60687	Arabidopsis thalia
109	7	3.0	436	13	AAW26505	Adrenalin receptor	182	6	2.6	68	21	AAW21112	Arabidopsis thalia
110	7	3.0	467	22	AAW50896	Human DR4. Homo s	183	6	2.6	68	21	AAW28554	Arabidopsis thalia
111	7	3.0	468	19	AAW64483	Human DR4. Homo s	184	6	2.6	68	21	AAW34705	Arabidopsis thalia
112	7	3.0	468	20	AAW93609	Human DR4 protein.	185	6	2.6	68	21	AAW47081	Arabidopsis thalia
113	7	3.0	468	20	AAW93609	Human DR4 protein.	186	6	2.6	69	21	AAW52668	Arabidopsis thalia
114	7	3.0	468	21	AAW72022	Human Death Domain	187	6	2.6	69	21	AAW41928	Arabidopsis thalia
115	7	3.0	468	21	AAW72023	Human Death Domain	188	6	2.6	70	22	AAW44399	Propionibacterium
116	7	3.0	468	21	AAW80546	Amino acid sequenc	189	6	2.6	70	22	AAW06357	Human foetal prote
117	7	3.0	468	21	AAW80546	TNF-related apopt	190	6	2.6	71	21	AAW74316	Neisseria meningit
118	7	3.0	468	22	AAW49241	Human DR4 protein.	191	6	2.6	74	21	AAW34066	Arabidopsis thalia
119	7	3.0	477	22	AAW70765	Human beta1-adreno	192	6	2.6	74	21	AAW35084	Arabidopsis thalia
120	7	3.0	482	22	AAW58143	Propionibacterium	193	6	2.6	74	22	ABW60037	Novel human diagno
121	7	3.0	498	21	AAW52714	Arabidopsis thalia	194	6	2.6	75	22	ABW604503	Novel human diagno
122	7	3.0	513	21	AAW52713	Arabidopsis thalia	195	6	2.6	75	22	ABW14408	Novel human diagno
123	7	3.0	521	21	AAW52712	Arabidopsis thalia	196	6	2.6	75	22	ABW14461	Novel human diagno
124	7	3.0	537	21	AAW84870	Amino acid sequenc	197	6	2.6	75	22	ABW16989	Novel human diagno
125	7	3.0	551	21	AAW84870	Human ORFX ORF1813	198	6	2.6	75	22	ABW17397	Novel human diagno
126	7	3.0	576	21	AAW24204	Human vesicle asso	199	6	2.6	75	22	AAW89055	Human immune/haema
127	7	3.0	576	22	AAW95100	Human protein sequ	200	6	2.6	77	22	AAW42266	Propionibacterium
128	7	3.0	677	22	ABW61957	Drosophila melanog	201	6	2.6	79	22	AAW00856	Human bone marrow
129	7	3.0	1247	22	ABW61174	Rat brain alpha-II	202	6	2.6	80	22	AAW50707	Propionibacterium
130	7	3.0	1792	22	ABW66477	Rat T-type voltage	203	6	2.6	83	21	AAW34660	Arabidopsis thalia
131	7	3.0	1835	20	AAW14597	Amino acid sequenc	204	6	2.6	84	21	AAW74315	Neisseria meningit
132	7	3.0	3739	21	AAW18658	S. venezuelae macr	205	6	2.6	84	22	AAW22575	Novel human colon
133	7	3.0	3739	21	AAW18658	S. venezuelae macr	206	6	2.6	84	22	AAW92538	Human digestive sy
134	7	3.0	3739	21	AAW77193	Narbonolide syntha	207	6	2.6	85	21	AAW19540	Propionibacterium
135	7	3.0	3739	21	AAW77201	S. venezuelae pik	208	6	2.6	85	22	AAW48698	Arabidopsis thalia
136	7	3.0	3739	21	AAW67202	S. venezuelae pik	209	6	2.6	86	22	ABW26420	Novel human diagno
137	7	3.0	12199	21	AAW77180	Human secreted pro	210	6	2.6	87	17	AAW92991	Homologous sequenc
138	6	2.6	13	18	AAW38117	SH3-binding peptid	211	6	2.6	88	18	AAW20911	H. pylori cytoplas
139	6	2.6	14	17	AAW05449	Human secreted pro	212	6	2.6	88	22	AAW45191	Propionibacterium
140	6	2.6	14	18	AAW37657	Human secreted pro	213	6	2.6	91	20	AAW00202	Enterococcus faeca
141	6	2.6	16	21	AAW00224	Human secreted pro	214	6	2.6	91	20	AAW00202	Enterococcus faeca
142	6	2.6	16	21	AAW00224	Human secreted pro	215	6	2.6	93	22	AAW80048	Human protein SEQ
143	6	2.6	17	7	AAW61749	Human secreted pro	216	6	2.6	93	22	AAW80048	Human protein SEQ
144	6	2.6	23	22	AAW60685	Human secreted pro	217	6	2.6	95	19	AAW21419	Human high mobil
145	6	2.6	25	19	AAW59638	Human secreted pro	218	6	2.6	96	21	AAW34659	Arabidopsis thalia
146	6	2.6	32	19	AAW79213	Human secreted pro	219	6	2.6	97	15	AAW57475	Human secreted pro
147	6	2.6	33	22	AAW60686	Human secreted pro	220	6	2.6	97	17	AAW92078	Human secreted pro
148	6	2.6	33	22	AAW60686	Human secreted pro	221	6	2.6	97	22	AAW92078	Human secreted pro
149	6	2.6	34	22	AAW37085	Human secreted pro	222	6	2.6	97	22	AAW37085	Human secreted pro
150	6	2.6	34	22	AAW30561	Human secreted pro	223	6	2.6	97	22	AAW05174	Human secreted pro
151	6	2.6	37	22	AAW43274	Human secreted pro	224	6	2.6	98	21	AAW16621	Human secreted pro
152	6	2.6	37	22	AAW26323	Human secreted pro	225	6	2.6	98	21	AAW19539	Human secreted pro
153	6	2.6	37	22	AAW64183	Human secreted pro	226	6	2.6	98	21	AAW44934	Human secreted pro
154	6	2.6	37	22	AAW70100	Human secreted pro	227	6	2.6	98	21	AAW01380	Human secreted pro
155	6	2.6	40	22	AAW37118	Human secreted pro	228	6	2.6	99	21	AAW21111	Human secreted pro
156	6	2.6	40	22	AAW60689	Human secreted pro	229	6	2.6	99	21	AAW28553	Human secreted pro
157	6	2.6	41	22	AAW85060	Human secreted pro	230	6	2.6	99	21	AAW34704	Human secreted pro

231	6	2.6	99	21	AA652667	Arabidopsis thalia	304	6	2.6	131	22	ABR23066	Protein #5065 enco
232	6	2.6	99	21	AA652671	Arabidopsis thalia	305	6	2.6	131	22	AAW58399	Human brain expres
233	6	2.6	99	21	AA650044	Human secreted pro	306	6	2.6	131	22	AAW70885	Human bone marrow
234	6	2.6	100	18	AAW13527	Anti-melanoma anti	307	6	2.6	131	22	AAW18715	Peptide #5149 enco
235	6	2.6	100	20	AAW19277	Arabidopsis thalia	308	6	2.6	131	22	AAW31177	Peptide #5214 enco
236	6	2.6	101	20	AAW29245	Amino acid sequenc	309	6	2.6	131	22	AAW31177	S. epidermidis ope
237	6	2.6	105	21	AAW44933	Zea mays protein f	310	6	2.6	133	22	ABR68834	Drosophila melanog
238	6	2.6	105	22	ABR65119	Drosophila melanog	311	6	2.6	133	22	ABR62686	Murine OR-1 like pol
239	6	2.6	105	22	ABR65122	Drosophila melanog	312	6	2.6	134	21	AAW24064	Arabidopsis thalia
240	6	2.6	105	22	ABR67261	Drosophila melanog	313	6	2.6	134	21	AAW24064	Arabidopsis thalia
241	6	2.6	105	22	AAW31125	Peptide #5162 enco	314	6	2.6	135	21	AAW80291	Humanised anti-Fas
242	6	2.6	106	22	AAW82034	S. epidermidis ope	315	6	2.6	135	21	AAW80292	Humanised anti-Fas
243	6	2.6	107	22	AAW54125	Propionibacterium	316	6	2.6	135	22	AAW44502	Propionibacterium
244	6	2.6	109	21	AAW34350	Zea mays protein f	317	6	2.6	136	17	AAW57481	Humanised 1308F VH
245	6	2.6	110	17	AAW88692	Allergen Alt a 12	318	6	2.6	136	17	AAW82084	Humanised antibody
246	6	2.6	111	19	AAW83192	Wheat 4-alpha-gluc	319	6	2.6	136	22	ABG17564	Novel human diagno
247	6	2.6	111	21	AAW12573	Zea mays protein f	320	6	2.6	138	22	AAW62797	Propionibacterium
248	6	2.6	111	22	ABR38499	Peptide #6005 enco	321	6	2.6	138	22	AAW66337	Novel human diagno
249	6	2.6	111	22	ABR23651	Protein #5650 enco	322	6	2.6	138	22	ABG01165	Novel human diagno
250	6	2.6	111	22	AAW59115	Human brain expres	323	6	2.6	138	22	ABG26296	Novel human diagno
251	6	2.6	111	22	AAW1650	Human bone marrow	324	6	2.6	138	22	ABG28151	Novel human diagno
252	6	2.6	111	22	AAW19253	Peptide #5687 enco	325	6	2.6	139	21	AAW75079	Neisseria gonorrh
253	6	2.6	111	22	AAW31944	Peptide #5981 enco	326	6	2.6	139	21	AAW75080	Neisseria meningit
254	6	2.6	112	20	AAW18127	Clone 1 of A. thal	327	6	2.6	139	21	AAW75081	Neisseria meningit
255	6	2.6	112	20	AAW21110	Arabidopsis thalia	328	6	2.6	139	21	AAW75081	S. epidermidis ope
256	6	2.6	112	21	AAW28552	Arabidopsis thalia	329	6	2.6	140	22	ABG26230	Novel human diagno
257	6	2.6	112	21	AAW34703	Arabidopsis thalia	330	6	2.6	142	21	AAW47049	Arabidopsis thalia
258	6	2.6	112	21	AAW52666	Arabidopsis thalia	331	6	2.6	142	21	AAW47064	Arabidopsis thalia
259	6	2.6	112	21	AAW52670	Arabidopsis thalia	332	6	2.6	142	21	AAW57167	Arabidopsis thalia
260	6	2.6	113	21	AAW04869	Arabidopsis thalia	333	6	2.6	142	22	AAW41513	Propionibacterium
261	6	2.6	113	21	AAW41926	Arabidopsis thalia	334	6	2.6	144	22	ABG13852	Novel human diagno
262	6	2.6	113	21	AAW47050	Arabidopsis thalia	335	6	2.6	145	19	AAW60119	Mycobacterium vacc
263	6	2.6	113	21	AAW47065	Arabidopsis thalia	336	6	2.6	145	20	AAW14865	Novel human diagno
264	6	2.6	113	21	AAW47080	Arabidopsis thalia	337	6	2.6	145	20	ABG16992	Novel human diagno
265	6	2.6	113	22	ABR39444	Peptide #6350 enco	338	6	2.6	146	18	AAW22841	Human anti-tumour
266	6	2.6	113	22	ABR24209	Protein #6208 enco	339	6	2.6	146	21	AAW46658	Arabidopsis thalia
267	6	2.6	113	22	AAW60131	Human brain expres	340	6	2.6	148	22	AAW10299	Human polypeptide
268	6	2.6	113	22	AAW2745	Human bone marrow	341	6	2.6	149	22	ABR59178	Drosophila melanog
269	6	2.6	113	22	AAW32973	Peptide #7010 enco	342	6	2.6	151	21	AAW44246	Arabidopsis thalia
270	6	2.6	114	22	AAW44336	Propionibacterium	343	6	2.6	151	22	AAW03604	Human polypeptide
271	6	2.6	114	22	AAW11521	Human polypeptide	344	6	2.6	153	21	AAW00836	Human secreted pro
272	6	2.6	116	22	ABG25103	Novel human diagno	345	6	2.6	153	21	AAW33173	Eucalyptus grandis
273	6	2.6	117	15	AAW57476	CDR-grafted anti-R	346	6	2.6	155	21	AAW17607	Arabidopsis thalia
274	6	2.6	117	16	AAW6296	Human immunoglobul	347	6	2.6	155	21	AAW56304	Propionibacterium
275	6	2.6	117	16	AAW66334	Human immunoglobul	348	6	2.6	155	22	AAW13344	Novel human secret
276	6	2.6	117	17	AAW62079	Murine 1308F VH CD	349	6	2.6	157	21	AAW17606	Arabidopsis thalia
277	6	2.6	119	18	AAW13526	Anti-melanoma anti	350	6	2.6	158	22	AAW39656	Propionibacterium
278	6	2.6	119	22	ABR40557	Peptide #8063 enco	351	6	2.6	158	22	AAW16464	Human novel secret
279	6	2.6	119	22	ABR24855	Protein #6854 enco	352	6	2.6	158	22	AAW38515	Gorilla olfactory
280	6	2.6	119	22	AAW61415	Human bone marrow	353	6	2.6	160	22	ABG26487	Novel human diagno
281	6	2.6	119	22	AAW74205	Human bone marrow	354	6	2.6	161	22	ABG29965	Novel human diagno
282	6	2.6	119	22	AAW43439	Peptide #8356 enco	355	6	2.6	165	22	AAW05113	Human polypeptide
283	6	2.6	120	15	AAW47491	Humanised anti-CD1	356	6	2.6	166	22	AAW07352	Interleukin-X (IL-
284	6	2.6	120	18	AAW27551	Human Ab heavy cha	357	6	2.6	168	21	AAW04868	Arabidopsis thalia
285	6	2.6	120	18	AAW27551	Human Ab heavy cha	358	6	2.6	168	21	AAW04868	Arabidopsis thalia
286	6	2.6	120	22	AAW07768	Human polypeptide	359	6	2.6	168	21	AAW04868	Arabidopsis thalia
287	6	2.6	120	22	AAW02535	Anti-adipocyte mon	360	6	2.6	172	21	AAW47063	Arabidopsis thalia
288	6	2.6	123	19	AAW79228	Heavy chain variab	361	6	2.6	172	22	ABG07576	Novel human diagno
289	6	2.6	123	22	AAW19814	B. burgdorferi ant	362	6	2.6	172	22	ABG14155	Novel human diagno
290	6	2.6	123	22	ABG16390	Novel human diagno	363	6	2.6	172	22	ABG14414	Novel human diagno
291	6	2.6	123	22	ABG26294	Novel human diagno	364	6	2.6	172	22	AAW32808	Novel human secret
292	6	2.6	125	20	AAW13036	Human secreted pro	365	6	2.6	175	22	ABR62382	Drosophila melanog
293	6	2.6	125	21	AAW47079	Arabidopsis thalia	366	6	2.6	176	22	AAW55201	Propionibacterium
294	6	2.6	126	15	AAW45609	Monoclonal antibod	367	6	2.6	178	22	ABG14807	Novel human diagno
295	6	2.6	126	21	AAW00026	Human secreted pro	368	6	2.6	180	22	AAW66383	Human partial olfa
296	6	2.6	126	22	AAW92417	C glutamicum prote	369	6	2.6	182	21	AAW82504	Human adenovirus t
297	6	2.6	129	21	AAW46659	Arabidopsis thalia	370	6	2.6	184	21	AAW42698	Propionibacterium
298	6	2.6	129	21	AAW32669	Arabidopsis thalia	371	6	2.6	184	22	ABG06690	Novel human diagno
299	6	2.6	129	21	AAW64703	Human 5' EST relat	372	6	2.6	184	22	ABG14160	Novel human diagno
300	6	2.6	129	21	AAW21859	Human cardiovascular	373	6	2.6	184	22	ABG19507	Novel human diagno
301	6	2.6	130	22	AAW57218	Human prostate can	374	6	2.6	185	19	AAW98220	H. pylori GHPO 234
302	6	2.6	130	22	ABR63591	Drosophila melanog	375	6	2.6	187	22	ABG16394	Novel human diagno
303	6	2.6	130	22	AAW46604	Propionibacterium	376	6	2.6	189	22	AAW42341	Propionibacterium
	6	2.6	131	22	ABR37784	Peptide #5290 enco		6	2.6	191	21	AAW39548	Arabidopsis thalia

377	6	2.6	192	16	AAR69640	Hepatitis C virus	450	2.6	249	16	AAR77611	Humanised 5G1.1 VH
378	6	2.6	192	16	AAR69658	Hepatitis C virus	451	2.6	249	18	AAW24061	Human W5X receptor
379	6	2.6	192	16	AAR69656	Hepatitis C virus	452	2.6	250	21	AAW24061	Human ORFX ORF2721
380	6	2.6	192	16	AAR69644	Hepatitis C virus	453	2.6	250	22	ABG07012	Novel human diago
381	6	2.6	192	17	AAR89527	Hepatitis C virus	454	2.6	250	22	AAW78506	Human protein sequ
382	6	2.6	192	17	AAR89529	Hepatitis C virus	455	2.6	250	22	AAW78506	Human protein sequ
383	6	2.6	192	17	AAR89511	Hepatitis C virus	456	2.6	252	22	ABG22238	Novel human diago
384	6	2.6	192	17	AAR89515	Hepatitis C virus	457	2.6	253	22	ABG11941	Human CGI-97 prote
385	6	2.6	192	19	AAW1596	Hepatitis C virus	458	2.6	253	22	AAW79490	Human protein sequ
386	6	2.6	192	22	ABG15682	Novel human diago	459	2.6	254	21	AAW33010	Human secreted pro
387	6	2.6	194	21	AAW10530	Arbidopsis thalia	460	2.6	254	22	AAW78341	Human protein sequ
388	6	2.6	194	21	AAW24413	Arbidopsis thalia	461	2.6	256	22	ABG14800	Novel human diago
389	6	2.6	194	22	AAW31017	Novel human secret	462	2.6	256	22	AAW2545	C glutamic prote
390	6	2.6	195	21	AAW40635	Human ORFX ORF399	463	2.6	256	22	AAW2545	Murine OR-1like pol
391	6	2.6	196	22	AAW80871	Lipid biosynthesis	464	2.6	257	21	AAW07568	Arbidopsis thalia
392	6	2.6	196	22	AAW83319	P patens lipid met	465	2.6	257	21	AAW17567	Arbidopsis thalia
393	6	2.6	201	21	AAW47048	Arbidopsis thalia	466	2.6	262	21	AAW24248	Human ORFX ORF2262
394	6	2.6	201	22	AAW68183	Arbidopsis thalia	467	2.6	263	22	ABG06689	Novel human diago
395	6	2.6	202	17	AAW89497	Penicillin acylase	468	2.6	263	22	ABG16991	Novel human diago
396	6	2.6	202	17	AAW89495	Penicillin acylase	469	2.6	264	22	ABG14668	Novel human diago
397	6	2.6	202	17	AAW89496	Penicillin acylase	470	2.6	264	22	AAW16528	Novel human diago
398	6	2.6	202	22	AAW72674	Murine OR-1like pol	471	2.6	265	22	AAW48363	Proprionibacterium
399	6	2.6	204	22	AAW10920	Human gene 12 enco	472	2.6	268	21	AAW11289	Arbidopsis thalia
400	6	2.6	205	22	AAW69885	Ox40 protein. Uni	473	2.6	268	21	AAW49632	Arbidopsis thalia
401	6	2.6	208	22	AAW5399	Human protein sequ	474	2.6	269	22	ABG16993	Novel human diago
402	6	2.6	210	20	AAW07103	Colon cancer assoc	475	2.6	271	22	AAW53107	Novel human diago
403	6	2.6	210	21	AAW39547	Arbidopsis thalia	476	2.6	271	22	ABG15685	Novel human diago
404	6	2.6	211	18	AAW14495	Urease accessory m	477	2.6	271	22	ABG19951	Novel human diago
405	6	2.6	211	22	ABW1181	Peptide #3832 enco	478	2.6	272	21	AAW70732	Klebsiella oxytoca
406	6	2.6	211	22	ABW36378	Peptide #3884 enco	479	2.6	272	22	ABW11203	Drosophila melanog
407	6	2.6	211	22	ABW21732	Protein #3731 enco	480	2.6	272	22	AAW40815	Human polypeptide
408	6	2.6	211	22	AAW57143	Human brain expres	481	2.6	272	22	AAW19621	Human diagnostic a
409	6	2.6	211	22	AAW69536	Human bone marrow	482	2.6	273	19	AAW60128	M. vaccae antigen
410	6	2.6	211	22	AAW17366	Peptide #3800 enco	483	2.6	273	20	AAW14874	Partial amino acid
411	6	2.6	211	22	AAW29876	Peptide #3913 enco	484	2.6	274	22	ABW58196	Drosophila melanog
412	6	2.6	211	22	AAW05055	Peptide #3737 enco	485	2.6	274	22	ABG20434	Novel human diago
413	6	2.6	212	22	ABW11999	Drosophila melanog	486	2.6	275	14	AAW43390	Sequence specific
414	6	2.6	213	22	AAW60357	Chicken atonal hom	487	2.6	275	17	AAW89933	Neisseria gonorrhoe
415	6	2.6	218	14	AAW33259	Sj23-1-like protein.	488	2.6	275	21	AAW67400	N. gonorrhoe spec
416	6	2.6	218	22	ABW60938	Drosophila melanog	489	2.6	278	22	ABG07552	Novel human diago
417	6	2.6	219	21	AAW96302	Human tGFAM-14 imm	490	2.6	279	21	AAW320607	Arbidopsis thalia
418	6	2.6	219	22	ABW58448	Drosophila melanog	491	2.6	284	22	AAW59854	Proprionibacterium
419	6	2.6	220	22	AAW94801	Human protein sequ	492	2.6	284	22	ABW07559	Novel human diago
420	6	2.6	221	22	AAW57429	Proprionibacterium	493	2.6	286	22	ABW62405	Drosophila melanog
421	6	2.6	222	21	AAW10529	Arbidopsis thalia	494	2.6	287	22	ABG14156	Novel human diago
422	6	2.6	222	21	AAW24412	Arbidopsis thalia	495	2.6	289	22	AAW16031	Human novel secret
423	6	2.6	222	22	ABW58672	Drosophila melanog	496	2.6	291	22	ABG07730	Novel human diago
424	6	2.6	222	22	ABW38154	Novel human diago	497	2.6	292	22	ABG24151	Novel human diago
425	6	2.6	224	19	AAW98587	H. pylori GHPO 85	498	2.6	294	22	ABW60740	Drosophila melanog
426	6	2.6	226	21	AAW07569	Arbidopsis thalia	499	2.6	294	22	AAW52463	Mycobacterium tube
427	6	2.6	226	21	AAW11062	Arbidopsis thalia	500	2.6	295	21	AAW68463	Mouse testis speci
428	6	2.6	226	21	AAW17568	Arbidopsis thalia	501	2.6	295	22	ABG03705	Novel human diago
429	6	2.6	228	22	AAW35239	Enterococcus faeca	502	2.6	297	22	AAW78949	C. glutamicum SRT
430	6	2.6	228	22	AAW05775	Rice invertase inh	503	2.6	298	22	AAW72939	Human olfactory re
431	6	2.6	230	21	AAW46657	Arbidopsis thalia	504	2.6	298	22	AAW72939	Human olfactory re
432	6	2.6	231	22	ABG05553	Novel human diago	505	2.6	298	22	AAW72935	Human olfactory re
433	6	2.6	232	22	ABW60555	Drosophila melanog	506	2.6	299	22	AAW72931	Human olfactory re
434	6	2.6	232	22	ABW07577	Novel human diago	507	2.6	299	22	AAW72936	Human olfactory re
435	6	2.6	235	21	AAW44245	Arbidopsis thalia	508	2.6	299	22	AAW72937	Human olfactory re
436	6	2.6	235	22	AAW61793	Proprionibacterium	509	2.6	300	22	ABG14415	Novel human diago
437	6	2.6	236	22	ABG33665	Novel human diago	510	2.6	300	22	AAW72932	Human olfactory re
438	6	2.6	237	22	AAW79065	Human protein sequ	511	2.6	300	22	AAW72933	Human olfactory re
439	6	2.6	238	21	AAW34396	Arbidopsis thalia	512	2.6	300	22	AAW72934	Human olfactory re
440	6	2.6	239	22	AAW79064	Human protein sequ	513	2.6	301	22	AAW72927	Human olfactory re
441	6	2.6	241	22	ABG04939	Novel human diago	514	2.6	302	19	AAW98243	H. pylori GHPO 852
442	6	2.6	241	22	AAW33231	Novel human secret	515	2.6	305	22	AAW66367	Human partial olfa
443	6	2.6	242	21	AAW15137	Anti-murine CTLA-4	516	2.6	305	22	AAW66389	Human partial olfa
444	6	2.6	245	22	AAW67619	Human leukocyte an	517	2.6	306	21	AAW16164	S. avermitilis HRP
445	6	2.6	247	18	AAW20248	H. pylori cytoplas	518	2.6	311	22	ABG19950	Novel human diago
446	6	2.6	247	18	ABG29563	Novel human diago	519	2.6	312	22	AAW66377	Human partial olfa
447	6	2.6	248	16	AAW77616	Humanised CDR-graf	520	2.6	313	19	AAW53955	Bacillus subtilis
448	6	2.6	248	16	AAW77607	Humanised CDR-graf	521	2.6	314	22	AAW24694	Human olfactory re
449	6	2.6	249	16	AAW77615	Humanised 5G1.1 VH	522	2.6	314	22	AAW24763	Human olfactory re

523	6	2.6	314	22	AA672151	Human olfactory re	596	6	2.6	362	19	AAW69717	Herpesviral VP22 p
524	6	2.6	315	22	AA673015	Olfactory receptor	597	6	2.6	362	21	AAW82497	Human adenovirus t
525	6	2.6	316	22	AAU16014	Human novel secret	598	6	2.6	362	22	AA662572	Follicular conjunc
526	6	2.6	317	22	AAE10692	G-protein coupled	599	6	2.6	366	18	AAW40248	B. cereus LeuDH pr
527	6	2.6	317	22	AAE11901	Human G-protein co	600	6	2.6	366	21	AA636484	Arabidopsis thalia
528	6	2.6	317	22	AA671408	Human olfactory re	601	6	2.6	366	22	AAW78703	Human protein SEQ
529	6	2.6	317	22	AA671703	Human olfactory re	602	6	2.6	367	21	AA613801	Arabidopsis thalia
530	6	2.6	317	22	AA672330	Human OR-like poly	603	6	2.6	367	21	AA640335	Arabidopsis thalia
531	6	2.6	317	22	AA672925	Human olfactory re	604	6	2.6	368	22	AA620307	Novel human diagno
532	6	2.6	317	22	AA672977	Olfactory receptor	605	6	2.6	369	22	ABG16527	Novel human diagno
533	6	2.6	318	22	AAU58952	Propionibacterium	606	6	2.6	370	20	AA114924	Amino acid sequenc
534	6	2.6	320	21	AA634713	Arabidopsis thalia	607	6	2.6	372	20	AAW14924	HSV-2 strain SB5 C
535	6	2.6	320	21	AA195055	Caridida albicans p	608	6	2.6	372	19	AAW72164	Thermotable alkai
536	6	2.6	321	22	AB803778	Human musculoskele	609	6	2.6	375	19	AAW44141	Drosophila melanog
537	6	2.6	321	22	AAU23231	Novel human enzyme	610	6	2.6	376	22	AB860164	Amino acid sequenc
538	6	2.6	321	22	AAU23757	Novel human enzyme	611	6	2.6	377	21	AA686643	Mastadenovirus 9 f
539	6	2.6	322	21	AA634712	Arabidopsis thalia	612	6	2.6	377	22	AA631728	Arabidopsis thalia
540	6	2.6	323	21	AA640336	Arabidopsis thalia	613	6	2.6	377	22	AA671711	Amino acid sequenc
541	6	2.6	324	22	AA693112	C glutamyl prote	614	6	2.6	378	21	AA646131	Arabidopsis thalia
542	6	2.6	324	22	AA679609	Arabidopsis thalia	615	6	2.6	378	22	AA668081	Amino acid sequenc
543	6	2.6	325	21	AA632391	Drosophila thalia	616	6	2.6	382	22	AAU48462	Propionibacterium
544	6	2.6	326	22	AB863538	Murine OR-like pol	617	6	2.6	383	22	AB865888	Drosophila melanog
545	6	2.6	326	22	AA672717	Novel human diagno	618	6	2.6	384	22	AB860223	Human brain P2X-1
546	6	2.6	327	22	ABG15678	Novel human diagno	619	6	2.6	388	18	AAW47066	HPORR amino acid s
547	6	2.6	327	22	ABG17556	Novel human diagno	620	6	2.6	388	19	AAW55035	Amino acid sequenc
548	6	2.6	328	22	AB858351	Drosophila melanog	621	6	2.6	388	22	AA684382	Amino acid sequenc
549	6	2.6	329	22	AB826298	Novel human diagno	622	6	2.6	388	22	AA668075	Arabidopsis thalia
550	6	2.6	330	22	AAU38133	Salmonella typhi c	623	6	2.6	389	21	AA646130	Arabidopsis thalia
551	6	2.6	331	21	AA695072	Novel human diagno	624	6	2.6	391	21	AA636483	Arabidopsis thalia
552	6	2.6	331	22	ABG16651	Novel human diagno	625	6	2.6	391	21	AA646129	Arabidopsis thalia
553	6	2.6	333	21	AA650874	Arabidopsis thalia	626	6	2.6	391	21	AB865335	Non-endogenous hum
554	6	2.6	333	22	AA671843	Human olfactory re	627	6	2.6	392	20	AAW00139	Enterococcus faeca
555	6	2.6	334	22	AA672928	Human olfactory re	628	6	2.6	392	22	AA696350	Putative P. abysci
556	6	2.6	335	22	AAU37137	Staphylococcus aur	629	6	2.6	392	22	AA668079	Amino acid sequenc
557	6	2.6	336	20	AA673733	Protein involved i	630	6	2.6	393	22	ABG20187	Novel human diagno
558	6	2.6	344	19	AA669762	Acetobacter xyliu	631	6	2.6	394	22	AAU32882	Novel human secret
559	6	2.6	344	22	AA664959	Human secreted pro	632	6	2.6	395	22	ABG03788	Novel human diagno
560	6	2.6	347	20	AAW08214	Rat glucuronyltran	633	6	2.6	395	22	ABG14173	Novel human diagno
561	6	2.6	347	20	AAW90057	Rat GlcAT-P protei	634	6	2.6	398	22	AB868073	Amino acid sequenc
562	6	2.6	348	21	AA636485	Arabidopsis thalia	635	6	2.6	399	22	AB860049	Drosophila melanog
563	6	2.6	350	18	AAW09968	HSV-1 (F) protease	636	6	2.6	401	22	ABG17572	Novel human diagno
564	6	2.6	350	18	AAW09978	HSV-1 (F) protease	637	6	2.6	402	22	AB860625	Drosophila melanog
565	6	2.6	350	18	AAW09977	HSV-1 (F) protease	638	6	2.6	404	21	AAW47067	Human brain P2X-2
566	6	2.6	350	18	AAW09976	HSV-1 (F) protease	639	6	2.6	405	21	AA645447	Human secreted pro
567	6	2.6	350	18	AAW09975	HSV-1 (F) protease	640	6	2.6	405	22	ABG10424	Novel human diagno
568	6	2.6	350	18	AAW09974	HSV-1 (F) protease	641	6	2.6	407	18	AAW08384	Novel human diagno
569	6	2.6	350	18	AAW09973	HSV-1 (F) protease	642	6	2.6	408	22	AAE12887	Human chordin-like
570	6	2.6	350	18	AAW09972	HSV-1 (F) protease	643	6	2.6	409	22	AAU38241	Salmonella typhi c
571	6	2.6	350	18	AAW09971	HSV-1 (F) protease	644	6	2.6	410	19	AAW60054	Brain-associated l
572	6	2.6	350	18	AAW09970	HSV-1 (F) protease	645	6	2.6	410	20	AAV31663	Mouse neuroserpin.
573	6	2.6	350	18	AAW09969	HSV-1 (F) protease	646	6	2.6	410	20	AAV31664	Human brain-associ
574	6	2.6	350	18	AAW09967	HSV-1 (F) protease	647	6	2.6	410	21	AA619550	Human neuroserpin.
575	6	2.6	350	18	AAW09965	HSV-1 (F) protease	648	6	2.6	410	21	AA619550	Human neuroserpin.
576	6	2.6	350	18	AAW09964	HSV-1 (F) protease	649	6	2.6	410	21	AA619550	Human neuroserpin.
577	6	2.6	350	18	AAW09963	HSV-1 (F) protease	650	6	2.6	410	21	AA619550	Human neuroserpin.
578	6	2.6	350	18	AAW09962	HSV-1 (F) protease	651	6	2.6	410	21	AA619550	Human neuroserpin.
579	6	2.6	350	18	AAW09961	HSV-1 (F) protease	652	6	2.6	413	21	AA619550	Human neuroserpin.
580	6	2.6	350	18	AAW09960	HSV-1 (F) protease	653	6	2.6	413	21	AA619550	Human neuroserpin.
581	6	2.6	350	18	AAW09959	HSV-1 (F) protease	654	6	2.6	414	22	AA619550	Human neuroserpin.
582	6	2.6	350	18	AAW09958	HSV-1 (F) protease	655	6	2.6	415	13	AA619550	Human neuroserpin.
583	6	2.6	350	18	AAW09957	HSV-1 (F) protease	656	6	2.6	415	13	AA619550	Human neuroserpin.
584	6	2.6	350	18	AAW09956	HSV-1 (F) protease	657	6	2.6	416	22	ABG04597	Novel human diagno
585	6	2.6	350	18	AAW09955	HSV-1 (F) protease	658	6	2.6	417	22	ABG07733	Novel human diagno
586	6	2.6	350	18	AAW09954	HSV-1 (F) protease	659	6	2.6	417	22	ABG12837	Novel human diagno
587	6	2.6	353	22	AB862613	Drosophila melanog	660	6	2.6	417	22	AA680962	Human gpC85 #1.
588	6	2.6	353	22	AB860551	Novel human diagno	661	6	2.6	419	22	AA680962	Pseudomonas aerugi
589	6	2.6	353	22	AB860757	Novel human diagno	662	6	2.6	419	22	AA680962	Human gpC85 #3.
590	6	2.6	353	22	AA686441	Putative P. abysci	663	6	2.6	420	22	AAU35408	Haemophilus influe
591	6	2.6	355	22	AA683925	Human protein sequ	664	6	2.6	420	22	AAU35837	Helicobacter pylor
592	6	2.6	356	22	AA686082	Amino acid sequenc	665	6	2.6	420	22	AAU35837	Helicobacter pylor
593	6	2.6	357	22	AAU32816	Novel human secret	666	6	2.6	422	22	AA674772	Human secreted pro
594	6	2.6	359	21	AA693397	Amino acid sequenc	667	6	2.6	423	22	ABG03642	Novel human diagno
595	6	2.6	361	22	AA662563	Follicular conjunc	668	6	2.6	423	22	AA604796	Human aspartyl pro

669	6	2.6	423	22	AAB88479	Human membrane or	742	6	2.6	476	19	AAW72024	HSV-2 strain SB5 C
670	6	2.6	425	21	AAG23387	Arabidopsis thalia	743	6	2.6	478	22	ABG15687	Novel human diagno
671	6	2.6	425	22	AAB92792	Human protein sequ	744	6	2.6	481	22	AAG75592	Human colon cancer
672	6	2.6	427	22	ABR71359	Drosophila melanog	745	6	2.6	482	22	AAU38270	Salmonella typhi C
673	6	2.6	428	20	AAV05332	Inflammatory cyto	746	6	2.6	487	18	AAW15471	Hantaan virus poly
674	6	2.6	428	21	AAI12798	Rice alpha-Amy7-C	747	6	2.6	489	22	ABG14285	Novel human diagno
675	6	2.6	428	22	AAW50251	Rice alpha-amyase	748	6	2.6	494	21	AAAG48093	Arabidopsis thalia
676	6	2.6	428	22	AAAB97245	Alpha-amyase rela	749	6	2.6	496	22	ABAB69420	Drosophila melanog
677	6	2.6	429	16	AAAR76520	Alpha-amyase-7-C	750	6	2.6	498	21	AAAB10038	LCMV coat glycopro
678	6	2.6	429	18	AAAW22727	Membrane protein M	751	6	2.6	499	22	AAAG82195	S. epidermidis ope
679	6	2.6	429	22	AAE128866	Human choridin-like	752	6	2.6	500	19	AAW56791	L. lactis RI portl
680	6	2.6	429	22	AAAG1874	C glutamicum prote	753	6	2.6	502	22	AAU04832	E. coli cellular p
681	6	2.6	429	22	AAU02750	Novel Human Protei	754	6	2.6	503	20	AAV028637	Thermotoga neopol
682	6	2.6	429	22	AAAB76819	Corynebacterium q1	755	6	2.6	503	22	ABAB62843	Drosophila melanog
683	6	2.6	432	22	ABAB64855	Drosophila melanog	756	6	2.6	503	22	AAU35487	Haemophilus influe
684	6	2.6	433	15	AAAR55130	Rice alpha-amyase	757	6	2.6	505	22	AAU36334	pseudomonas aerugi
685	6	2.6	433	19	AAW72144	HSV-2 strain SB5 C	758	6	2.6	505	22	AAAG80974	Human nGPCR58 #2
686	6	2.6	433	19	AAW72012	HSV-2 strain SB5 C	759	6	2.6	506	22	ABAB61810	Drosophila melanog
687	6	2.6	433	22	AAU19572	Human diagnostic a	760	6	2.6	507	22	AAV82488	Human L-type amino
688	6	2.6	434	14	AAAR32987	Rice alpha-amyase	761	6	2.6	507	21	ABG11780	Novel human diagno
689	6	2.6	434	18	AAW10469	Rice alpha-amyase	762	6	2.6	507	22	ABG14659	Novel human diagno
690	6	2.6	434	18	AAW11871	Rice alpha-amyase	763	6	2.6	513	22	ABAG0546	Novel human diagno
691	6	2.6	434	20	AAV01375	O. sativa alpha-am	764	6	2.6	514	13	AAAR28643	Novel human diagno
692	6	2.6	434	20	AAW84385	Rice alpha-amyase	765	6	2.6	517	22	ABG16617	Novel human diagno
693	6	2.6	434	21	AAV8792	Rice alpha-amyase	766	6	2.6	518	19	AAW61362	Aspartic proteinas
694	6	2.6	435	22	ABAG29570	Novel human diagno	767	6	2.6	518	20	AAV41714	Human CP852 prote
695	6	2.6	436	22	ABG16422	Novel human diagno	768	6	2.6	518	20	AAV22239	Human CP56, aspar
696	6	2.6	439	22	AAU34200	Staphylococcus aur	769	6	2.6	518	20	AAV13799	Human aspartyl pro
697	6	2.6	439	22	AAAB80076	Amino acid sequenc	770	6	2.6	518	21	AAAB44270	Human aspartyl pro
698	6	2.6	443	22	AAAB68080	Amino acid sequenc	771	6	2.6	518	21	AAV88424	Human aspartyl pro
699	6	2.6	444	22	AAU30756	Novel human secret	772	6	2.6	518	21	AAV51063	S. tendae nicomycl
700	6	2.6	444	22	ABG05552	Novel human secret	773	6	2.6	518	21	AAV50817	Streptomyces tende
701	6	2.6	446	21	AAAB25414	Novel human diagno	774	6	2.6	518	22	AAE10628	Human aspartyl pro
702	6	2.6	447	22	AAU36154	Klebsiella pneumon	775	6	2.6	518	22	AAE10656	Human Asp 1 protei
703	6	2.6	448	22	AAAG1349	C glutamicum prote	776	6	2.6	518	22	AAU29059	Human pro polypept
704	6	2.6	449	22	AAAB75201	Drosophila gustato	777	6	2.6	518	22	AAE06858	Human aspartyl pro
705	6	2.6	451	21	AAV93382	Human PRO157 (UNQ	778	6	2.6	518	22	AAU06602	Human aspartyl pro
706	6	2.6	451	22	AAU29164	Human pro polypept	779	6	2.6	518	22	AAU07201	Human aspartyl pro
707	6	2.6	451	22	AAU02749	Novel Human Protei	780	6	2.6	518	22	AAE02580	Human aspartyl pro
708	6	2.6	451	22	AAAB87566	Human PRO1557. Ho	781	6	2.6	518	22	AAE02608	Human Aspartyl pro
709	6	2.6	451	22	AAAB66131	Protein of the inv	782	6	2.6	524	22	AAE05440	Novel human diagno
710	6	2.6	451	22	AAAB48069	Human extracellular	783	6	2.6	525	22	ABR71642	Drosophila melanog
711	6	2.6	452	21	AAAG13800	Arabidopsis thalia	784	6	2.6	526	10	AAAP90587	Polypeptide with m
712	6	2.6	452	21	AAAG40334	Arabidopsis thalia	785	6	2.6	527	22	ABG15862	Novel human diagno
713	6	2.6	453	22	ABG14171	Novel human diagno	786	6	2.6	528	22	ABG13737	Novel human diagno
714	6	2.6	455	22	ABG12029	Novel human diagno	787	6	2.6	529	19	AAW73045	Ply virus G glyco
715	6	2.6	457	22	ABBI2464	Human bone marrow	788	6	2.6	529	19	AAW73046	Chandipura virus G
716	6	2.6	458	18	AAAG09030	Neutonal nicotinic	789	6	2.6	529	21	AAV99528	Ply virus membran
717	6	2.6	458	22	ABG16999	Novel human diagno	790	6	2.6	529	21	AAV99529	Chandipura virus m
718	6	2.6	458	22	ABBI1778	Human FGF receptor	791	6	2.6	530	22	ABG16998	Novel human diagno
719	6	2.6	458	22	AAE12775	Human cholinergic	792	6	2.6	534	22	ABG04517	Novel human diagno
720	6	2.6	458	22	AAW79325	Human protein sequ	793	6	2.6	536	21	AAAB53136	Macaca mulatta rha
721	6	2.6	458	22	AAW25740	Human protein sequ	794	6	2.6	537	22	ABAB1550	Drosophila melanog
722	6	2.6	458	22	AAAG89932	C glutamicum prote	795	6	2.6	537	22	ABAB7157	Drosophila melanog
723	6	2.6	459	21	AAAG13799	Arabidopsis thalia	796	6	2.6	539	22	AAAB68074	Amino acid sequenc
724	6	2.6	461	18	AAW14006	Caenorhabditis ele	797	6	2.6	541	22	ABG17001	Novel human diagno
725	6	2.6	461	19	AAW14007	Caenorhabditis ele	798	6	2.6	542	22	ABAB6342	Castor bean calnex
726	6	2.6	462	18	AAW69359	Pyridine nucleotid	799	6	2.6	545	22	ABAB68867	Drosophila melanog
727	6	2.6	463	21	AAAG07155	Arabidopsis thalia	800	6	2.6	545	22	AAU38979	Drosophila G-prote
728	6	2.6	463	21	AAAG48101	Arabidopsis thalia	801	6	2.6	546	22	AAU04063	Mouse Interleukin-
729	6	2.6	466	22	ABG17916	Novel human diagno	802	6	2.6	546	22	AAAB5275	Mouse IL-20 recept
730	6	2.6	467	19	AAW72177	HSV-2 strain SB5 C	803	6	2.6	547	17	AAW06135	Choline oxidase us
731	6	2.6	468	21	AAV71295	Human orphan G pro	804	6	2.6	547	18	AAW22053	Choline oxidase de
732	6	2.6	468	21	AAAB02829	Human G protein co	805	6	2.6	547	22	AAE07054	Human gene 4 encod
733	6	2.6	468	22	AAAG1023	C glutamicum prote	806	6	2.6	549	22	AAAB68077	Amino acid sequenc
734	6	2.6	468	22	AAAB76815	Corynebacterium g1	807	6	2.6	549	22	AAAB68078	Amino acid sequenc
735	6	2.6	470	21	AAV94267	Human G-protein co	808	6	2.6	550	21	AAAG46256	Arabidopsis thalia
736	6	2.6	470	21	AAV94268	Human G-protein co	809	6	2.6	551	11	AAAR07282	Maltoetraose. Ps
737	6	2.6	470	22	AAE10175	Human lipoxin A4 r	810	6	2.6	554	21	AAAG46255	C glutamicum thalia
738	6	2.6	470	22	AAE04567	Human G-protein co	811	6	2.6	554	22	AAAG92535	C glutamicum prote
739	6	2.6	470	22	AAAB46838	Human G-protein co	812	6	2.6	554	22	AAAB79255	Corynebacterium g1
740	6	2.6	475	22	ABG14170	Novel human diagno	813	6	2.6	555	22	ABG06700	Novel human diagno
741	6	2.6	476	19	AAW72127	HSV-2 strain SB5 C	814	6	2.6	555	22	ABG12798	Novel human diagno



815	6	2.6	557	21	AA0808112	A polypheanol oxida	888	6	2.6	705	22	AA0293222	Human PRO polypept
816	6	2.6	561	18	AAW14440	Protein involved i	889	6	2.6	705	22	AAU04956	Human Interleukin
817	6	2.6	562	22	AB58411	Drosophila melanog	890	6	2.6	705	22	AA887606	Human PRO20040. H
818	6	2.6	565	22	ABG08794	Novel human diagno	891	6	2.6	705	22	AA661884	Chimeric zcytor14
819	6	2.6	567	21	AA818197	Plasmodium falcipa	892	6	2.6	706	22	AB866693	Drosophila melanog
820	6	2.6	569	16	AA84923	Splachn 2-oxogluta	893	6	2.6	707	20	AAW83395	Rabbit protein-con
821	6	2.6	569	22	AAU34910	Enterococcus faeca	894	6	2.6	707	22	ABG24674	Novel human diagno
822	6	2.6	571	22	AAU16075	Human novel secret	895	6	2.6	708	20	AAW74088	Human hPEP1 prote
823	6	2.6	575	22	AAU34647	E. coli cellular p	896	6	2.6	708	20	AAW74087	Gastro-intestinal-
824	6	2.6	575	22	AA81681	Human variant zcyt	897	6	2.6	708	20	AAW83394	Human protein-conp
825	6	2.6	585	20	AAU08485	Y. lipolytica Paec	898	6	2.6	717	10	AA891933	BI antigen. Toxop
826	6	2.6	588	22	AB869947	Drosophila melanog	899	6	2.6	717	21	AA629902	Arabidopsis thalia
827	6	2.6	588	22	AA683117	S. epidermidis ope	900	6	2.6	717	22	ABG17438	Novel human diagno
828	6	2.6	592	9	AA804777	Pyruvate oxidase.	901	6	2.6	722	22	AAW39029	Human polypeptide
829	6	2.6	601	21	AA808123	A polypheanol oxida	902	6	2.6	730	22	ABG17073	Novel human diagno
830	6	2.6	603	13	AA828641	UL26 protease dele	903	6	2.6	735	21	AA627789	Arabidopsis thalia
831	6	2.6	608	21	AA629904	Arabidopsis thalia	904	6	2.6	735	21	AAU32806	Novel human secret
832	6	2.6	609	20	AAU14957	Amino acid sequenc	905	6	2.6	745	21	AA627788	Arabidopsis thalia
833	6	2.6	609	22	ABG07734	Novel human diagno	906	6	2.6	758	22	AB864656	Drosophila melanog
834	6	2.6	609	22	ABG14417	Novel human diagno	907	6	2.6	764	12	AA812504	Canine thyroid sti
835	6	2.6	609	22	AA883257	Murine FAFp3 parti	908	6	2.6	764	15	AA860568	Down-regulated in
836	6	2.6	610	20	AA821628	Ligand binding dom	909	6	2.6	775	22	ABG17239	Novel human diagno
837	6	2.6	612	17	AA891947	Brevibacterium fla	910	6	2.6	783	11	AA805804	C-terminal of natl
838	6	2.6	613	20	AAU14933	Amino acid sequenc	911	6	2.6	794	22	ABG08768	Novel human diagno
839	6	2.6	613	22	AB860220	Drosophila melanog	912	6	2.6	814	21	AA630844	Arabidopsis thalia
840	6	2.6	613	22	AAU34632	E. coli cellular p	913	6	2.6	815	22	ABG10390	Novel human diagno
841	6	2.6	613	22	AA883223	Murine FAFp3 SEQ I	914	6	2.6	816	12	AA814444	A. faecalis penticil
842	6	2.6	613	22	AA883271	Murine FAFp3 SEQ I	915	6	2.6	824	22	ABG25104	Novel human diagno
843	6	2.6	614	17	AAW07908	Pemphigus vulgaris	916	6	2.6	827	11	AA805049	Human villin. Hom
844	6	2.6	614	21	AA629903	Arabidopsis thalia	917	6	2.6	837	22	AB863623	Drosophila melanog
845	6	2.6	615	13	AA828642	UL26 protease dele	918	6	2.6	865	21	AA826153	Neospora NC-p65 ve
846	6	2.6	619	22	AB870767	Drosophila melanog	919	6	2.6	872	22	AB869476	Drosophila melanog
847	6	2.6	626	13	AA828640	Novel human diagno	920	6	2.6	885	17	AA892747	SAB virus gb glyco
848	6	2.6	627	22	ABG14169	UL26 protease dele	921	6	2.6	903	20	AAU37116	Protein involved i
849	6	2.6	635	13	AA828634	UL26 protease. He	922	6	2.6	930	22	ABG04240	Novel human diagno
850	6	2.6	635	13	AA828630	UL26 protease subs	923	6	2.6	930	22	ABG17993	Novel human diagno
851	6	2.6	635	13	AA828649	UL26 protease subs	924	6	2.6	999	14	AA830742	Human pemphigus vu
852	6	2.6	635	13	AA828651	UL26 protease subs	925	6	2.6	999	22	AA859815	Tutd protein #6.
853	6	2.6	635	13	AA828652	UL26 protease subs	926	6	2.6	1014	22	ABG12435	Novel human diagno
854	6	2.6	635	13	AA828648	UL26 protease subs	927	6	2.6	1018	22	AB861379	Drosophila melanog
855	6	2.6	635	13	AA828648	UL26 protease subs	928	6	2.6	1059	22	ABG07732	Novel human diagno
856	6	2.6	635	16	AA817031	HSV-1 UL26 gene pr	929	6	2.6	1059	22	AAU32823	Novel human secret
857	6	2.6	636	22	AB862805	Drosophila melanog	930	6	2.6	1060	22	ABG20068	Novel human diagno
858	6	2.6	636	13	AA828635	UL26 protease inse	931	6	2.6	1062	22	ABG14418	Novel human diagno
859	6	2.6	636	13	AA828636	UL26 protease inse	932	6	2.6	1087	22	AA878992	Human cancer-inhib
860	6	2.6	636	13	AA828637	UL26 protease inse	933	6	2.6	1088	21	AAU06527	Human WAKR2, ortho
861	6	2.6	637	22	AAU32818	Novel human secret	934	6	2.6	1088	21	AA807663	Amino acid sequenc
862	6	2.6	643	22	AAW39119	Human polypeptide	935	6	2.6	1088	21	AA807664	Amino acid sequenc
863	6	2.6	643	22	AA870155	DNA encoding human	936	6	2.6	1088	22	AA862429	Human kidney ankyr
864	6	2.6	647	22	AAW40905	Human polypeptide	937	6	2.6	1097	22	ABG21941	Novel human diagno
865	6	2.6	651	20	AAW86313	Kidney injury asso	938	6	2.6	1099	17	AAW05177	Lats large tumour
866	6	2.6	652	22	AB864920	Drosophila melanog	939	6	2.6	1099	21	AAU70393	Drosophila melanog
867	6	2.6	654	22	AA894772	Human protein sequ	940	6	2.6	1101	22	AA882299	Wheat starch branc
868	6	2.6	655	22	AA894770	Human protein sequ	941	6	2.6	1105	22	AB858401	Drosophila melanog
869	6	2.6	658	22	ABG03643	Novel human diagno	942	6	2.6	1121	22	AA879244	Amino acid sequenc
870	6	2.6	663	21	AA630846	Arabidopsis thalia	943	6	2.6	1135	15	AA850037	Hantaan virus GI/
871	6	2.6	664	16	AA875190	Osteoinductive ret	944	6	2.6	1135	21	AA868784	Amino acid sequenc
872	6	2.6	669	20	AAU00141	Enterococcus faeca	945	6	2.6	1141	14	AA831961	Human cardiac CGT
873	6	2.6	671	15	AA861135	Delta-pyrroline-5-	946	6	2.6	1165	21	AA843016	Human OREF OREF2780
874	6	2.6	671	18	AAW42386	Delta1-pyrroline-5	947	6	2.6	1165	22	ABG17468	Novel human diagno
875	6	2.6	672	21	AA630845	Arabidopsis thalia	948	6	2.6	1175	22	ABG17468	Novel human diagno
876	6	2.6	675	22	AA861885	Chimeric zcytor14	949	6	2.6	1191	22	ABG12436	Novel human diagno
877	6	2.6	683	22	AA692931	C glutamicum prote	950	6	2.6	1212	22	AA804368	Human kinase (PKIN
878	6	2.6	686	22	AB857992	Drosophila melanog	951	6	2.6	1216	18	AAW14487	Urease protein. M
879	6	2.6	687	22	AA894945	Canine retrovirus	952	6	2.6	1219	22	ABG17469	Novel human diagno
880	6	2.6	688	22	AA861883	Chimeric zcytor14	953	6	2.6	1233	20	AAU55954	Mouse STE20-relate
881	6	2.6	692	22	AA861880	Human cytokine rec	954	6	2.6	1236	22	AB865297	Drosophila melanog
882	6	2.6	694	22	AA690113	C glutamicum prote	955	6	2.6	1239	20	AAU55931	Human zc1 protein.
883	6	2.6	697	21	AA627790	Arabidopsis thalia	956	6	2.6	1257	22	AB867273	Drosophila melanog
884	6	2.6	697	21	AA631652	Novel human diagno	957	6	2.6	1268	22	ABG29502	Novel human diagno
885	6	2.6	700	22	AB859209	Drosophila melanog	958	6	2.6	1272	22	AA884881	Murine protein, SE
886	6	2.6	709	21	AA646254	Arabidopsis thalia	959	6	2.6	1272	22	AA884883	Murine protein, SE
887	6	2.6	703	19	AAW47389	Rice delta-1-pyrro	960	6	2.6	1291	22	ABG28604	Novel human diagno

961	6	2.6	1307	22	ABB63936	Drosophila melanog
962	6	2.6	1311	22	ABB60748	Drosophila melanog
963	6	2.6	1329	22	AAU34519	E. coli cellular p
964	6	2.6	1372	21	ABG24404	Novel human diago
965	6	2.6	1428	21	AAV97033	Caspase 8-interact
966	6	2.6	1477	16	AAE67691	S. cerevisiae scau
967	6	2.6	1477	18	AAAI0424	Saccharomyces cere
968	6	2.6	1477	20	AAV06819	Fumonisin-resistan
969	6	2.6	1480	22	ABBS9227	Drosophila melanog
970	6	2.6	1583	22	ABAS9828	Protein #5 encoded
971	6	2.6	1596	22	ABH70845	Drosophila melanog
972	6	2.6	1638	20	AAV00138	Enterococcus faeca
973	6	2.6	1638	20	AAV00140	Enterococcus faeca
974	6	2.6	1638	20	AAV00142	Enterococcus faeca
975	6	2.6	1655	22	ABG17466	Novel human diago
976	6	2.6	1730	22	ABAS2049	Corn earworm Bt to
977	6	2.6	1742	22	ABBS9031	Drosophila melanog
978	6	2.6	1959	12	AAI10562	Mutant protease (d
979	6	2.6	1962	12	AAI10560	Mutant protease (K
980	6	2.6	1962	12	AAI10561	Mutant protease (N
981	6	2.6	1962	12	AAI10557	Mutant protease (A
982	6	2.6	1962	12	AAI10558	Mutant protease (A
983	6	2.6	1962	12	AAI10559	Mutant protease (A
984	6	2.6	1962	12	AAI10563	Mutant protease (A
985	6	2.6	1968	12	AAI10941	Mutant protease (d
986	6	2.6	1974	12	AAI10940	Mutant protease (d
987	6	2.6	2037	22	ABBS6909	Drosophila melanog
988	6	2.6	2225	22	ABB71877	Drosophila melanog
989	6	2.6	2243	22	ABBS4884	Mutrin protein, SE
990	6	2.6	2724	22	ABG20119	Novel human diago
991	6	2.6	2737	22	ABG18288	Novel human diago
992	6	2.6	2771	22	ABBS6380	Drosophila melanog
993	6	2.6	2778	22	ABBS6683	Drosophila melanog
994	6	2.6	2819	22	ABBS5408	Human 07CG27 gene
995	6	2.6	3076	22	ABG07038	Novel human diago
996	6	2.6	3256	21	AAV50976	Human cell cycle p
997	6	2.6	3313	22	AAU30134	Novel human secre
998	6	2.6	3389	22	AAE07984	Dengue virus (DEN)
999	6	2.6	3391	12	AAI13166	Proteins encoded b
1000	6	2.6	3391	18	AAW06591	Polypeptide of att

## ALIGNMENTS

RESULT	ID	AAW64668	standard; Protein; 259 AA.
XX	AAW64668		
XX	AC		
XX	23-Oct-1998	(first entry)	
XX	Human TRID protein.		
XX	TRAIL receptor without intracellular domain; TRID; TNFR-5; human;		
KW	tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;		
KW	haematopoietic tissue; immune system; ligand; apoptosis; treatment.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..27	
FT		/label= signal	
FT	Protein	27..259	
FT		/label= TRID	
FT	Region	42..52	
FT		/label= epitope	
FT	Region	58..66	
FT		/label= epitope	
FT	Region	68..76	
FT		/label= epitope	
FT	Region	79..85	

FT		/label= epitope
FT	Region	91..102
FT		/label= epitope
FT	Region	110..122
FT		/label= epitope
FT	Region	126..136
FT		/label= epitope
FT	Region	142..148
FT		/label= epitope
XX		
XX	MO9830693-A2.	
XX		
XX	16-JUL-1998.	
XX		
PX	13-JAN-1998;	98WO-US00152.
XX		
PX	07-AUG-1997;	97US-0054885.
PR		
PR	14-JAN-1997;	97US-0035496.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Ebner R, Feng P, Gentz RL, NI J, Ruben SM, Wei Y;	
PI	Yu G;	
XX		
DR	WPI: 1998-399141/34.	
DR	N-PDB: AAV51348.	
XX		
PT	Human TRAIL receptor without an intracellular domain polypeptide -	
PT	used in the diagnosis of immune system-related disorder(s)	
PS		
PS	Claim 1b; Fig 1; 90pp; English.	
CC		
CC	This sequence represents a human "TRID (TNF-related	
CC	apoptosis-inducing ligand) receptor without an intracellular domain".	
CC	TRID is a member of the tumour necrosis factor receptor (TNFR) family	
CC	also known as TNFR-5. TRID is expressed in haematopoietic tissues and	
CC	other normal human tissues. For a number of immune system-related	
CC	disorders, substantially altered (whether increased or decreased) levels	
CC	of TRID gene expression can be detected, therefore the TRID polypeptides	
CC	nucleic acids and antibodies are useful in the diagnosis of such immune	
CC	system related disorders. Mutations of the TRID gene can also be	
CC	detected. TRID can also be used to identify ligands which may be useful	
CC	in the treatment of apoptosis related disorders. TRID is administered to	
CC	humans at a parenteral dose of 0.01 to 1 mg/kg/day.	
XX		
SQ	Sequence      259 AA;	

Query Match	100.0%	Score 233:	DB 19:	Length 259:
Best Local Similarity	100.0%	Pred. No. 2.4e-233:		
Matches 233:	Conservative	0:	Mismatches	0: Indels
				Gaps
				0
Qy	1	TTAROEENVPOQTVAAPDQQRHSFEKGECCPAGSHRSEHTGACNPCTEGVDYTNASNNPSCF	60	
Db	27	ttargeevpqqlvapqpgqhsfkgeecpagsnrseltgacnptegvdytnasnnpsctf	86	
Qy	61	PCTVCKSDQKHKSSCTMTBDYVCOCKEGTFRRNENSPDMCRKCSRCPGSEVQVSNCTSWDD	120	
Db	87	pctvcksdqkhkssctumtrdtvcqkegfrrnenspdmcrkscrcpsgevyansctswdd	146	
Qy	121	IOCVEEFGANATVEIPAAEETMTTSGTTPAPAAEETMTTSGTTPAPAAEETMTTSGTTPA	180	
Db	147	lqcvseefgnatveipaaeelmttspgtpapaaeelmttspgtpapaaeelmttspgtpa	206	
Qy	181	PAAEETMTTSGTTPAPAAEETMTTSGTTPAASSHYLSCTIVGIIVLVLIVP	233	
Db	207	paaeetmttspgtpapaaeelmttspgtpaasshylsctivgiivlvlivfv	259	
RESULT	2			
AAW88408				
ID	AAW88408	standard; Protein: 259	AA.	
XX				

AC		AAW88408;	
XX			
DT	26-APR-1999	(first entry)	
XX			
DE		Human Apo-2Dcr protein (amino acids 1-259).	
XX			
KM	Apo-2Dcr; human; apoptosis; tumor necrosis factor receptor;		
KX	neurodegeneration; autoimmune disease; inflammation; cancer;		
XX	therapy.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..29	"predicted signal peptide"
FT		/note=	
FT	Domain	1..161	"extracellular domain, this domain is specifically claimed in Claim 5"
FT		/note=	
FT	Domain	68..109	"cysteine-rich domain"
FT		/note=	
FT	Domain	110..149	"cysteine-rich domain"
FT		/note=	
FT	Peptide	162..176	"tandem repeat peptide"
FT		/note=	
FT	Peptide	177..191	"tandem repeat peptide"
FT		/note=	
FT	Peptide	192..206	"tandem repeat peptide"
FT		/note=	
FT	Peptide	207..221	"tandem repeat peptide"
FT		/note=	
FT	Peptide	222..236	"tandem repeat peptide"
FT		/note=	
FT	Region	225..259	"hydrophobic C-terminal region"
FT		/note=	
FT	Modified-site	77	"N-glycosylation"
FT		/note=	
FT	Modified-site	140	"N-glycosylation"
FT		/note=	
FT	Modified-site	156	"N-glycosylation"
FT		/note=	
FT	Modified-site	169	"N-glycosylation"
FT		/note=	
FT	Modified-site	184	"N-glycosylation"
FT		/note=	
PN	WO9858062-A1.		
PD	23-DEC-1998.		
XX			
PF	12-JUN-1998;	98WO-US12456.	
XX			
PR	18-JUN-1997;	97US-087818B.	
XX			
PA	(GETH ) GENENTECH INC.		
PI	Ashtkenazi AJ, Baker KP, Chuntharapai A, Gurney A;		
PI	Kim KJ, Wood WI;		
XX			
DR	WPI: 1999-095340/08.		
DR	N-PsDB: AAV84347.		
XX			
New Apo-2Dcr polypeptide - used for modulation and diagnosis of apoptosis, e.g. in neurodegeneration			
PS	Claim 1; Page 50-51; 88pp; English.		
XX			
CC	This polypeptide comprises human Apo-2Dcr, a novel member of the		
CC	tumor necrosis factor receptor family that binds to Apo-2 ligand.		
CC	its amino acid sequence was deduced from the nucleotide sequence		
CC	of an isolated cDNA clone (see AAU84347); an alternative translation		
CC	initiation site in this clone will encode a polypeptide (see		
CC	AAW8409) comprising amino acid residues -40 to 269 of Apo-2Dcr.		
CC	Apo-2Dcr shows more sequence identity to DR4 (60%) and Apo-2 (50%).		

PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.

(GETH ) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

DR WPI: 2001-408281/43.  
 DR N-PSDB: AAS21393.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical

XX Claim 12; Fig 300; 813pp: English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PMNCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.

XX Sequence 259 AA:

Query Match 100.0%; Score 233; DB 22; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAROEVPQDTVAPQOQRHSFKGECPAGSHRSHTGACNCTGADVDTNANNEPSCF 60  
 DB 27 ttarqeepvqgtvapgqrhskfgecpagshrshtgacnctgadvdtananepefcf 86  
 QY 61 PCTVCKSDQKHKSSCTMTRDVYCQCKEKTFRNENSPKCRKSCRPSEGVQVSNCTSMDD 120  
 DB 87 pctvcksdqkhkssctmtrdvcqckegktfrnenspmckrcscrpsegevyqsnctswdd 146  
 QY 121 IOCVEEFGANATVETPAAEETMTNTPGTPPAAEETMTNTPGTPPAAEETMTNTPGTPPA 180

DB 147 IqcvEEFGANATVETPAAEETMTNTPGTPPAAEETMTNTPGTPPAAEETMTNTPGTPPA 206  
 QY 181 PAAEETMTNTPGTPPAAEETMTNTPGTPPASSHYLSCTIVGIIVLVLIIVY 233  
 DB 207 paaEETMTNTPGTPPAAEETMTNTPGTPPASSHYLSCTIVGIIVLVLIIVY 259

#### RESULT 4

AA20111  
 ID AAB20111 standard; Protein; 259 AA.

AC AAB20111;

DT 30-APR-2001 (first entry)

DE Human immunostimulant PRO366 (Apo-2DCR).

KW PRO366; UNQ321; human; immune disease; autoimmune disease;  
 KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
 KW immunosuppressive; antidiabetic; antidiabetic; neuroprotective;  
 KW hepatotropic; virucide; dermatological; antipsoriatic;  
 KW antiallergic; antiallergic; immunostimulant; Apo-2DCR;  
 KW tumour necrosis factor receptor; apoptosis.

OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..29  
 FT Protein 30..259  
 FT Domain 240..257

FT Region 85..92  
 FT /note= "transmembrane domain"

FT Modified-site 126..130  
 FT /note= "TNFR/NGFR family cysteine-rich region"

FT Modified-site 56..62  
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 72..78  
 FT /note= "N-myristoylation site"

FT Modified-site 114..120  
 FT /note= "N-myristoylation site"

FT Modified-site 154..160  
 FT /note= "N-myristoylation site"

FT Modified-site 233..239  
 FT /note= "N-myristoylation site"

FT W0200105972-A1.

FT 25-JAN-2001.

FT 15-MAR-2000; 2000WO-US06884.

FT 20-JUL-1999; 99US-0144758.

FT (GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
 PI Wood WI;

DR WPI: 2001-103149/11.  
 DR N-PSDB: AAF30053.

XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes -

XX Claim 20; Fig 8; 127pp; English.

XX The present sequence is that of PRO366 (UNQ321), also designated

CC



RESULT 6  
AAB53091  
ID AAB53091 standard; Protein: 259 AA.  
XX  
AC AAB53091;  
XX  
D7 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO366, SEQ ID NO:152.  
XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0133957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoi NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI: 2001-090793/10.  
DR N-PSDB; AAC97488.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
PS Claim 69; Fig 56; 293pp; English.  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or

CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
CC invention.  
XX  
SQ Sequence 259 AA;

Query Match 100.0%; Score 233; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 2,4e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTARQEEVPOQVAPQOQRHSFKGECPCAGSRHSHTGACNCPRGVDTNANSNNEPSCF 60  
DB 27 ttaqeevppqvapqqrhshfkgeecpagsrshshgacncpctegvdytnasnnepscf 86  
OY 61 PCTWCKSDQKHKSSCTMTTRDTVCQCKEGTFRNENSPENCRCRCRSCPGSEVOVSNCTSMDD 120  
DB 87 pctwcksdqkhkssctmttrdtvcqckegtfrenenspencrcrcrspgsevoynctswdd 146  
OY 121 IQCVSEFGANATVERPAAEETMTSPGTPAPAAETMTMTSGTPAPAAETMTTSPGTPA 180  
DB 147 iqcvsefganatvetrpaaeetmtspgtpapaaetmttspgtpapaaetmttspgtpa 206  
OY 181 PAAETMTTSPGTPAPAAETMTTSPGTPASASHYSTIGIVLIVLIVFV 233  
DB 207 paaetmttspgtpapaaetmttspgtpasashysctivlilvllivfv 259

RESULT 7  
AAB82181  
ID AAB82181 standard; Protein: 268 AA.  
XX  
AC AAB82181;  
XX  
D7 23-JUL-2001 (first entry)  
XX  
DE FLAG-TRID clone with a transmembrane domain.  
XX  
KW FLAG-epitope tag; transmembrane domain; death domain; apoptosis;  
KW cell suicide; tissue homeostasis; cell proliferation;  
KW cell-cell signalling; Trail Receptor without Intracellular Domain; TRID.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= signal\_peptide  
FT Protein 24..268  
FT /label= FLAG-TRID-protein  
FT Peptide 27..34  
FT /label= FLAG-epitope\_TAG  
FT Region 250..268  
FT /label= Transmembrane\_region  
PN WO200114542-A1.  
PD 01-MAR-2001.  
XX

PF 23-AUG-2000; 2000MO-US23112.  
 PR 25-AUG-1999; 9905-0150747.  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 PA Denome SA, Swain PM, Tzellas N;  
 XX  
 PI WPI: 2001-374162/39.  
 DR N-PSDB; AAH19325.  
 XX  
 PT Identifying a transmembrane domain of a membrane-spanning protein  
 PT useful in defining processes in cell suicide and tissue homeostasis,  
 PT comprises modifying the nucleic acid encoding a death domain-lacking  
 PT membrane spanning protein -  
 XX  
 PS Disclosure; Fig 1; 38pp; English.  
 XX  
 CC The present invention relates to methods for identifying a transmembrane  
 CC domain (TM) of a membrane-spanning protein. The method comprises  
 CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane  
 CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID)  
 CC by replacing the nucleic acid encoding the TM of the DD-lacking  
 CC membrane-spanning protein with a candidate nucleic acid sequence to  
 CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
 CC protein. The modified nucleic acid is then transfected into a host cell,  
 CC which expresses a DD-containing receptor. The absence of apoptosis of the  
 CC host cell is determined following exposure of the transfected cell to an  
 CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
 CC apoptosis of the host cell. The modified nucleic acid encoding the  
 CC modified death domain-lacking membrane-spanning protein can also include  
 CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
 CC a FLAG-TRID clone, which was used in the method of the present invention.  
 CC This sequence comprises human TRID protein and the FLAG-epitope tag. The  
 CC FLAG-epitope is a useful marker to purify proteins encoded by the  
 CC modified DD-lacking membrane-spanning protein. The identified TM and  
 CC membrane-spanning proteins may be used in defining processes involved in  
 CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat  
 CC events, such as cell proliferation and cell-cell signalling pathways.  
 CC  
 XX  
 SO Sequence 268 AA:

Query Match 100.0%; Score 233; DB 22; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRQEEVPOQYVAPQOQRHSFKGEECPAGSHSEHTGACNPCTEGVDYTNASNNEPSCF 60  
 DB 36 tIarqeevPqqtVApqqrHsfxgEECPagshSEhtgacnPCtegydytnasnepscF 95  
 QY 61 PCIVCSDDOKHKSSCTTRTVCCKEGRFNRNENSPCKRCSCRGCEVOVSNCTGMD 120  
 DB 96 pCivcsddqhksscttrtvcckEgrfNrnenSPcmrckscrgceVqvsncTsgwd 155  
 QY 121 IOCVEEFGANATETPAAEETMNTSPGTPAPAAETMNTSPGTPAPAAETMNTSPGTPA 180  
 DB 156 iGveeEfganAtetpAaeetmNtspGtpaPAAetmNtspGtpaPAAetmNtspGtpa 215  
 QY 181 PAAEETMNTSPGTPAPAAETMNTSPGTPASSNYLCTIGIIVLIVLVFV 233  
 DB 216 pAaeetmNtspGtpaPAAetmNtspGtpassnylctIvgiivlIvlfv 268

RESULT 8  
 AAW76331  
 ID AAW76331 standard; Protein; 299 AA.  
 XX  
 AC AAW76331;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Human tumour necrosis related receptor TR5.

XX Tumour necrosis related receptor; TR5; human; inflammation;  
 KM arthritis; septicemia; transplant rejection; autoimmune disease;  
 KM inflammatory bowel disease; graft versus host disease; infection;  
 KM stroke; ischemia; acute respiratory disease syndrome; psoriasis;  
 KM restenosis; brain injury; AIDS; bone disease; cancer;  
 KM atherosclerosis; Alzheimer's disease; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..165  
 FT /label= Sig\_peptide  
 FT Protein 66..299  
 FT /label= Mat\_protein  
 XX  
 PN EP867509-A2.  
 XX  
 PD 30-SEP-1998.  
 XX  
 PD 04-FEB-1998; 98EP-0300827.  
 XX  
 PR 28-JUL-1997; 97US-0901469.  
 PR 05-FEB-1997; 97US-0795910.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Lyn SDP, Tan KB, Truneh A, Young PR;  
 XX  
 DR WPI: 1998-497862/43.  
 DR N-PSDB; AAV56990.  
 XX  
 PT New polynucleotide encoding TR5 polypeptide - used to diagnose,  
 PT prevent and treat e.g. inflammation, arthritis, septicemia,  
 PT autoimmune diseases, infections, stroke, ischemia, ARDS, psoriasis,  
 PT restenosis, brain injury, AIDS and bone diseases  
 XX  
 PS Claim 5; Fig 1; 22pp; English.

This is the amino acid sequence of human tumour necrosis related  
 receptor TR5, as deduced from the sequence of an isolated cDNA  
 clone (see AAV56990). The protein is characterised as a GPI-linked  
 protein that has a membrane proximal O-glycosylation region. The  
 CC invention provides methods for the recombinant production of TR5  
 CC and its use in diagnostic and therapeutic methods. Treatment of a  
 CC subject in need of enhanced TR5 activity comprises administering an  
 CC agonist to the polypeptide and/or providing TR5 polynucleotide in a  
 CC form so as to effect production of the polypeptide activity in vivo.  
 CC Treatment of a subject with the need to inhibit TR5 polypeptide  
 CC activity comprises administering an antagonist to the polypeptide,  
 CC administering a nucleic acid that inhibits the expression of the  
 CC nucleotide sequence encoding the polypeptide and/or administering a  
 CC polypeptide that competes with the polypeptide for its ligand,  
 CC substrate or receptor. Diagnosing a disease or a susceptibility  
 CC to a disease related to expression or activity of TR5 polypeptide,  
 CC comprises determining the presence or absence of mutation in the  
 CC nucleotide sequence encoding the TR5 polypeptide in the genome of  
 CC the subject and/or analysing for the presence or amount of TR5  
 CC polypeptide expression in a sample. Identification of compounds  
 CC which bind to TR5 comprises contacting host cells with a candidate  
 CC compound and assessing the ability of it to bind to the cells. The  
 CC active agents can be used for the treatment of chronic and acute  
 CC inflammation, arthritis, septicemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis), transplant rejection,  
 CC graft vs host disease, infection, stroke, ischemia, acute  
 CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone  
 CC diseases, cancer (e.g. lymphoproliferative disorders),  
 CC atherosclerosis and Alzheimer's disease.  
 XX  
 SO Sequence 299 AA:

Query Match 100.0%; Score 233; DB 19; Length 299;

Best Local Similarity 100.0%; Pred. No. 2,8e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TTAEOEEVPOOTVAPQOORHSFKGECPCAGSHRSRHTACPCTEGVYTNASNNPEPCF 60
    |||||||
Db 67 tlarqeevpgqlvapgqgrhskfgeecpagsrhrehtgacmpctegvdytnasnnepscf 126
QY 61 PCTVCKSDQKHKSCTMTTRDTVCOCKEGTFRNENSPEMCRKCSRCPSGEVOVSNCTSWDD 120
    |||||||
Db 127 pctrcksdqkhksctmttrdtvcqckegtfrenspemcrkcsrpsgegvsnctswdd 186
QY 121 IQCYEEGRANNTVETPPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPA 180
    |||||||
Db 187 iqcyeeigranativetppaaeetmtspgtpapaaeetmtspgtpapaaeetmtspgtpa 246
QY 181 PAAEETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIIYVLIIVFV 233
    |||||||
Db 247 paaeetmtspgtpapaaeetmtspgtpashylsctivgiiyvlivlvfv 299
```

## RESULT 9

AAV29864  
ID AAV29864 standard; Protein: 299 AA.

AC AAV29864;

DT 17-NOV-1999 (first entry)

XX Human secreted protein clone ijj1442\_1.

XX Human: secreted protein; biological activity: nutritional; cytokine;  
KW cell proliferation; differentiation; immune stimulating; vaccine;  
KW haematopoiesis regulation; tissue growth; haemostatic; thrombolytic;  
KW anti-inflammatory; tumour inhibition.

XX Homo sapiens.

OS

PN W09946287-A1.

PD 16-SEP-1999.

XX

PE 11-MAR-1999: 99MO-US05243.

XX

PR 11-MAR-1998: 98US-0077521.

PR 14-MAY-1998: 98US-0079124.

PR 10-MAR-1999: 99US-0266105.

XX

PA (GEMV ) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, Lavallic ER, Collins-Racie LA, Evans C;

XX Merberg D, Treacy M, Agostino MJ, Steininger RJ;

XX WPI; 1999-551362/46.

DR N-PSDB; AA221096.

XX

PT Polynucleotides encoding secreted human proteins, derived from human

PT fetal brain, human adult blood, human adult bladder, or human adult

PT neural tissue cDNA libraries.

XX

Claim 17; Page 104; 118pp; English.

AA221093 to AA221102 encode new human secreted proteins and AAV29861 to

AAV29873 represent the secreted proteins encoded by the polynucleotide

sequences. AA221103 to AA221112 represent probes for the secreted

proteins. The polynucleotides and proteins are predicted to have

biological activities which would make them suitable for treating,

preventing or ameliorating medical conditions in humans and animals,

although no supporting data is given. Suggested activities include

nutritional activity, cytokine and cell proliferation/differentiation

activity, immune stimulating (e.g. as vaccines) or suppressing activity,

haematopoiesis regulating activity, tissue growth activity,

CC actinin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory

CC

CC

CC

CC

CC

CC

CC

CC activity, cadherin/tumour invasion suppressor activity, and tumour  
CC inhibition activity. The polynucleotides and proteins can also be used  
CC as nutritional sources or supplements. Such uses include use as a protein  
CC or amino acid supplement, use as a carbon source, use as a nitrogen  
CC source and use as a source of carbohydrate. They may also have utility  
CC in compositions used for bone, cartilage, tendon, ligament, and/or nerve  
CC tissue growth or regeneration, as well as for wound healing and tissue  
CC repair and replacement, and in the treatment of burns, incisions and  
CC ulcers. The proteins which induce cartilage and/or bone growth in  
CC circumstances where bone is not normally formed, have application in  
CC the healing of bone fractures and cartilage damage or defects in humans  
CC and other animals.

Sequence 299 AA;

Query Match 100.0%; Score 233; DB 20; Length 299;

Best Local Similarity 100.0%; Pred. No. 2,8e-233;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TTAEOEEVPOOTVAPQOORHSFKGECPCAGSHRSRHTACPCTEGVYTNASNNPEPCF 60
    |||||||
Db 67 tlarqeevpgqlvapgqgrhskfgeecpagsrhrehtgacmpctegvdytnasnnepscf 126
QY 61 PCTVCKSDQKHKSCTMTTRDTVCOCKEGTFRNENSPEMCRKCSRCPSGEVOVSNCTSWDD 120
    |||||||
Db 127 pctrcksdqkhksctmttrdtvcqckegtfrenspemcrkcsrpsgegvsnctswdd 186
QY 121 IQCYEEGRANNTVETPPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPA 180
    |||||||
Db 187 iqcyeeigranativetppaaeetmtspgtpapaaeetmtspgtpapaaeetmtspgtpa 246
QY 181 PAAEETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIIYVLIIVFV 233
    |||||||
Db 247 paaeetmtspgtpapaaeetmtspgtpashylsctivgiiyvlivlvfv 299
```

## RESULT 10

AAV05744  
ID AAV05744 standard; Protein: 299 AA.

AC AAV05744;

DT 19-JUL-1999 (first entry)

XX Tumour necrosis factor receptor TR5.

XX

KW Tumour necrosis factor receptor; TR5; TR1D; DCRL; agonist;

KW antagonist; screening; human; cancer; AIDS; Alzheimer's disease;

KW inflammation; arthritis; septicemia; autoimmune disease;

KW psoriasis; inflammatory bowel disease; transplant rejection;

KW graft versus host disease; infection; stroke; ischaemia;

KW acute respiratory disease syndrome; restenosis; brain injury;

KW bone disease; atherosclerosis; therapy.

XX

OS Homo sapiens.

PN EP911633-A1.

PD 28-APR-1999.

XX

PE 02-OCT-1998: 98EP-0203332.

PR 08-OCT-1997: 97US-0061334.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX McDonnell PC, Young PR, Zou J;

XX WPI; 1999-246560/21.

DR

XX

XX

XX

XX

XX

XX

XX

Identifying agonists and antagonists of tumor necrosis factor  
related receptors TR1, TR3 and of ligand TR3, useful for



PT treatment of cancer, AIDS, Alzheimer's disease, bone disease etc  
 XX Disclosure; Page 13-14; 23pp; English.  
 XX  
 CC The present sequence represents tumour necrosis factor receptor  
 CC (TNFR) TR5, also known as TR1D or DCRI. The invention relates  
 CC to TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and  
 CC their ligand TR3 (see AAY05745). TR1, TR3, TR5 and TR3 are used in  
 CC claimed methods of identifying agonists and antagonists, i.e.  
 CC compounds that bind to the receptors or ligand, and which activate  
 CC (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or  
 CC TR3. A screening kit for identifying agonists, antagonists,  
 CC ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or  
 CC TR3 polypeptides is provided. The agonists and antagonists are  
 CC useful for treatment of chronic and acute inflammation, arthritis,  
 CC septicemia, autoimmune disease e.g. inflammatory bowel disease,  
 CC psoriasis, transplant rejection, graft versus host disease,  
 CC infection, stroke, ischaemia, acute respiratory disease syndrome,  
 CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.  
 CC lymphoproliferative disorders), atherosclerosis and Alzheimer's  
 CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TR3.  
 CC  
 XX  
 SQ Sequence 299 AA;  
 Query Match 100.0%; Score 233; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTAAROEVPQOQTVAPQOORHSFKGEECPAGSHREHTGACNPTCEGVDTYNASNNPSCF 60  
 Db 67 ttarqeepvqqlvapgqqrhsfkgeecpagsrhrehtgacncptcegvdytnasnnepscf 126  
 QY 61 PCTVCKSDOKHKSSCTMTROTVCOCKEGTFRNENSPENCRCSCSPSEGVVSNCTSDMD 120  
 Db 127 pcvcksdqkhkssctmtrdvocqkegtfrnenspencrcscspsegvvsnctswdd 186  
 QY 121 IQCVEEFGANATVETPAAEETMTNTPSGTPAPAEETMTNTPSGTPAPAEETMTNTPSGTPA 180  
 Db 187 iqveefganatvetpaaeetmtntspgtppaaeetmtntspgtppaaeetmtntspgtppa 246  
 QY 181 PAAEETMTNTPSGTPAPAEETMTNTPSGTPASSHLSCTIVGIIYLVLLIVFV 233  
 Db 247 paaeetmtntspgtppaaeetmtntspgtppasshlylsctivgiiylvllivfv 299  
 RESULT 11  
 ID AAY00933 standard; Protein; 299 AA.  
 XX  
 AC AAY00933;  
 XX  
 DT 02-JUN-1999 (first entry)  
 XX  
 DE Human TRAIL-R3 protein sequence.  
 XX  
 KW Human; DR5; TRAIL-R3; apoptosis related condition; cancer; therapy;  
 KW autoimmune disease; viral infection; degenerative disorder;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischaemic injury;  
 KW cerebellar degeneration; myelodysplastic syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9909165-A1.  
 XX  
 PD 25-FEB-1999.  
 XX  
 PF 14-AUG-1998; 98WO-US16945.  
 XX  
 PR 15-AUG-1997; 97US-0055906.  
 XX  
 PA (IDUN-) IDUN PHARM INC.

PI Alnemri ES;  
 XX  
 DR WPI; 1999-181035/15.  
 DR N-PSDB; AAX27280.  
 XX  
 PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
 PT protein - useful in for screening for (ant)agonists that modulate  
 PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
 XX  
 PS Claim 16; Page 62-63; 71pp; English.  
 XX  
 CC This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An  
 CC antibody against the TRAIL receptors is useful for detecting mammalian  
 CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
 CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
 CC (Ant)agonists identified by the assay are useful for modulating the  
 CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
 CC related conditions which are treated in this way, include cancer  
 CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
 CC erythematosus and immune-mediated glomerulonephritis), viral infections  
 CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
 CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
 CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
 CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial  
 CC infarction and stroke). The polynucleotides can also be used to treat  
 CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
 CC used to form a composition that is useful for inhibiting expression of a  
 CC human DR5 or TRAIL-R3 protein.  
 XX  
 SQ Sequence 299 AA;  
 Query Match 100.0%; Score 233; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTAAROEVPQOQTVAPQOORHSFKGEECPAGSHREHTGACNPTCEGVDTYNASNNPSCF 60  
 Db 67 ttarqeepvqqlvapgqqrhsfkgeecpagsrhrehtgacncptcegvdytnasnnepscf 126  
 QY 61 PCTVCKSDOKHKSSCTMTROTVCOCKEGTFRNENSPENCRCSCSPSEGVVSNCTSDMD 120  
 Db 127 pcvcksdqkhkssctmtrdvocqkegtfrnenspencrcscspsegvvsnctswdd 186  
 QY 121 IQCVEEFGANATVETPAAEETMTNTPSGTPAPAEETMTNTPSGTPAPAEETMTNTPSGTPA 180  
 Db 187 iqveefganatvetpaaeetmtntspgtppaaeetmtntspgtppaaeetmtntspgtppa 246  
 QY 181 PAAEETMTNTPSGTPAPAEETMTNTPSGTPASSHLSCTIVGIIYLVLLIVFV 233  
 Db 247 paaeetmtntspgtppaaeetmtntspgtppasshlylsctivgiiylvllivfv 299  
 RESULT 12  
 ID AAW94671 standard; Protein; 299 AA.  
 XX  
 AC AAW94671;  
 XX  
 DT 04-MAY-1999 (first entry)  
 XX  
 DE Human TNF-related apoptosis-inducing ligand binding protein.  
 XX  
 KW Human; TNF-related apoptosis-inducing ligand binding protein; clotting;  
 KW TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy;  
 KW thrombotic microangiopathy; thrombotic thrombocytopenic purpura;  
 KW haemolytic-uraemic syndrome; systemic lupus erythematosus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9900423-A1.  
 XX  
 PD 07-JAN-1999.

XX 25-JUN-1998; 98WO-US13491.  
 XX 26-JUN-1997; 97US-0883529.  
 XX (IMMUNEX CORP.  
 XX Smith CA, Malczak H;  
 XX WPI: 1999-095685/08.  
 DR N-PSDB: AAX16692.  
 XX  
 XX New isolated TRAIL binding protein - which binds to a tumour  
 PT necrosis factor-related apoptosis inducing ligand, used in the  
 PT diagnosis and treatment of TRAIL-mediated disorders  
 XX  
 PS Claim 1; Fig 1; 47pp; English.  
 XX  
 CC The present sequence is human tumour necrosis factor (TNF)-related  
 CC apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be  
 CC used for inhibiting the biological activities of TRAIL or for purifying  
 CC TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated  
 CC disorder such as T cell death in HIV-infected patients. They can be used  
 CC for treating thrombotic microangiopathies such as thrombotic  
 CC thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small  
 CC blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic  
 CC acids can also be used for gene therapy. They can also be used as  
 CC carriers for delivering attached agents to cells bearing TRAIL.  
 XX  
 SQ Sequence 299 AA;

Query Match 100.0%; Score 233; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAQOEVPQQTVAPOQORHSFKGECPAGSGHRSHTACNPTBGVYTANSNNEPSCF 60  
 |||||||  
 Db 67 tlarqeevpgqlvapgqgrhshkgeecpagsrhshetlqacnptevgydnasnepacf 126  
 QY 61 PCTWCKSDQKHSCTMTROTVCOCKEGTFRNENSPKCRKRCRCPSEGVVSNCTSD 120  
 |||||||  
 Db 127 pcvcksdqkhsctmtrotdvcoqekgltrnenspmcrrkscrcpsgevyvsnctswdd 186  
 QY 121 IQCVEEFGANATVETPAEETMTNTSPGTAPAEETMTNTSPGTAPAEETMTNTSPGTPA 180  
 |||||||  
 Db 187 lqcvcefganavetpaeetmtntspgtapaeetmtntspgtapaeetmtntspgtpa 246  
 QY 181 PAAEETMTNTSPGTAPAEETMTNTSPGTAPASSHLSCTIVGIIIVLLIVFV 233  
 |||||||  
 Db 247 paaeetmtntspgtapaeetmtntspgtapashylsctivgiiivllivfv 299

RESULT 13  
 AAW88409  
 ID AAW88409 standard; Protein: 299 AA.  
 XX  
 AC AAW88409;  
 XX  
 DT 26-APR-1999 (first entry)  
 XX  
 DE Human Apo-2DcR protein (amino acids -40 to 259).  
 XX  
 KM Apo-2DcR; human; apoptosis; tumour necrosis factor receptor;  
 KM neurodegeneration; autoimmune disease; inflammation; cancer;  
 KM therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..40  
 FT /note= "-40 to -1 region of Apo-2DcR"  
 FT Peptide 41..69

FT Domain /note= "predicted signal peptide"  
 FT 41..201  
 FT /note= "extracellular domain, this domain is  
 FT specifically claimed in claim 5"  
 FT Domain 108..149  
 FT /note= "cysteine-rich domain"  
 FT Domain 150..189  
 FT /note= "cysteine-rich domain"  
 FT Peptide 202..216  
 FT /note= "tandem repeat peptide"  
 FT Peptide 217..231  
 FT /note= "tandem repeat peptide"  
 FT Peptide 232..246  
 FT /note= "tandem repeat peptide"  
 FT Peptide 247..261  
 FT /note= "tandem repeat peptide"  
 FT Peptide 262..276  
 FT /note= "tandem repeat peptide"  
 FT Region 265..299  
 FT /note= "hydrophobic C-terminal region"  
 FT Modified-site 117  
 FT /note= "N-glycosylation"  
 FT Modified-site 180  
 FT /note= "N-glycosylation"  
 FT Modified-site 196  
 FT /note= "N-glycosylation"  
 FT Modified-site 209  
 FT /note= "N-glycosylation"  
 FT Modified-site 224  
 FT /note= "N-glycosylation"  
 FT Modified-site 224  
 FT /note= "N-glycosylation"

XX WO9858062-A1.  
 XX 23-DEC-1998.  
 XX  
 XX 12-JUN-1998; 98WO-US12456.  
 XX  
 XX 18-JUN-1997; 97US-0878168.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 PI Askenazi AJ, Baker KP, Chuntharapai A, Gurney A;  
 PI Kim KU, Wood WI;  
 DR WPI: 1999-095340/08.  
 DR N-PSDB: AAW84347.  
 XX  
 PT New Apo-2DcR polypeptide - used for modulation and diagnosis of  
 PT apoptosis, e.g. in neurodegeneration  
 PS Claim 9; Page 53-54; 88pp; English.  
 XX  
 CC This polypeptide comprises human Apo-2DcR, a novel member of the  
 CC tumour necrosis factor receptor family that binds to Apo-2 ligand.  
 CC Its amino acid sequence was deduced from the nucleotide sequence  
 CC of an isolated cDNA clone (see AAW84347); an alternative translation  
 CC initiation site in this clone will encode a polypeptide (see  
 CC AAW88408) lacking the first 40 amino acid residues of this sequence.  
 CC Apo-2DcR shows more sequence identity to DR4 (60%) and Apo-2 (50%)  
 CC than to other apoptosis-linked receptors. The polypeptide can be  
 CC obtained by expression in host cells using the vector deposited as  
 CC ATCC 209087. The invention provides vectors and host cells for  
 CC recombinant production of Apo-2DcR polypeptides, antibodies, and  
 CC transgenic and knockout animals (useful e.g. for screening and  
 CC developing drugs that protect against excessive apoptosis).  
 CC Apo-2DcR, or chimeras comprising Apo-2DcR or its (claimed)  
 CC extracellular domain fused to a heterologous polypeptide are used  
 CC to modulate apoptosis of mammalian cells (claimed) and/or NF-kappaB  
 CC activation by Apo-2 ligand, and may be expressed in vivo or ex vivo  
 CC for gene therapy. They can be used in methods for the modulation  
 CC and diagnosis of apoptosis e.g. in cases of neurodegeneration,  
 CC autoimmune diseases and inflammation. Most human tumour cells do  
 CC not express Apo-2DcR transcripts, but normal tissues do, suggesting

CC that Apo-2DR may permit selective killing of cancer cells by Apo-2  
 CC ligand, possibly by protecting normal, but not cancerous, cells.  
 XX  
 XX  
 SO Sequence 299 AA;

Query Match 100.0%; Score 233; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRAQEEVPQOTYAPQOQRHSFKGECPAGSHRSEHTGACNPGCEGYDYNASNNESCF 60  
 DB 67 ttrageevpqvltvapqqrirshfygeecpagshrsehlgacnpgcegydylnasnepsc 126  
 QY 61 PCYVCKSDOKHKSCTTRPTVCCKEGTRFNENSPMCRCRCSRCPGGEVQVSNCTGMD 120  
 DB 127 pcvcksdqghksscttrptvcckegtrfnenpamcrkscspggevqvsncstwd 186  
 QY 121 IQCVEEFGANATVETPAAEETMTNTSPGTPAPAAEETMTNTSPGTPAPAAEETMTNTSPGTPA 180  
 DB 187 iqcvееfganatvetpaaеetmtntspgtpapaeetmtntspgtpapaeetmtntspgt 246  
 QY 181 PAAEETMTNTSPGTPAPAAEETMTNTSPGTPASSHLSCTIVGIIVLVLLIVFV 233  
 DB 247 paaеetmtntspgtpapaeetmtntspgtpasshlsctivgiivlvllivfv 299

## RESULT 14

AAB01343  
 ID AAB01343 standard; Protein: 299 AA.

AC AAB01343;

DT 25-SEP-2000 (first entry)

XX Death receptor.

XX UL144; death receptor; apoptosis; programmed cell death; FAS;

KW TNF- $\alpha$ ; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;

KM human.

XX Homo sapiens.

XX WO200034335-A2.

PD 15-JUN-2000.

PF 03-DEC-1999; 99WO-US26035.

XX 04-DEC-1998; 98US-0205018.

XX (SCHE) SCHERING CORP.

XX Leong C, Phillips JH;

XX WPI; 2000-423383/36.

XX Purified or recombinant polypeptide for modulating apoptosis comprises

PT a sequence which binds to an antibody specific for UL144 or its

PT fragments

XX Disclosure; Page 75-76; 76pp; English.

XX A pure or recombinant polypeptide which binds to a polyclonal antibody

CC specific for the mature UL144 is useful for screening molecules which

CC block induction of apoptosis or interfere with antiapoptotic activity.

CC The polypeptide is also useful for modulating apoptosis and useful in

CC treatment of conditions associated with abnormal physiology or

CC development, such as cancer or degenerative conditions and for

CC regulation of viral infection and replication. At least five

CC different death receptors are known, which include the CD95

CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated

CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related

CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.  
 XX  
 XX  
 SO Sequence 299 AA;

Query Match 100.0%; Score 233; DB 21; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRAQEEVPQOTYAPQOQRHSFKGECPAGSHRSEHTGACNPGCEGYDYNASNNESCF 60  
 DB 67 ttrageevpqvltvapqqrirshfygeecpagshrsehlgacnpgcegydylnasnepsc 126  
 QY 61 PCYVCKSDOKHKSCTTRPTVCCKEGTRFNENSPMCRCRCSRCPGGEVQVSNCTGMD 120  
 DB 127 pcvcksdqghksscttrptvcckegtrfnenpamcrkscspggevqvsncstwd 186  
 QY 121 IQCVEEFGANATVETPAAEETMTNTSPGTPAPAAEETMTNTSPGTPAPAAEETMTNTSPGTPA 180  
 DB 187 iqcvееfganatvetpaaеetmtntspgtpapaeetmtntspgtpapaeetmtntspgt 246  
 QY 181 PAAEETMTNTSPGTPAPAAEETMTNTSPGTPASSHLSCTIVGIIVLVLLIVFV 233  
 DB 247 paaеetmtntspgtpapaeetmtntspgtpasshlsctivgiivlvllivfv 299

## RESULT 15

AAB82182  
 ID AAB82182 standard; Protein: 249 AA.

AC AAB82182;

DT 23-JUL-2001 (first entry)

XX FLAG-TRID clone without a transmembrane domain.

XX FLAG-epitope tag; transmembrane domain; death domain; apoptosis;

KW cell suicide; tissue homeostasis; cell proliferation;

KM cell-cell signaling; Trail Receptor without Intracellular Domain; TRID.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..23

XX Protein /label= Signal\_peptide

XX Peptide /label= FLAG-TRID

XX MISC-difference 249

XX /note= "Insertion site for candidate sequences"

XX WO200114542-A1.

XX 01-MAR-2001.

XX 23-AUG-2000; 2000WO-US23112.

XX 25-AUG-1999; 99US-0150747.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Denome SA, Swain PM, Tzellas N;

XX WPI; 2001-374162/39.

XX N-PSDB; AAH19326.

XX Identifying a transmembrane domain of a membrane-spanning protein

PT useful in defining processes in cell suicide and tissue homeostasis,

PT comprises modifying the nucleic acid encoding a death domain-lacking

PT membrane spanning protein -

PS Disclosure; Fig 2; 38pp; English.

XX The present invention relates to methods for identifying a transmembrane  
 CC domain (TM) of a membrane-spanning protein. The method comprises  
 CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane  
 CC spanning protein (e.g., TRAIL Receptor without Intracellular Domain; TRID)  
 CC by replacing the nucleic acid encoding the TM of the DD-lacking  
 CC membrane-spanning protein with a candidate nucleic acid sequence to  
 CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
 CC protein. The modified nucleic acid is then transfected into a host cell,  
 CC which expresses a DD-containing receptor. The absence of apoptosis of the  
 CC host cell is determined following exposure of the transfected cell to an  
 CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
 CC apoptosis of the host cell. The modified nucleic acid encoding the  
 CC modified death domain-lacking membrane-spanning protein can also include  
 CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
 CC a FLAG-TRID clone, which was used in the method of the present invention.  
 CC This sequence comprises human TRID protein and the FLAG-epitope tag. The  
 CC FLAG-epitope is a useful marker to purify proteins encoded by the  
 CC modified DD-lacking membrane-spanning protein. The identified TM and  
 CC membrane-spanning proteins may be used in defining processes involved in  
 CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat  
 CC events, such as cell proliferation and cell-cell signalling pathways.

XX Sequence 249 AA:

Query Match 91.8%; Score 214; DB 22; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-213;  
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAROEYVPOQTVAAPQOQRHSFKGEECPAGSHRSEHTGACNPGTEGVDTNANSPSCF 60  
 DB 36 ttarqeepqgtvpaqgrhshfkgeecpagsrhsehtgacnpgtegvdytnasnepscfcf 95  
 QY 61 PCTVCKSDQKHKSCTMTRTDVTCCCKECTFRNENSPKCRKCRSPGSEVOVSNCTSMDD 120  
 DB 96 pctvcksdqkhkssctmtldvtccckegltfrnenspckrcscrgsgvgsnctswdd 155  
 QY 121 IQCYEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA 180  
 DB 156 iqcyeeifganatvetpaaeeetmntspgtpapaaeeetmntspgtpapaaeeetmtspgtpa 215  
 QY 181 PAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY 214  
 DB 216 paaeeetmtspgtpapaaeeetmtspgtpasshy 249

#### RESULT 16

AAW93578 standard; Protein: 259 AA.

AAW93578:

18-JUN-1999 (first entry)

Human hAPO9 protein.

XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;  
 KM developmental abnormality; gestational abnormality; prostate cancer;  
 KM APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;  
 KM cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;  
 KM apoptosis; human.

OS Homo sapiens.

PN W09911791-A2.

PD 11-MAR-1999.

PF 04-SEP-1998; 98WO-US18393.

PR 05-SEP-1997; 97US-0924634.

XX

PA (UNIV ) UNIV WASHINGTON.

PI Chaudhary PM.

XX WPI: 1999-205191/17.

DR N-PSDB: AAX23412.

XX New Tumor Necrosis Factor family receptor polypeptides and ligands -  
 PT useful for diagnosis and treatment of prostate cancer and  
 PT developmental or gestational abnormalities

XX Claim 24; Fig 6; 156pp; English.

PS This invention describes isolated Tumor Necrosis Factor (TNF) family  
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active  
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or  
 CC their active fragments. APO4 is useful for diagnosing prostate cancer  
 CC by determining levels of APO4 in an individual. Prostate cancer can also  
 CC be treated using APO4 selective binding agents linked to a therapeutic  
 CC moiety. APO4 polypeptides are also useful for identifying selective  
 CC binding agents, useful in diagnosis/treatment of disease by binding of  
 CC agents to the polypeptide/active fragment which is extracellular, or  
 CC expressed on the cell surface. The binding is preferably performed in  
 CC vivo. APO4 polypeptides/active fragments are also useful for screening  
 CC for agonists and antagonists by binding and observing the change in APO4  
 CC activity. Effective pharmacological agents useful in diagnosis or  
 CC treatment of disease are also identified using APO4 polypeptides/active  
 CC fragments and APO4 signal transducer molecules that specifically interact  
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4  
 CC activity. The method is performed in vivo or in vitro. APO polypeptides  
 CC are all useful as immunogens for preparing antibodies. APO4 is also  
 CC useful for diagnosis/treatment of developmental or gestational  
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line  
 CC MCF-7, and induced apoptosis.

XX Sequence 259 AA:

Query Match 79.4%; Score 185; DB 20; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-183;  
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAROEYVPOQTVAAPQOQRHSFKGEECPAGSHRSEHTGACNPGTEGVDTNANSPSCF 60  
 DB 27 ttarqeepqgtvpaqgrhshfkgeecpagsrhsehtgacnpgtegvdytnasnepscfcf 86  
 QY 61 PCTVCKSDQKHKSCTMTRTDVTCCCKECTFRNENSPKCRKCRSPGSEVOVSNCTSMDD 120  
 DB 87 pctvcksdqkhkssctmtldvtccckegltfrnenspckrcscrgsgvgsnctswdd 146  
 QY 121 IQCYEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA 180  
 DB 147 iqcyeeifganatvetpaaeeetmntspgtpapaaeeetmntspgtpapaaeeetmtspgtpa 206  
 QY 181 PAAEE 185  
 DB 207 paaee 211

#### RESULT 17

AAV05726 standard; Protein: 259 AA.

AAV05726:

19-JUL-1999 (first entry)

Tumour necrosis factor receptor TRAIL-R3.

XX TRAIL-3; tumour necrosis factor receptor; apoptosis; cancer;  
 KM therapy.

OS Mammalia.

```

XX Key Location/Qualifiers
FH Peptide 1..24
FT /note="signal peptide"
FT Protein 25..259
FT /note="mature protein"
FT Region 162..175
FT /note="TAPE repeat"
FT Region 176..191
FT /note="TAPE repeat"
FT Region 192..206
FT /note="TAPE repeat"
FT Region 207..221
FT /note="TAPE repeat"
FT Region 222..236
FT /note="TAPE repeat"
FT Domain 238..259
FT /note="Transmembrane domain"
XX
XX WO912963-A2.
XX 18-MAR-1999.
XX
XX 11-SEP-1998; 98WO-US19029.
XX
XX 06-MAY-1998; 98US-0084422.
XX 12-SEP-1997; 97US-0058631.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Tschopp J;
XX
XX WPI; 1999-276942/23.
XX N-PSDB; AAX25349.
XX
XX Novel tumor necrosis factor receptor proteins TRAIL-R2 and TRAIL-R3
XX
XX Disclosure; Page 28; 28pp; English.
XX
XX The present sequence represents TRAIL-R3, a novel mammalian
XX cysteine-rich receptor of the tumour necrosis factor receptor family.
XX The invention is related to novel receptors for TRAIL, i.e. TRAIL-2
XX (see AAY05725) and TRAIL-3. TRAIL-3 is highly glycosylated. It is
XX a putative glycosylphosphatidylinositol-anchored protein, which is
XX either cell-associated or processed and secreted. Secreted
XX TRAIL-R3 competes for the binding of TRAIL to TRAIL-R1 and/or
XX TRAIL-R2, thereby acting as an inhibitor of apoptosis. Expression
XX of TRAIL-R3 is restricted to peripheral blood lymphocytes and
XX skeletal muscle. It is likely that TRAIL-3 acts as an important
XX regulator of TRAIL-R2 and -R3 induced cell death in vivo. A method
XX for preventing or reducing the advancement, severity or effects of
XX an immunological disease involves administering a TRAIL-R2 or
XX TRAIL-R3 blocking agent such as a soluble TRAIL-R (preferably
XX comprising a human immunoglobulin Fc domain) and an antibody. A
XX method of treating cancer involves administration of antibodies
XX against TRAIL-R3 or TRAIL-R2. A method of inducing cell death
XX involves administration of an agent capable of inhibiting the
XX binding of TRAIL-R2 or -R3 to its ligand.
XX
XX Sequence 259 AA:

```

```

Query Match 60.1%; Score 140; DB 20; Length 259;
Best Local Similarity 100.0%; Pred. No. 6.8e-137;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 94 NSPEMCKKCSGPGEGVQVSNCTSWDIOCYEEFGANATVETPAAEETMTMTSPGTPAPAA 153
DB 120 nspemckkcsrpgsvncstswddiqcveefganatvetpaaeeemntspgtpapaa 179
QY 154 EETNTNTSGTPAPAAEETMTSPGTPAPAAEETMTSGTPAPAAEETMTSPGTPASSH 213
DB 180 eetntntspgtpapaaeeemntspgtpapaaeeemntspgtpapaaeeemntspgtpassh 239

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```

QY 214 YLSCTGIIVLIVLIVFV 233
DB 240 ylsctgiivliviivfv 259

```

```

RESULT 18
AAW88450
ID AAW88450 standard; Peptide; 48 AA.
XX
AC AAW88450;
XX
DE 26-APR-1999 (first entry)
XX
DE Human Apo-2DCR peptide.
XX
KW Apo-2DCR; human; apoptosis; tumour necrosis factor receptor;
KW neurodegeneration; autoimmune disease; inflammation; cancer;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO9858062-A1.
XX
PD 23-DEC-1998.
XX
PF 12-JUN-1998; 98WO-US12456.
XX
PR 18-JUN-1997; 97US-0878168.
XX
XX (GETH ) GENENTECH INC.
XX
PA Ashkenazi AJ, Baker KP, Chuntcharapai A, Gurney A;
PI Kim KJ, Wood WJ;
XX
XX WPI; 1999-095340/08.
XX
XX New Apo-2DCR polypeptide - used for modulation and diagnosis of
XX apoptosis, e.g. in neurodegeneration
XX
XX Example 1; Page 39; 88pp; English.
XX
XX This peptide is encoded by DNA21705, a cDNA clone obtained by
XX PCR amplification (see AAW84349-50) of human breast carcinoma cDNA.
XX The peptide shows homology to a peptide (see AAW88449) derived from
XX human tumour necrosis factor receptor 1 (TNFR1). DNA21705 was used
XX as a probe to screen a human foetal lung library, yielding a clone
XX (see AAV84347) encoding Apo-2DCR, a novel member of the TNFR family
XX that binds to Apo-2 ligand and is involved in apoptosis. Apo-2DCR
XX polypeptides can be used in methods for the modulation and
XX diagnosis of apoptosis e.g. in cases of neurodegeneration,
XX autoimmune diseases and inflammation.
XX
XX Sequence 48 AA:

```

```

Query Match 20.6%; Score 48; DB 20; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.6e-42;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 40 CNPCTEGVDYTNASNEPSCFCTVCKSDQKHKSSCTWTRDTVCQCKE 87
DB 1 cnpctegvdytnasnepsfcctvcksdqkhhkssctwtrdtvcqcke 48

```

```

RESULT 19
AAW98200
ID AAW98200 standard; Protein; 386 AA.
XX
AC AAW98200;
XX
DE 05-JUL-1999 (first entry)
XX

```

DE RTD, inhibitor of Apo-2 ligand-induced apoptosis.  
 XX RTD; tumour necrosis factor receptor; trail receptor; Apo-2 ligand;  
 KW apoptosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT 1..55  
 FT /note= "signal peptide"  
 FT 56..386  
 FT /note= "mature protein"  
 FT 56..212  
 FT /note= "extracellular domain, specifically claimed  
 in Claim 6"  
 FT Domain  
 FT 213..232  
 FT /note= "transmembrane domain"  
 FT 233..386  
 FT /note= "intracellular domain"  
 FT Modified-site  
 FT 127  
 FT /note= "N-glycosylated"  
 FT Modified-site  
 FT 171  
 FT /note= "N-glycosylated"  
 FT Modified-site  
 FT 182  
 FT /note= "N-glycosylated"  
 FT Misc-difference  
 FT 310  
 FT /label= Ser, Leu  
 FT 99..139  
 FT /note= "cysteine-rich domain"  
 FT 141..180  
 FT /note= "cysteine-rich domain"  
 FT 1..212  
 FT /note= "extracellular domain polypeptide,  
 specifically claimed in Claim 7"  
 FT Protein  
 FT 99..139  
 FT /note= "extracellular domain polypeptide,  
 specifically claimed in Claim 8"  
 FT Protein  
 FT 141..180  
 FT /note= "extracellular domain polypeptide,  
 specifically claimed in Claim 9"  
 XX  
 XX  
 PN WO9910484-A1.  
 PD 04-MAR-1999.  
 XX  
 XX 14-JUL-1998; 98WO-US14552.  
 XX 26-AUG-1997; 97US-0918874.  
 XX (GERTH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Gurney A;  
 XX WPI: 1999-254218/21.  
 DR N-PSDB: AAX25093.  
 XX  
 XX A new polypeptide, designated RTD  
 PS Claim 4; Page 40-52; 58pp; English.  
 XX  
 CC The present sequence is human RTD, a novel protein capable of  
 CC binding Apo-2 ligand. RTD is a receptor for tumour necrosis  
 CC factor, belonging to the family of trail receptors. It is an  
 CC inhibitor of Apo-2 ligand-induced apoptosis, and acts as a decoy  
 CC receptor, lacking an intracellular signalling death domain. RTD  
 CC polypeptides can be obtained by expressing the polypeptide  
 CC encoded by the cDNA insert of the vectors deposited as ATCC 209201  
 CC or ATCC 209202 (see also AAX25093). These cDNAs differ in sequence  
 CC at a single nucleotide, resulting in serine or leucine at amino  
 CC acid position 310 of RTD. Isolated RTD polypeptides, especially  
 CC the extracellular domain (ECD), chimeric molecules including RTD or  
 CC its ECD, and nucleic acids encoding such polypeptides are claimed,  
 CC as are antibodies, vectors, host cells (especially CHO, yeast and

CC E. coli cells), transgenic and knockout animals, and a method of  
 CC modulating apoptosis in mammalian cells by exposing the cells to  
 CC RTD polypeptide. This therapy can be accomplished e.g. using in  
 CC vivo or ex vivo gene therapy techniques. RTD chimeric molecules  
 CC comprising immunoglobulin sequences can be used to inhibit Apo-2  
 CC ligand activities, e.g. apoptosis or NF-kappa B induction or the  
 CC activity of another ligand to which RTD binds.  
 XX  
 XX Sequence 386 AA;  
 SQ  
 Query Match 6.0%; Score 14; DB 20; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 37 TGACNPTCEGYDYT 50  
 Db 93 TGACNPTCEGYDYT 106  
 RESULT 20  
 AAY04144  
 ID AAY04144 standard; Protein: 386 AA.  
 XX  
 XX AAY04144;  
 XX  
 XX 15-JUN-1999 (first entry)  
 DT  
 XX Human Tango-74 protein.  
 DE  
 XX Human; Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;  
 KW detection.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9907850-A1.  
 PN 18-FEB-1999.  
 PD  
 XX 06-AUG-1998; 98WO-US16502.  
 PF  
 XX 05-SEP-1997; 97US-0058108.  
 PR 06-AUG-1997; 97US-0054966.  
 XX  
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 PA  
 PI Goodearl ADJ, Holtzman DA;  
 XX WPI: 1999-167426/14.  
 DR N-PSDB: AAX19957.  
 XX  
 XX New TANGO polypeptides and nucleic acids encoding them - useful as  
 PT diagnostic agents and for treating disorders caused by aberrant  
 PT expression of TANGO  
 XX  
 XX Claim 8; Fig 3; 84pp; English.  
 PS  
 XX The present sequence represents human Tango-74. Tango polypeptides are  
 CC useful for identifying compounds which bind the polypeptide via direct  
 CC binding, competition binding assays or Tango-71, -73, -74, 76 or -83-  
 CC mediated signal transduction. Tango polypeptides are also useful for  
 CC identifying modulating compounds by determining effect on Tango activity.  
 CC Tango polypeptides and nucleic acids are useful for diagnosing diseases  
 CC related to aberrant expression of Tango, and Tango polypeptides are  
 CC useful for raising antibodies which can be used in diagnostic assays for  
 CC detection of Tango, and also for generating anti-idiotypic antibodies for  
 CC prevention and protection.  
 CC  
 XX Sequence 386 AA;  
 SQ  
 Query Match 6.0%; Score 14; DB 20; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 TGACNPCTEGVDYT 50  
 |||||  
 Db 93 tgacnpctegvdyt 106

RESULT 21  
 ID AAM99018 standard; Protein: 386 AA.

XX AC AAM99018;  
 XX 12-MAY-1999 (first entry)  
 XX  
 DE Human TRAIL receptor 4A.

KW Human; TRAIL; TRAIL receptor; immunoreactive; thrombotic microangiopathy;  
 KW HIV infection; tumour necrosis factor related apoptosis inducing ligand;  
 KW TNF related apoptosis inducing ligand; systemic lupus erythematosus;  
 KW multiple sclerosis.

XX OS Homo sapiens.  
 XX WO9903992-A1.  
 XX 28-JAN-1999.

XX PF 10-JUL-1998; 98WO-US14410.  
 XX PR 15-JUL-1997; 97US-0892119.

XX PA (IMMV ) IMMUNEX CORP.

XX PI Degli-Esposti M;

XX DR WPI; 1999-132236/11.  
 DR N-PSDB; AAX18926.

XX PT New isolated TRAIL receptor polypeptides - used to develop products  
 PT for treating e.g. thrombotic microangiopathy, multiple sclerosis,  
 PT systemic lupus erythematosus or HIV infection

XX PS Claim 1; Fig 1; 51pp; English.

CC The present sequence is a human tumour necrosis factor (TNF)-related  
 CC apoptosis-inducing ligand (TRAIL) receptor designated TRAILR4A. TRAILR  
 CC proteins can be used for binding TRAIL, e.g. to measure or inhibit the  
 CC biological activity of TRAIL. TRAILR proteins can be used for treating  
 CC thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura  
 CC (TTP) or haemolytic-uraemic syndrome (HUS), clotting of small blood  
 CC vessels in e.g. AIDS, multiple sclerosis or systemic lupus erythematosus  
 CC or for reducing TRAIL-mediated death of T cells in HIV-infected patients.  
 CC They can also be used to purify TRAIL or TRAIL-expressing cells or as  
 CC carriers for delivering agents to cells bearing TRAIL.

XX SQ Sequence 386 AA;

Query Match 6.0%; Score 14; DB 20; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 TGACNPCTEGVDYT 50  
 |||||  
 Db 93 tgacnpctegvdyt 106

RESULT 22  
 ID AAM99019 standard; Protein: 386 AA.

XX AC AAM99019;

XX DT 12-MAY-1999 (first entry)  
 XX  
 DE Human TRAIL receptor 4B.

KW Human; TRAIL; TRAIL receptor; immunoreactive; thrombotic microangiopathy;  
 KW HIV infection; tumour necrosis factor related apoptosis inducing ligand;  
 KW TNF related apoptosis inducing ligand; systemic lupus erythematosus;  
 KW multiple sclerosis.

XX OS Homo sapiens.  
 XX WO9903992-A1.  
 XX 28-JAN-1999.

XX PF 10-JUL-1998; 98WO-US14410.  
 XX PR 15-JUL-1997; 97US-0892119.

XX PA (IMMV ) IMMUNEX CORP.

XX PI Degli-Esposti M;

XX DR WPI; 1999-132236/11.  
 DR N-PSDB; AAX18927.

XX PT New isolated TRAIL receptor polypeptides - used to develop products  
 PT for treating e.g. thrombotic microangiopathy, multiple sclerosis,  
 PT systemic lupus erythematosus or HIV infection

XX PS Claim 1; Fig 2; 51pp; English.

CC The present sequence is a human tumour necrosis factor (TNF)-related  
 CC apoptosis-inducing ligand (TRAIL) receptor designated TRAILR4B. TRAILR  
 CC proteins can be used for binding TRAIL, e.g. to measure or inhibit the  
 CC biological activity of TRAIL. TRAILR proteins can be used for treating  
 CC thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura  
 CC (TTP) or haemolytic-uraemic syndrome (HUS), clotting of small blood  
 CC vessels in e.g. AIDS, multiple sclerosis or systemic lupus erythematosus  
 CC or for reducing TRAIL-mediated death of T cells in HIV-infected patients.  
 CC They can also be used to purify TRAIL or TRAIL-expressing cells or as  
 CC carriers for delivering agents to cells bearing TRAIL.

XX SQ Sequence 386 AA;

Query Match 6.0%; Score 14; DB 20; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 TGACNPCTEGVDYT 50  
 |||||  
 Db 93 tgacnpctegvdyt 106

RESULT 23  
 ID AAM92792 standard; Protein: 386 AA.

XX AC AAM92792;

XX DT 12-APR-1999 (first entry)

XX DE Human TNF receptor TR10 protein.

KW TR10; tumour necrosis factor receptor; TNF; human; agonist; treatment;  
 KW disease; apoptosis; inhibition; cancer; lymphoma; carcinoma; tumour;  
 KW autoimmune disease; viral infection; inflammation; graft rejection; AIDS;  
 KW graft versus host disease; antagonist; neurodegenerative disorder;  
 KW myelodysplastic syndrome; ischemic injury; liver disease; drug screening;  
 KW septic shock; cachexia; anorexia; detection; diagnosis.

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..55  
 FT /label= signal\_peptide  
 FT Protein 56..386  
 FT /label= TR10  
 FT Domain 56..212  
 FT /label= extracellular\_domain  
 FT Domain 213..230  
 FT /label= transmembrane\_domain  
 FT Domain 231..386  
 FT /label= intracellular\_domain  
 XX  
 PN WO9854202-A1.  
 XX  
 PD 03-DEC-1998.  
 XX  
 PF 29-MAY-1998; 98WO-US10981.  
 XX  
 PR 09-DEC-1997; 97US-0069112.  
 PR 30-MAY-1997; 97US-0050936.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI NI J, Rosen CA.  
 PT  
 DR MPI: 1999-059803/05.  
 DR N-PSDB; AAV72101.  
 XX  
 PT New isolated human tumour necrosis factor-like receptor TR10 - used  
 PT to develop products for treating, e.g. cancers, autoimmune  
 PT disorders, viral infections, inflammation, graft rejection,  
 PT neurodegenerative disorders or septic shock  
 XX  
 PS Claim 3; Fig 1A-D; 85pp; English.  
 XX  
 CC This sequence represents a novel human tumour necrosis factor (TNF)  
 CC receptor, TR10. TR10 polypeptides or agonists can be used for treating  
 CC diseases and disorders associated with inhibition of apoptosis, e.g.  
 CC cancers (e.g. follicular lymphomas, carcinomas with p53 mutations, and  
 CC hormone-dependent tumours, such as breast cancer, prostate cancer,  
 CC Kaposi's sarcoma and ovarian cancer), autoimmune disorders (e.g. systemic  
 CC lupus erythematosus and immune-related glomerulonephritis rheumatoid  
 CC arthritis), viral infections (e.g. herpes viruses, pox viruses and  
 CC adenoviruses), inflammation, graft versus host disease, acute graft  
 CC rejection and chronic graft rejection. Antagonists can be used for  
 CC treating diseases and disorders associated with increased apoptosis,  
 CC e.g. AIDS, neurodegenerative disorders (e.g. Alzheimer's disease,  
 CC Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa,  
 CC cerebellar degeneration), myelodysplastic syndromes (e.g. aplastic  
 CC anemia), ischemic injury (e.g. as caused by myocardial infarction, stroke  
 CC and reperfusion injury), toxin-induced liver disease (e.g. as caused by  
 CC alcohol), septic shock, cachexia and anorexia. Antagonists can also be  
 CC used for treating inflammatory diseases and disorders, e.g. inflammatory  
 CC bowel disease, rheumatoid arthritis, osteoarthritis, psoriasis and  
 CC septicemia. The products can also be used for detection, diagnosis and  
 CC drug screening.  
 XX  
 SO Sequence 386 AA;

Query Match 6.0%; Score 14; DB 20; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGACNPCTEGVDYT 50  
 ||||||||||||  
 Db 93 tgacnpctegydyt 106

RESULT 24  
 AAB01341

ID AAB01341 standard; Protein; 386 AA.  
 XX  
 AC AAB01341;  
 XX  
 DT 25-SEP-2000 (first entry)  
 XX  
 DE TNF-related apoptosis inducing ligand (TRAIL) receptor-3.  
 XX  
 DE U1144; death receptor; apoptosis; programmed cell death; FAS;  
 KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200034335-A2.  
 XX  
 PD 15-JUN-2000.  
 XX  
 PF 03-DEC-1999; 99WO-US26035.  
 XX  
 PR 04-DEC-1998; 98US-0205018.  
 XX  
 PA (SCHE) SCHERING CORP.  
 XX  
 PI Leong C, Phillips JH;  
 PT  
 DR MPI: 2000-423383/36.  
 XX  
 PT Purified or recombinant polypeptide for modulating apoptosis comprises  
 PT a sequence which binds to an antibody specific for U1144 or its  
 PT fragments  
 XX  
 PS Disclosure; Page 73-74; 76pp; English.  
 XX  
 CC A pure or recombinant polypeptide which binds to a polyclonal antibody  
 CC specific for the mature U1144 is useful for screening molecules which  
 CC block induction of apoptosis or interfere with antiapoptotic activity.  
 CC The polypeptide is also useful for modulating apoptosis and useful in  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, such as cancer or degenerative conditions and for  
 CC regulation of viral infection and replication. At least five  
 CC different death receptors are known, which include the CD95  
 CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated  
 CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related  
 CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.  
 XX  
 SO Sequence 386 AA;

Query Match 6.0%; Score 14; DB 21; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGACNPCTEGVDYT 50  
 ||||||||||||  
 Db 93 tgacnpctegydyt 106

RESULT 25  
 AAY69991  
 ID AAY69991 standard; Protein; 386 AA.  
 XX  
 AC AAY69991;  
 XX  
 DT 31-MAY-2000 (first entry)

Human receptor-associated protein from Incyte clone 3472455.  
 DE  
 DE Human receptor-associated protein; HRAP; Incyte clone 3472455;  
 KW cytosolic; immunomodulatory; antiinflammatory; cardiac; antianaemic;  
 KW antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;  
 KW antiasthmatic; osteopapalic; antiallergic; antidiabetic; dermatological;  
 KW neuroprotective; diagnosis; treatment; prevention; reproductive disorder;



KW cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;  
 KW gastroenteritis; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;  
 KW arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;  
 KW multiple sclerosis; irritable bowel syndrome.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 XX FH Modified-site 13 /note= "Potential phosphorylation site"  
 FT Modified-site 77 /note= "Potential phosphorylation site"  
 FT Modified-site 87 /note= "Potential phosphorylation site"  
 FT Modified-site 126 /note= "Potential phosphorylation site"  
 FT Modified-site 133 /note= "Potential phosphorylation site"  
 FT Modified-site 145 /note= "Potential phosphorylation site"  
 FT Modified-site 157 /note= "Potential phosphorylation site"  
 FT Modified-site 173 /note= "Potential phosphorylation site"  
 FT Modified-site 189 /note= "Potential phosphorylation site"  
 FT Modified-site 231 /note= "Potential phosphorylation site"  
 FT Modified-site 263 /note= "Potential phosphorylation site"  
 FT Modified-site 281 /note= "Potential phosphorylation site"  
 FT Modified-site 291 /note= "Potential phosphorylation site"  
 FT Modified-site 310 /note= "Potential phosphorylation site"  
 FT Modified-site 345 /note= "Potential phosphorylation site"  
 FT Modified-site 352 /note= "Potential phosphorylation site"  
 FT Modified-site 361 /note= "Potential phosphorylation site"  
 FT Modified-site 369 /note= "Potential phosphorylation site"  
 FT Modified-site 127 /note= "Potential phosphorylation site"  
 FT Modified-site 182 /note= "Potential N-glycosylation site"  
 FT Modified-site 277 /note= "Potential N-glycosylation site"  
 FT Binding-site 185..192 /note= "Potential N-glycosylation site"  
 FT Region /label= ATP/GTP-binding\_site  
 FT /label= Signature\_sequence  
 FT /note= "TNFR/NGFR cysteine-rich region"  
 PN MO200008155-A2.  
 XX 17-FEB-2000.  
 PD 17-FEB-2000.  
 XX 06-AUG-1999; 99MO-US17777.  
 XX 07-AUG-1998; 98US-0160065.  
 PR 01-SEP-1998; 98US-0098703.  
 XX (INCYTE) INCYTE PHARM INC.  
 XX Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;  
 PI Corley NC, Baughn MR;  
 XX WPI: 2000-205710/18.  
 DR N-PSDB; AA250893.  
 XX

PT New human receptor-associated proteins (HRAP) useful for the diagnosis,  
 PT treatment and prevention of cell proliferative, autoimmune,  
 PT inflammatory, reproductive, cardiovascular, and gastrointestinal  
 PT disorders -

XX Claim 1; Page 78-79; 99pp; English.

XX The present sequence is a human receptor-associated protein  
 CC (HRAP) from Incyte clone 3472455 obtained from LUNG0727 cDNA library.  
 CC This sequence is expressed in musculoskeletal, cardiovascular  
 CC and urologic tissues. HRAP has cytosolic, immunomodulatory,  
 CC antiinflammatory, cardiac, antiarteriosclerotic, hepatotropic,  
 CC antirheumatic, antirheumatic, osteopathic, antiallergic, antianemic,  
 CC antiasthmatic, antidiabetic, dermatological and neuroprotective  
 CC activities. The present sequence is useful in the diagnosis, treatment  
 CC and prevention of disorders associated with HRAP expression, especially  
 CC cell proliferative, autoimmune/inflammatory, reproductive,  
 CC cardiovascular and gastrointestinal disorders (e.g. atherosclerosis,  
 CC cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia,  
 CC asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and  
 CC irritable bowel syndrome).

XX Sequence 386 AA;

Query Match 6.0%; Score 14; DB 21; Length 386;

Best Local Similarity 100.0%; Pred. No. 4.5e-06; Mismatches 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGACNPGCTEGVDYPT 50

Db 93 tgaenpctegvdyt 106

|||||

RESULT 26  
 AAU12341  
 ID AAU12341 standard; Protein: 386 AA.

XX AAU12341;

XX 24-OCT-2001 (first entry)

XX Human PRO288 polypeptide sequence.

KW Human secretory and transmembrane; PRO: mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX MO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000MO-US32678.

XX 01-DEC-1999; 99MO-US28301.

XX 01-DEC-1999; 99MO-US28634.

XX 02-DEC-1999; 99MO-US28551.

XX 02-DEC-1999; 99MO-US28564.

XX 02-DEC-1999; 99MO-US28565.

XX 09-DEC-1999; 99US-0170262.

XX 16-DEC-1999; 99MO-US30095.

XX 20-DEC-1999; 99MO-US30911.

XX 30-DEC-1999; 99MO-US31243.

XX 06-JAN-2000; 2000MO-US00276.

XX 11-FEB-2000; 2000MO-US03565.

XX 18-FEB-2000; 2000MO-US04341.

XX 18-FEB-2000; 2000MO-US04342.

XX 22-FEB-2000; 2000MO-US04414.



PI	Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI	Paoi NF, Roy MA, Stewart TR, Tunas D, Watanabe CK, Williams PM;
PI	Wood WI, Zhang Z;
XX	WPI: 2001-050091/06.
DR	N-PSDB; AAC86979.
XX	
PT	Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT	transmembrane polypeptide is useful for gene therapy and identification
PT	of related polypeptides -
XX	
PS	Claim 12; Fig 18; 244p; English.
XX	
CC	The present sequence represents a human secreted and transmembrane
CC	polypeptide. The specification describes human polypeptides, designated
CC	PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC	PRO365, PRO1361, PRO1308, PRO1183, PRO172, PRO1419, PRO499, PRO7170,
CC	PRO248, PRO353, PRO1318, PRO1600, PRO9540, PRO533, PRO301, PRO187,
CC	PRO337, PRO1411, PRO2356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC	PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC	can be modulated with agents that bind to these polypeptides, resulting
CC	in the death of the cells. The polynucleotides encoding these
CC	polypeptides are useful in the recombinant production of the
CC	polypeptides, as a hybridisation probe to screen libraries to isolate
CC	homologous sequences, or to map the gene. They may also be used for
CC	analysing genetic disorders, and to produce transgenic animals which are
CC	useful for the development and screening of therapeutically useful
CC	reagents. The polynucleotides can also be used in gene therapy e.g. to
CC	replace a defective gene.
XX	
SQ	Sequence 386 AA;
XX	
Query Match	6.0%; Score 14; DB 22; Length 386;
Best Local Similarity	100.0%; Pred. No. 4,5e-06;
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
YY	
QY	37 TGACNPTCTEGVDYT 50
DB	93 tgacnptctegvydt 106
XX	
RESULT 28	
AAB50892	
ID	AAB50892 standard; Protein: 386 AA.
XX	
AC	AAB50892;
XX	
DT	19-MAR-2001 (first entry)
XX	
DE	Human TR10 receptor.
XX	
KW	Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective;
KW	antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiact;
KW	vasotrophic; antiallergic; antidiabetic; vulnerary; ophthalmologically;
KW	antiviral; antibacterial; antifungal; antiparasitic; gene therapy;
KW	tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder;
KW	apoptosis; cardiovascular disorder; inflammatory disease; wound;
KW	infection; neurological disease; protein coordinate data.
XX	
OS	Homo sapiens.
XX	
PN	WO200073321-A1.
XX	
PD	07-DEC-2000.
XX	
PE	26-MAY-2000; 2000WO-US14554.
XX	
PR	28-MAY-1999; 99US-0136786.
XX	
PR	07-JUL-1999; 99US-0142563.
XX	
PR	15-JUL-1999; 99US-0144023.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.

Pt	Rosen CA; Ni J;
Xx	
Xx	WPI: 2001-025250/03.
Dd	N-Psdb; AAC91408.
Xx	
Pt	Nucleic acid encoding a tumor necrosis factor receptor 10, useful in
Pt	the diagnosis, treatment or prevention of cancer, autoimmune disorders,
Pt	and diseases and disorders associated with apoptosis -
Xx	
Xx	Claim 20; Fig 1; 212pp; English.
Ps	
Cc	The present sequence is given in a specification relating to an isolated
Cc	nucleic acid encoding a human tumour necrosis factor receptor TR10.
Cc	The TR10 polynucleotide, polypeptide, antiodies, agonists and
Cc	antagonists are useful in the diagnosis, treatment or prevention of
Cc	cancer, such as breast and ovarian cancer and leukaemia; autoimmune
Cc	disorders such as multiple sclerosis, Crohn's disease and graft versus
Cc	host disease; diseases associated with increased apoptosis such as AIDS,
Cc	Alzheimer's disease and Parkinson's disease; cardiovascular disorders
Cc	such as limb ischaemia and congenital heart defects; inflammatory
Cc	diseases e.g. allergy; wound healing; disorders associated with
Cc	neovascularisation, e.g. diabetic retinopathy; infectious diseases such
Cc	as viral, bacterial, fungal and parasitic infections; and neurological
Cc	diseases such as amyotrophic lateral sclerosis.
Sq	
Sq	Sequence      386 AA;
Oy	
Oy	Query Match                 6.0%; Score 14; DB 22; Length 386; Best Local Similarity     100.0%; Pred. No. 4.3e-06; Matches    14; Conservative   0; Mismatches   0; Indels    0; Gaps    0;
Db	37 TGACNPGTEGVDTT 50       93 tgaacnpgtegvdytt 106
Result_29	
AAB68231	
ID	AAB68231 standard; Protein; 109 AA.
Xx	
Ac	AAB68231;
Xx	
Dt	26-MAR-2002 (first entry)
Xx	
Dd	Drosophila melanogaster polypeptide SEQ ID NO 31485.
Xx	
Kw	Drosophilaa: developmental biology; cell signalling; insecticide;
Kw	pharmaceutical.
Xx	
Os	Drosophila melanogaster.
Xx	
Pn	WO200171042-A2.
Xx	
Pd	27-SEP-2001.
Xx	
Pf	23-MAR-2001; 2001WO-US09231.
Xx	
Pr	23-MAR-2000; 2000US-191637P.
Pk	11-JUL-2000; 2000US-061415O.
Xx	
Pa	(PEKE ) PE CORP NY.
Xx	
Pt	Venter JC, Adams M, Li PWD, Myers EW;
Xx	
Dr	WPI: 2001-656860/75.
DR	N-PSDB; ABL12334.
Xx	
Pt	New isolated nucleic acid detection reagent for detecting 1000 or more
Pt	genes from Drosophila and for elucidating cell signalling and cell-cell
Pt	-interactions -
Xx	

PS Disclosure; SEQ ID NO 31485; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
CC useful in developmental biology and in elucidating cell signaling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
CC sequences (AB101840-AB16175) and the encoded proteins  
CC (AB57737-AB572072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
CC  
XX  
SQ Sequence 109 AA;  
  
Query Match 3.4%; Score 8; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 220 VGIIVLIIV 227  
|||||  
Db 27 VGIIVLIIV 34  
  
RESULT 30  
AAB93909  
ID AAB93909 standard; Protein; 217 AA.  
XX  
AC AAB93909;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human protein sequence SEQ ID NO:13873.  
XX  
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000EP-0116126.  
XX  
PR 29-JUL-1999; 99JP-0248036.  
PR 27-AUG-1999; 99JP-0300253.  
PR 11-JAN-2000; 2000JP-0118776.  
PR 02-MAY-2000; 2000JP-0183767.  
PR 09-JUN-2000; 2000JP-0241899.  
XX  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX  
XX WPI; 2001-318749/34.  
XX  
PT Primer sets for synthesizing polynucleotides, particularly the 5602  
PT full-length cDNAs defined in the specification, and for the detection  
PT and/or diagnosis of the abnormality of the proteins encoded by the  
PT full-length cDNAs -  
XX  
XX  
PS Claim 8; SEQ ID 13873; 2537pp + CD ROM; English.  
XX  
CC The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AA003166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
CC AAB95993 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.  
CC  
XX  
SQ Sequence 217 AA;  
  
Query Match 3.4%; Score 8; DB 22; Length 217;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 141 TMNTSPGT 148  
|||||  
Db 19 tmtspgt 26  
  
RESULT 31  
AAM41810  
ID AAM41810 standard; Protein; 272 AA.  
XX  
AC AAM41810;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 6741.  
XX  
KM Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KM peripheral nervous system; neuropathy; central nervous system; CNS;  
KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;  
KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KM leukaemia.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000MO-US34263.  
XX  
PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI; 2001-442253/47.  
XX  
DR N-PSDB; AAI60966.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -

XX	Example 2; SEQ ID NO 6741; 10078pp; English.
PS	
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilisation of the activities such as: Immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
CC	
XX	
SQ	Sequence 272 AA;
OY	Query Match 3.4%; Score 8; DB 22; Length 272; Best Local Similarity 100.0%; Pred. No. 5.5; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DG	141 TMNTPSGT 148         15 tmntspgt 22
RESULT 32	
ID	AAM41811
AA	AAM41811 standard; Protein: 272 AA.
AC	AAM41811;
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 6742.
XX	
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokineic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
KW	
OS	Homo sapiens.
XX	
PN	WO200153312-A1.
XX	
PD	26-JUL-2001.
PF	26-DEC-2000; 2000WO-US34263.
XX	
PR	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	
PA	(HYSEQ-) HYSEQ INC.
PI	Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J; Zhao Q, Zhou P, Goodrich R, Drmanac RT;
DR	WPt: 2001-442253/47.

DR	N-PSDB: AAI60967.
XX	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
PS	Example 2: SEQ ID NO 6742; 10078bp; English.
XX	
CC	The invention relates to human nucleic acids (AA15798-AA161369) and
CC	the encoded polypeptides (AAW38642-AAW42213) with nootropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilisation of the activities such as: immune system suppression,
CC	Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
CC	
XX	
SO	Sequence 272 AA;
	Query Match 3.4%; Score 8; DB 22; Length 272;
	Best Local Similarity 100.0%; Pred. No. 5.5;
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	141 TWNTSPGT 148
DB	15 tmtspgt 22
RESULT 33	
AAW76828	
XX	AAW76828 standard; Protein; 303 AA.
XX	
AC	AAW76828;
XX	
DT	25-JAN-1999 (first entry)
XX	
DE	Human TR6 partial protein.
XX	
KM	TR6; tumour necrosis factor related receptor; human; treatment; stroke;
XX	inflammation; arthritis; septicemia; autoimmune disease; restenosis;
KM	transplant rejection; infection; ischaemia; brain injury; bone disease;
KM	acute respiratory disease syndrome; acquired autoimmune disease syndrome;
KM	AIDS; cancer; atherosclerosis; Alzheimers disease.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Protein
XX	
XX	Location/Qualifiers
FT	1..303
XX	/note= "Partial sequence. Start codon missing"
PN	EP870827-A2.
XX	
PD	14-OCT-1998.
XX	
PF	23-DEC-1997; 97EP-0310562.
XX	
PR	22-AUG-1997; 97US-0916625.
PR	14-MAR-1997; 97US-0041230.
PR	09-MAY-1997; 97US-0853684.
XX	
PA	(SMK ) SMTKLINE BEECHAM CORP.
XX	
PI	Deen KC, Young PR;
DR	WPI, 1998-523156/45.

DR N-PSDB; AAV63095.  
XX  
PT DNA encoding tumour necrosis factor receptor TR6 - and corresponding  
PT polypeptide, antibody, agonist, antagonist, etc  
XX  
PS Disclosure; Page 30-31; 34pp; English.  
XX  
CC This sequence represents a novel human tumour necrosis factor related  
CC receptor, TR6. TR6 polypeptides and polynucleotides can be used in the  
CC treatment of chronic and acute inflammation, arthritis, septicemia,  
CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),  
CC transplant rejection, graft vs. host disease, infection, stroke,  
CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,  
CC (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g.  
CC lympho-proliferative disorders), atherosclerosis and Alzheimers disease.  
XX  
SQ Sequence 303 AA;  
  
Query Match 3.4%; Score 8; DB 19; Length 303;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 95 SPEMCRKC 102  
DB 41 spemcrkc 48  
|||||||  
  
RESULT 34  
AAB48349  
ID AAB48349 standard; Protein: 303 AA.  
AC AAB48349;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Partial amino acid sequence of human TR6.  
XX  
KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human;  
KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;  
KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;  
KW nootropic; neuroprotective; antiarthritic; antirheumatic; antischismic;  
KW gene therapy; vaccine; TNF-alpha; bone disease; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200077191-A1.  
XX  
PD 21-DEC-2000.  
XX  
PF 12-JUN-2000; 2000WO-US16134.  
XX  
PR 15-JUN-1999; 99US-033593.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;  
XX WPI: 2001-112223/12.  
DR N-PSDB; AAC84744.  
XX  
XX New tumor necrosis factor related receptor TR6 polynucleotides and  
PT polypeptides useful for e.g. for treating chronic and acute  
PT inflammation, arthritis, septicemia, autoimmune diseases, infection,  
PT cancer, bone diseases -  
XX  
XX Disclosure; Page 16-17; 47pp; English.  
XX  
CC The invention relates to a human tumour necrosis factor (TNF) related  
CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.  
CC The TR6 polypeptides are useful for treating chronic and acute  
CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases  
CC (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft

CC vs. host disease, infection, stroke, ischaemia, acute respiratory disease,  
CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,  
CC atherosclerosis, and Alzheimer's disease. These may also be used to  
CC inhibit production of TNF-alpha and eicosanoids, as research reagents and  
CC materials for discovering treatments and diagnostics to animal and human  
CC diseases. The polypeptides may further be used as immunogens to produce  
CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides  
CC may also be used as hybridization probes for cDNA and genomic DNA, for  
CC isolating full-length cDNAs and genomic clones encoding TR6 and of other  
CC genes having high sequence similarity to TR6 gene, and for chromosome  
CC identification. The present sequence represents a partial amino acid  
CC sequence of human TR6.  
XX  
SQ Sequence 303 AA;  
  
Query Match 3.4%; Score 8; DB 22; Length 303;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 95 SPEMCRKC 102  
DB 41 spemcrkc 48  
|||||||  
  
RESULT 35  
AAV00934  
ID AAV00934 standard; Protein: 350 AA.  
AC AAV00934;  
XX  
DT 02-JUN-1999 (first entry)  
XX  
DE Human DR5s protein sequence.  
XX  
KW Human; DR5; TRAIL-R3; apoptosis related condition; cancer; therapy;  
KW autoimmune disease; viral infection; degenerative disorder;  
KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischaemic injury;  
KW cerebellar degeneration; myelodysplastic syndrome; splice variant.  
XX  
OS Homo sapiens.  
XX  
PN WO9909165-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 14-AUG-1998; 98WO-US16945.  
XX  
PR 15-AUG-1997; 97US-0055906.  
XX  
PA (IDUN-) IDUN PHARM INC.  
XX  
PI Alnemrl ES;  
XX WPI: 1999-181035/15.  
DR N-PSDB; AAX27281.  
XX  
XX Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
PT protein - useful in for screening for (ant)agonists that modulate  
PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
XX  
XX Claim 16; Fig 5; 71pp; English.  
XX  
XX This sequence is the human TRAIL receptor DR5s of the invention. An  
CC antibody against the TRAIL receptor is useful for detecting mammalian  
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
CC (Ant)agonists identified by the assay are useful for modulating the  
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
CC related conditions which are treated in this way, include cancer  
CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
CC erythematosus and immune-mediated glomerulonephritis), viral infections  
CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders

CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial  
CC infarction and stroke). The polynucleotides can also be used to treat  
CC these diseases. Antisense oligonucleotides can be used to inhibit  
CC the expression of a human DR5 or TRAIL-R3 protein.

XX  
SQ Sequence 350 AA;

Query Match 3.4%; Score 8; DB 20; Length 350;  
Best Local Similarity 100.0%; Pred. No. 6.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRKC 102  
Db 149 SPEMCRKC 156

RESULT 36

ID AAW79261 standard; Protein; 411 AA.

XX AAW79261;

DT 15-FEB-1999 (first entry)

DE Tumour necrosis factor receptor related protein Tango-63e.

XX Tango-63e; tumour necrosis factor receptor related protein; human;  
KM apoptosis; cancer; autoimmune disease; neurodegenerative disease.

XX Homo sapiens.

XX W09846643-A1.

XX 22-OCT-1998.

XX 16-APR-1998; 98WO-US07694.

XX 16-APR-1997; 97US-0843652.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Holtzman D;

XX WPI; 1998-594562/50.

XX N-PSDB; AAV62673.

PT Isolated tumour necrosis factor related proteins - used to develop  
PT products for the diagnosis and treatment of apoptosis-related  
PT disorders, e.g. cancers, autoimmune disorders or neurodegenerative  
PT disorders

XX Claim 6; Fig 2; 88pp; English.

XX This is the amino acid sequence of Tango-63e, a new member of the  
CC human tumour necrosis factor receptor superfamily. It was deduced  
CC from a human prostate cDNA clone sequence (see AAV62673). Two  
CC different forms of Tango-63, i.e. Tango-63e and Tango-63d (see  
CC AAW79260), have been identified. These are identical with the  
CC exception of the deletion of amino acids 183-211 of Tango-63d in  
CC Tango-63e. The invention also encompasses nucleic acid molecules  
CC encoding Tango-63d and -63e, vectors containing these nucleic acid  
CC molecules, cells harboring recombinant DNA encoding Tango-63d and/or  
CC -63e, fusion proteins that include Tango-63d and/or -63e, transgenic  
CC animals that express Tango-63d and/or -63e, and recombinant knockout  
CC animals that fail to express Tango-63d and/or -63e. Methods are  
CC provided for the diagnosis and treatment of disorders associated  
CC with either an abnormally high or an abnormally low rate of  
CC apoptotic cell death. Inhibitors can be used for treating e.g.  
CC cancers, autoimmune disorders (e.g. systemic lupus erythematosus

CC and immune-mediated glomerulonephritis), and viral infections (e.g.  
CC herpesviruses, poxviruses, and adenoviruses). Agonists can be used  
CC for treating e.g. neurodegenerative diseases, e.g. Alzheimer's  
CC disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS),  
CC Huntington's disease, retinitis pigmentosa, spinal muscular atrophy,  
CC various forms of cerebellar degeneration, anaemia, myelodysplastic  
CC syndrome, ischaemic injury, myocardial infarction, cerebral ischaemia  
CC or toxin-induced injury. In addition, T cell mediated diseases,  
CC including AIDS, autoimmune diseases such as rheumatoid arthritis,  
CC and type I diabetes, septic shock, cerebral malaria, graft  
CC rejection, cytotoxicity, cachexia, and inflammation can be treated  
CC by altering the expression or activity of the polypeptides. The  
CC products can also be used for detection, diagnosis and screening  
CC assays.

XX  
SQ Sequence 411 AA;

Query Match 3.4%; Score 8; DB 19; Length 411;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRKC 102  
Db 149 SPEMCRKC 156

RESULT 37

ID AAW76827 standard; Protein; 411 AA.

XX AAW76827;

DT 25-JAN-1999 (first entry)

XX Human TR6 protein.

XX TR6; tumour necrosis factor related receptor; human; treatment; stroke;  
KM inflammation; arthritis; septicemia; autoimmune disease; restenosis;  
KM transplant rejection; infection; ischaemia; brain injury; bone disease;  
KM acute respiratory disease syndrome; acquired autoimmune disease syndrome;  
KM AIDS; cancer; atherosclerosis; Alzheimer's disease.

XX Homo sapiens.

XX EP870827-A2.

XX 14-OCT-1998.

XX 23-DEC-1997; 97EP-0310562.

XX 22-AUG-1997; 97US-0916625.

XX 14-MAR-1997; 97US-0041230.

XX 09-MAY-1997; 97US-0853684.

XX (SMK ) SMITHKLINE BEECHAM CORP.

XX Deen KC, Young PR;

XX WPI; 1998-523156/45.

XX N-PSDB; AAV63094.

PT DNA encoding tumour necrosis factor receptor TR6 - and corresponding  
PT polypeptide, antibody, agonist, antagonist, etc

XX Claim 1; Page 27-29; 34pp; English.

XX This sequence represents a novel human tumour necrosis factor related  
CC receptor. TR6 polypeptides and polynucleotides can be used in the  
CC treatment of chronic and acute inflammation, arthritis, septicemia,  
CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),  
CC transplant rejection, graft vs. host disease, infection, stroke,  
CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,

CC (acquired autoimmune disease syndrome) AIDS; bone diseases; cancer (e.g.  
 CC lympho-proliferative disorders), atherosclerosis and Alzheimer's disease.  
 XX  
 SO Sequence 411 AA;

Query Match 3.4%; Score 8; DB 19; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRKC 102  
 |||||  
 Db 149 spemcrkc 156

RESULT 38  
 AAM79083  
 ID AAM79083 standard; Protein: 411 AA.  
 XX  
 AC AAM79083;

DT 11-JAN-1999 (first entry)  
 XX

DE Human death domain containing receptor 5 (DR5).

XX  
 KW Death domain containing receptor 5; DR5; human; apoptosis;  
 KW tumour necrosis factor receptor; cancer; autoimmune disease;  
 KW inflammation; infection; AIDS; graft versus host disease;  
 KW neurodegeneration; systemic lupus erythematosus;  
 KW glomerulonephritis; rheumatoid arthritis; graft rejection;  
 KW osteoarthritis; psoriasis; septicemia; inflammatory bowel disease;  
 KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;  
 KW amyotrophic lateral sclerosis; aplastic anaemia; ischaemia;  
 KW septic shock; cachexia; anorexia; agonist; antagonist; therapy;  
 KW diagnosis.  
 XX

OS Homo sapiens.  
 XX

PH Key Location/Qualifiers  
 FT Peptide 1..51

FT /label= Sig-peptide  
 FT Protein 52..411

FT /label= Mat-protein  
 FT Domain 52..184

FT /label= Extracellular  
 FT Domain 185..208

FT /label= Transmembrane  
 FT Domain 209..411

FT /label= Intracellular  
 FT Domain 324..391

FT /label= Death  
 FT

XX WO9841629-A2.  
 XX

PD 24-SEP-1998.  
 XX

PE 17-MAR-1998; 98WO-US05377.  
 XX

PR 29-JUL-1997; 97US-0054021.  
 PR 17-MAR-1997; 97US-0040846.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX

XX Gentz RL, NI J, Rosen CA, Su JY, Yu G;  
 PI  
 XX WPI: 1998-531568/45.  
 DR N-PSDB; AAV61469.  
 XX

XX New isolated death domain containing receptor 5 - used to develop  
 PT products for treating e.g. cancers, autoimmune disorders, viral  
 PT infections, inflammation, graft-versus-host disease or  
 PT neurodegenerative disorders  
 XX

PS Claim 4; Fig 1A-B; 89pp; English.  
 XX

CC This is the amino acid sequence of human death domain containing  
 CC receptor 5 (DR5), deduced from an isolated DR5 nucleic acid (see  
 CC AAV61469). DR5 is a novel member of the tumour necrosis factor  
 CC receptor (TNFR) family that has been shown to bind TRAIL, and which  
 CC has the ability to induce apoptosis. It shows homology to human  
 CC TNFR1, FAS and DR3. DR5 cDNA has been identified in primary  
 CC dendritic cells, endothelial tissue, spleen, chronic lymphocytic  
 CC leukaemia, and human thymus stromal cells. The isolated nucleic  
 CC acid can be used in the recombinant production of DR5 polypeptides,  
 CC e.g. the extracellular, transmembrane, intracellular domains,  
 CC mature protein or soluble polypeptides lacking the transmembrane  
 CC domain; vectors, host cells and recombinant methods of producing  
 CC the polypeptides are claimed. DR5 polypeptides can be used to  
 CC identify agonists and antagonists, and to raise antibodies.  
 CC Agonists, which increase DR5 mediated signalling, can be used to  
 CC treat diseases in which decreased apoptosis is exhibited, e.g.  
 CC cancers, autoimmune disorders (such as systemic lupus erythematosus  
 CC and immune-related glomerulonephritis rheumatoid arthritis) and  
 CC viral infections (such as herpes viruses, pox viruses and  
 CC adenoviruses). Inflammation, graft versus host disease and  
 CC rejection, chronic graft rejection, rheumatoid arthritis, acute graft  
 CC rejection, osteoarthritis, psoriasis, septicemia, and inflammatory bowel  
 CC disease. Antagonists, which decrease DR5 mediated signalling, can  
 CC be used to treat diseases in which apoptosis is exhibited, e.g.  
 CC AIDS, neurodegenerative disorders (such as Alzheimer's disease,  
 CC Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
 CC pigmentosa, cerebellar degeneration), myelodysplastic syndromes  
 CC (such as aplastic anaemia), ischemic injury (such as that caused by  
 CC myocardial infarction, stroke and reperfusion injury), toxin-induced  
 CC liver disease (such as that caused by alcohol), septic shock,  
 CC cachexia and anorexia. The products can also be used for detection,  
 CC diagnosis and drug screening.  
 XX

SO Sequence 411 AA;

Query Match 3.4%; Score 8; DB 19; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRKC 102  
 |||||  
 Db 149 spemcrkc 156

RESULT 39  
 AAM93608

ID AAM93608 standard; Protein: 411 AA.  
 XX  
 AC AAM93608;

XX  
 DT 18-JUN-1999 (first entry)  
 XX

DE Human killer adriamycin-inducible protein.  
 XX

XX Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis;  
 KW p53-inducible; apoptosis-mediating activity; treatment; animal model;  
 KW neoplastic disease.  
 KW  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 PN WO9902653-A1.  
 PD 21-JAN-1999.  
 XX  
 PF 10-JUL-1998; 98WO-US14495.  
 XX  
 PR 11-MAR-1998; 98US-0077661.  
 PR 11-JUL-1997; 97US-0052305.  
 PR 04-AUG-1997; 97US-0054710.  
 PR 30-SEP-1997; 97US-0060473.





PS Claim 16; Page 58-60; 71pp; English.  
XX  
CC This sequence is the human TRAIL receptor DR5 of the invention. An  
CC antibody against the TRAIL receptors is useful for detecting mammalian  
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
CC (ant)agonists identified by the assay are useful for modulating the  
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
CC related conditions which are treated in this way, include cancer  
CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
CC erythematosus and immune-mediated glomerulonephritis), viral infections  
CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
CC syndromes (e.g. aplastic anaemia) and ischemic injury (e.g. myocardial  
CC infarction and stroke). The polynucleotides can also be used to treat  
CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
CC used to form a composition that is useful for inhibiting expression of a  
CC human DR5 or TRAIL-R3 protein.  
XX  
SQ Sequence 411 AA;  
  
OY 95 SPEMCRKC 102  
| | | | | | | |  
Db 149 spemcrkc 156  
  
RESULT 42  
AAW88410  
ID AAW88410 standard; Protein: 411 AA.  
XX  
AC AAW88410;  
XX  
DT 26-APR-1999 (first entry)  
XX  
DE Human Apo-2 ligand.  
XX  
KW Apo-2 ligand; Apo-2DCR; human; tumour necrosis factor receptor;  
KW neurodegeneration; autoimmune disease; inflammation; cancer;  
KW apoptosis; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..53  
FT /note= "signal peptide"  
FT Protein 54..411  
FT /note= "mature protein"  
FT Domain 54..182  
FT /note= "extracellular domain"  
FT Domain 183..208  
FT /note= "transmembrane domain"  
FT Domain 209..411  
FT /note= "intracellular domain"  
FT Region 96..137  
FT /note= "cysteine-rich region"  
FT Region 138..179  
FT /note= "cysteine-rich region"  
FT Domain 324..391  
FT /note= "death domain"  
FT Misc-difference 410  
FT /label= Met, Leu  
FT /note= "encoded by WTG"  
XX  
PN WO9858062-A1.  
XX  
PD 23-DEC-1998.  
XX

PF 12-JUN-1998; 98WO-US12456.  
XX  
PR 18-JUN-1997; 97US-0878168.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;  
PI Kim KJ, Wood WI;  
XX  
XX WPI: 1999-095340/08.  
DR N-PSDB; AAW84352.  
DR  
XX  
PT New Apo-2DCR polypeptide - used for modulation and diagnosis of  
PT apoptosis, e.g. in neurodegeneration  
XX  
PS Example 5; Page 61-62; 88pp; English.  
XX  
CC This polypeptide comprises human Apo-2 ligand. The amino acid  
CC sequence was deduced from a nucleotide sequence (see AAW84352)  
CC produced from overlapping cDNA clones obtained from human kidney  
CC and pancreatic cDNA libraries. The invention relates to Apo-2DCR  
CC (see AAW88408), a novel member of the tumour necrosis factor receptor  
CC family that binds to Apo-2 ligand and is involved in apoptosis;  
CC Apo-2DCR polypeptides are used to modulate apoptosis of mammalian  
CC cells (claimed) e.g. in the treatment of neurodegeneration,  
CC autoimmune diseases and inflammation. The Apo-2DCR polypeptides  
CC are optionally used in conjunction with Apo-2 ligand, the  
CC bioavailability of which is increased by antibody-mediated blockade  
CC of Apo-2DCR.  
XX  
SQ Sequence 411 AA;  
  
OY 95 SPEMCRKC 102  
| | | | | | | |  
Db 149 spemcrkc 156  
  
RESULT 43  
AAW83321  
ID AAW83321 standard; Protein: 411 AA.  
XX  
AC AAW83321;  
XX  
DT 16-MAR-1999 (first entry)  
XX  
DE Human Apo-2 protein.  
XX  
KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
KW TNF cytokine.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 410  
FT /label= unknown  
FT /note= "encoded by WTG"  
XX  
PN WO9851793-A1.  
XX  
PD 19-NOV-1998.  
XX  
PF 14-MAY-1998; 98WO-US09704.  
XX  
PR 09-FEB-1998; 98US-0020746.  
PR 15-MAY-1997; 97US-0857216.  
XX  
PA (GETH ) GENENTECH INC.

XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim RJ;  
 XX WPI: 1999-045228/04.  
 DR N-PSDB; AAV72526.  
 XX  
 PT Human Apo-2 polypeptide inducing apoptosis - useful to treat  
 PT conditions linked with decreased apoptosis e.g. cancer, and produce  
 PT antibodies to increase or decrease apoptosis  
 PS Claim 1; Fig 1; 134pp; English.  
 XX  
 CC The present sequence represents human Apo-2. Apo-2 can be used  
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer.  
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
 CC can be used to identify agents activating Apo-2, useful to treat  
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
 CC therapeutically (e.g. those containing immunoglobulin sequences can be  
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
 CC antibodies). It can be used to produce antibodies which can be combined  
 CC with a (particularly pharmaceutically acceptable) carrier in compositions  
 CC or used to produce dimeric molecules (especially homodimeric molecules  
 CC comprising first and second Apo-2 antibodies). Agonistic (especially  
 CC single-chain) antibodies can be administered to induce apoptosis in  
 CC mammalian cancer cells, and antagonistic antibodies used to block  
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
 CC antibodies may also be used diagnostically e.g. to detect Apo-2  
 CC expression in cells/tissues and in Apo-2 purification.  
 XX  
 SQ Sequence 411 AA;  
 QY 95 SPEMCRKC 102  
 Db 149 spemcrkc 156  
 RESULT 44  
 AAB29790  
 ID AAB29790 standard; Protein: 411 AA.  
 AC AAB29790;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Human death domain containing receptor-5 (DR5).  
 XX  
 XX Human death domain containing receptor-5; DR5; anti-DR5 antibody;  
 KW TRAIL binding; TNF-related apoptosis-inducing ligand; pro-apoptotic;  
 KW tumour necrosis factor receptor family; TNFR; graft-versus-host disease;  
 KW viral infection; cancer; leukaemia; immunodeficiency; autoimmune disease;  
 KW T-cell mediated immune response; osteoarthritis; psoriasis; septicaemia;  
 KW inflammatory bowel disease; parasitic infection; bacterial infection;  
 KW restenosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20006156-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 04-MAY-2000; 2000WO-US12041.  
 XX  
 PR 04-MAY-1999; 99US-0132498.  
 PR 07-MAY-1999; 99US-0133238.

PR 13-AUG-1999; 99US-0148939.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ni J, Gentz RL, Yu G, Rosen CA;  
 XX  
 DR WPI: 2000-687447/67.  
 DR N-PSDB; AAC81544.  
 XX  
 PT Treating graft-versus-host disease, viral infection, cancer, leukemia,  
 PT immunodeficiency, or an autoimmune disorder comprising administering an  
 PT antibody to death domain containing receptor (DR5) and a second agent -  
 XX  
 PS Claim 1; Fig 1A-B; 266pp; English.  
 XX  
 CC The invention relates to a novel method for treating graft-versus-host  
 CC disease, viral infection, cancer, leukemia, immunodeficiency, or an  
 CC autoimmune disorder. The method comprises administering an antibody  
 CC specific for human death domain containing receptor-5 (DR5); AAB29790  
 CC and a second agent selected from TRAIL (TNF-related apoptosis-inducing  
 CC ligand), a tumour necrosis factor (TNF), a TNF blocking agent, an  
 CC immunosuppressive agent, an antibiotic, an antiinflammatory agent, a  
 CC chemotherapeutic agent, or a cytokine. DR5 is a member of the TNF  
 CC receptor (TNFR) family, and is a mediator of apoptosis, being able to  
 CC bind TRAIL. The method of the invention is useful for the treatment of  
 CC graft-versus-host disease, viral infection, cancer, leukemia,  
 CC immunodeficiency, or an autoimmune disorder. The DR-5 antibody is useful  
 CC for treating or preventing diseases and conditions associated with  
 CC increased cell survival and/or insensitivity to apoptosis-inducing  
 CC agents. Examples of such diseases are solid tissue cancers and  
 CC leukemias. Antagonists of DR5 are useful for inhibiting T-cell mediated  
 CC immune responses, and preventing and/or treating diseases and conditions  
 CC associated with T-cell mediated immune responses such as graft-versus-  
 CC host responses, osteoarthritis, psoriasis, septicaemia, inflammatory  
 CC bowel disease, autoimmune diseases and leukaemia. DR5 nucleotides and  
 CC proteins are useful for diagnosis, prevention and/or treatment of  
 CC parasitic, bacterial, and viral infections, restenosis and autoimmune  
 CC disorders. The present sequence represents human DR5.  
 XX  
 SQ Sequence 411 AA;  
 QY 95 SPEMCRKC 102  
 Db 149 spemcrkc 156  
 RESULT 45  
 AAY55805  
 ID AAY55805 standard; Protein: 411 AA.  
 AC AAY55805;  
 XX  
 DT 29-FEB-2000 (first entry)  
 XX  
 DE Human Apo-2 polypeptide.  
 XX  
 XX Apo-2 polypeptide; immunization; antigen; polyclonal antibody; cancer;  
 KW monoclonal antibody; Apo-2L receptor; therapy; apoptosis; autoimmune;  
 KW immune-mediated cell death; neurodegenerative; inflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 PN Key Location/Qualifiers  
 FH Misc-difference 410  
 FT /label= unknown  
 FT /note= "encoded by WTG"  
 XX  
 PN WO9964461-A2.

XX 16-DEC-1999.  
PD  
XX  
XX 10-JUN-1999; 99WO-US13197.  
XX  
XX 12-JUN-1998; 98US-0096637.  
PR  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Chuntharapal A, Kim KJ;  
PI  
XX WPI: 2000-097520/08.  
DR N-PSDB: AA233630.  
XX  
XX Preparation of antibodies using 2 or more different antigens, used for  
PT producing antibodies against Apo-2 ligand receptors useful for inducing  
PT apoptosis, particularly in cancer cells -  
XX  
XX  
PS Disclosure: Fig 5; 57pp: English.  
XX  
XX The invention provides a method for producing antibodies (Abs) by  
CC immunizing an animal with at least two different antigens. The method  
CC comprises: (a) immunizing an animal with at least two different antigens,  
CC to generate polyclonal Abs against each antigen in the animal; (b)  
CC preparing monoclonal Abs (MAbs) using immune cells of the above animal;  
CC and(c) screening the MAbs to identify one or more MAbs which bind to each  
CC antigen. The Abs obtained are Apo-2L receptor (ant)agonists and can be  
CC used for therapy. The Apo-2L receptor Abs can be used for enhancing  
CC immune-mediated cell death in cells expressing Apo-2L receptors.  
CC Agonistic Abs which specifically cross-react with 2 or more different  
CC Apo-2L receptors can be used for inducing apoptosis in mammalian cancer  
CC cells. Antagonistic Abs can be used for blocking apoptosis, e.g. in  
CC neurodegenerative disease, or to block potential autoimmune/inflammatory  
CC effects of Apo-2 resulting from NF-approx .KB activation. The Abs can also  
CC be used for detection, diagnosis and affinity purification. The method  
CC can reduce the number of animals that need to be immunized and sacrificed  
CC in order to make 2 or more MAbs with differing antigen-binding  
CC specificities. The present sequence represents a human Apo-2 polypeptide.  
XX  
SQ Sequence 411 AA;  
QY 95 SPENCRCRC 102  
Db 149 spencrcrc 156  
RESULT 46  
AAU04038  
ID AAU04038 standard; Protein: 411 AA.  
XX  
AC AAU04038;  
XX  
DT 23-OCT-2001 (first entry)  
XX  
DE Human apoptotic protein, Apo-2.  
XX  
KW Human; Apo-2; Apo-2L receptor; immunogen; monoclonal antibody;  
KW cancer; tumour; apoptosis; lymphoma; blastoma; sarcoma; leukaemia;  
KW 3H3.14.5.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH MISC-difference 410 /label= OTHER  
FT /note= "Other= Leu or Met"  
XX  
PN US6252050-B1.

XX 26-JUN-2001.  
PD  
XX  
XX 10-JUN-1999; 99US-0329633.  
XX  
XX 12-JUN-1998; 98US-0089253.  
PR  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Chuntharapal A, Kim KJ;  
PI  
XX WPI: 2001-424490/45.  
DR N-PSDB: AAS07626.  
XX  
XX Novel human monoclonal antibody for inducing apoptosis in mammalian  
PT cancer cells, specifically cross-reacts with two or more different  
PT Apo-2 ligand receptors -  
XX  
XX  
PS Example 1; Fig 5; 29pp: English.  
XX  
XX The sequence represents human Apo-2, an apoptotic protein used as an  
CC immunogen to make the monoclonal antibodies of the invention. The  
CC invention relates to an isolated antibody which specifically cross-reacts  
CC with two or more different Apo-2 ligand (Apo-2L) receptors. Apoptosis by  
CC monoclonal antibody 3H3.14.5 after crosslinking with anti-mouse Ig was  
CC tested. Human 9D cells in complete RPMI medium were added. Cells were  
CC incubated with the monoclonal antibody in 100 micro on ice for 15  
CC minutes. Cells were then incubated with goat anti-mouse IgG FC complete  
CC RPMI medium overnight at 37 degrees C. After washing once with PBS, cells  
CC were resuspended in PBS containing 0.5% BSA and incubated with FITC-  
CC Annexin and propidium iodide for 15 minutes in the dark. Dead cells were  
CC detected by FACSscan. The 3H3.14.5 antibody was able to inhibit apoptosis  
CC induced by interaction between Apo-2L and Apo-2. This antibody was  
CC further capable of inducing apoptosis of 9D cells in the presence of an  
CC anti-PC antibody to cross-link antibodies. The antibodies are useful for  
CC inducing apoptosis in mammalian cancer cells for treating cancer  
CC including carcinoma, lymphoma, blastoma, sarcoma and leukaemia, and are  
CC useful in diagnostic assays for their antigen, e.g. detecting its  
CC expression in specific cells, tissues or serum and for affinity  
CC purification of antigen from recombinant cell culture or natural sources.  
XX  
SQ Sequence 411 AA;  
QY 95 SPENCRCRC 102  
Db 149 spencrcrc 156  
RESULT 47  
AAB73442  
ID AAB73442 standard; Protein: 411 AA.  
XX  
AC AAB73442;  
XX  
DT 25-JUN-2001 (first entry)  
XX  
DE Human Apo-2 receptor precursor, SEQ ID NO:2.  
XX  
KW Human Apo-2 receptor; caspase-dependent apoptosis induction;  
KW programmed cell death; pro-apoptotic; death domain;  
KW agonistic antibody; nuclear factor kappa B;  
KW NF-kappa-B activation; cancer; tumour; lung cancer;  
KW colon cancer; glioma.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..53

FT	Protein	/note- "Signal peptide"
FT		54..411
FT	Domain	/note- "Mature human Apo-2 receptor"
FT		54..182
FT		/note- "Extracellular domain. This domain is
FT		alternatively residues 1-182, or residues 1-130
FT	Disulfide-bond	81..94
FT	Domain	96..137
FT	Disulfide-bond	/note- "Cysteine-rich pseudorepeat domain #1"
FT	Binding-site	97..113
FT		106
FT	Binding-site	/note- "Binds Apo-2L"
FT		112
FT	Disulfide-bond	/note- "Binds Apo-2L"
FT	Disulfide-bond	116..129
FT	Disulfide-bond	119..137
FT	Domain	138..183
FT		/note- "Cysteine-rich pseudorepeat domain #2"
FT	Disulfide-bond	139..153
FT	Disulfide-bond	156..170
FT	Disulfide-bond	160..178
FT	Domain	183..208
FT		/note- "Transmembrane domain"
FT	Domain	209..411
FT		/note- "Intracellular domain"
FT	Domain	324..391
FT		/note- "Death domain"
FT	Misc-difference	410
FT		/label= Met, Leu
FT		/note- "Encoded by WTC. This residue is Met in kidney
FT		Apo-2, and is Leu in pancreatic Apo-2"
PN	WO200119861-A2.	
PD	22-MAR-2001.	
XX		
XX	14-SEP-2000; 2000WO-US25436.	
XX	15-SEP-1999; 99US-0396710.	
XX		
XX	(GETH ) GENENTECH INC.	
PA	Ashkenazi AJ, Chuntherapai A, Kim KJ;	
PI	WPI: 2001-266005/27.	
XX	N-PSDB; AAF84481.	
DR		
XX		
PT	Inducing apoptosis in mammalian cells for treating cancer, comprises	
PT	exposing mammalian cells or cancer cells expressing Apo-2 receptor, to	
PT	Apo-2 agonist antibody	
XX		
PS	Example 1; Fig 1; 90pp: English.	
XX		
CC	The invention relates to a method for inducing apoptosis in mammalian	
CC	cells which express the Apo-2 receptor protein (AAB3442, AAB3443).	
CC	The method involves exposing the cells to an Apo-2 agonistic antibody,	
CC	which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor	
CC	(also referred to simply as Apo-2) is a member of the tumour	
CC	necrosis factor receptor (TNFR) family, and its natural ligand is the	
CC	Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able	
CC	to trigger caspase-dependent apoptosis, and is also able to activate	
CC	NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an	
CC	approximately 45 kD type I transmembrane protein, and contains a death	
CC	domain in the cytoplasmic region (residues 324-392). It exhibits	
CC	significantly more sequence identity to the apoptosis-linked receptor	
CC	DR4, which also binds Apo-2L, than other apoptosis-associated proteins.	
CC	The Apo-2 receptor agonist monoclonal antibodies used in the method of	
CC	the invention are 3F11.39.7, 3H3.14, 5, 3D5.1.10 and 3H1.18.10. The	
CC	method of the invention is used to induce apoptosis in Apo-2-expressing	
CC	cells, particularly cancer cells. It may therefore be used for treating	
CC	mammalian cancers, especially lung cancer, colon cancer and glioma.	
CC	The present sequence represents human Apo-2 as encoded by cDNA isolated	
CC	in an exemplification of the invention.	

CC	Note: The present sequence differs from the human Apo-2 receptor precursor given in AAB73443 in that residue 410 of this sequence can be Met or Leu, rather than Leu.
CC	
CC	
xx	
SQ	Sequence      411 AA:
OY	95 SPEKCRKC 102 
DB	149 spemcrkc 156
 RESULT 48	
AAB73443	
ID	AAB73443 standard; Protein; 411 AA.
xx	
AC	AAB73443;
xx	
DT	25-JUN-2001 (first entry)
xx	
DE	Human Apo-2 receptor precursor, SEQ ID NO:6.
xx	
KW	Human Apo-2 receptor; caspase-dependent apoptosis induction; programmed cell death; pro-apoptotic; death domain; agonistic antibody; nuclear factor kappa B; NF-kappa-B activation; cancer; tumour; lung cancer; colon cancer; glioma.
KW	
xx	
OS	Homo sapiens.
xx	
RH	Key          Location/Qualifiers
FT	Peptide     1..53
FT	/note= "Signal peptide"
FT	Protein     54..411
FT	/note= "Mature human Apo-2 receptor"
FT	Domain     54..182
FT	/note= "Extracellular domain. This domain is alternatively residues 1-182, or residues 1-130"
FT	Disulfide-bond    81..94
FT	Domain     96..137
FT	/note= "Cysteine-rich pseudorepeat domain #1"
FT	Disulfide-bond    97..113
FT	Binding-site     106
FT	/note= "Binds Apo-2L"
FT	Binding-site     112
FT	/note= "Binds Apo-2L"
FT	Disulfide-bond    116..129
FT	Disulfide-bond    119..137
FT	Domain     138..183
FT	/note= "Cysteine-rich pseudorepeat domain #2"
FT	Disulfide-bond    139..153
FT	Disulfide-bond    156..170
FT	Disulfide-bond    160..178
FT	Domain     183..208
FT	/note= "Transmembrane domain"
FT	Domain     209..411
FT	/note= "Intracellular domain"
FT	Domain     324..391
FT	/note= "Death domain"
FT	Misc-difference   410
FT	/note= "Encoded by wrg"
xx	
PN	WO200119861-AZ.
xx	
PD	22-MAR-2001.
xx	
PF	14-SEP-2000; 2000WO-US25436.
xx	
PR	15-SEP-1999; 99US-0396710.

XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Chuntherapai A, Kim KJ;  
 XX WPI: 2001-266005/27.  
 DR N-PSDB: AAF84481.  
 XX  
 PT Inducing apoptosis in mammalian cells for treating cancer, comprises  
 PT exposing mammalian cells or cancer cells expressing Apo-2 receptor, to  
 PT Apo-2 agonist antibody -  
 XX  
 XX Example 1: Fig 2A; 90pp; English.  
 PS  
 XX The invention relates to a method for inducing apoptosis in mammalian  
 CC cells which express the Apo-2 receptor protein (AAB74442, AAB74443).  
 CC The method involves exposing the cells to an Apo-2 agonistic antibody,  
 CC which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor  
 CC (also referred to simply as Apo-2) is a member of the tumour  
 CC necrosis factor receptor (TNFR) family, and its natural ligand is the  
 CC Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able  
 CC to trigger caspase-dependent apoptosis, and is also able to activate  
 CC NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an  
 CC approximately 45 kD type I transmembrane protein, and contains a death  
 CC domain in the cytoplasmic region (residues 324-392). It exhibits  
 CC significantly more sequence identity to the apoptosis-linked receptor  
 CC DR4, which also binds Apo-2L, than other apoptosis-associated proteins.  
 CC The Apo-2 receptor agonist monoclonal antibodies used in the method of  
 CC the invention are 3F11.39.7, 3H3.14, 5, 3D5.1.10 and 3H1.18.10. The  
 CC method of the invention is used to induce apoptosis in Apo-2-expressing  
 CC cells, particularly cancer cells. It may therefore be used for treating  
 CC mammalian cancers, especially lung cancer, colon cancer and glioma.  
 CC The present sequence represents human Apo-2 as given in figure 2A.  
 CC Note: The present sequence differs from the human Apo-2 receptor  
 CC precursor given in AAB34442 in that residue 410 of this sequence is Leu,  
 CC rather than Met or Leu.  
 CC  
 XX Sequence 411 AA;  
 SQ

Query Match 3.4%; Score 8; DB 22; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 SPENCRCRC 102  
 |||||||  
 Db 149 spencrcrc 156

RESULT 49  
 AAB48348  
 ID AAB48348 standard; Protein: 411 AA.  
 XX  
 AC AAB48348;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Human tumour necrosis factor related receptor TR6.  
 XX  
 KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human;  
 KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;  
 KW antisthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;  
 KW neurotropic; neuroprotective; antiarthritic; antineumatic; antischismic;  
 KW gene therapy; vaccine; TNF-alpha; bone disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 290..324  
 FT /note="death domain"  
 XX  
 PN WO200077191-A1.

PD 21-DEC-2000.  
 XX  
 XX 12-JUN-2000; 2000WO-US16134.  
 XX  
 XX 15-JUN-1999; 99US-0333593.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PT Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;  
 XX WPI: 2001-112223/12.  
 DR N-PSDB: AAC84743.  
 XX  
 PT New tumor necrosis factor related receptor TR6 polynucleotides and  
 PT polypeptides useful for e.g. for treating chronic and acute  
 PT inflammation, arthritis, septicemia, autoimmune diseases, infection,  
 PT cancer, bone diseases -  
 XX  
 XX Claim 10: Page 14-15; 47pp; English.  
 PS  
 XX This represents a human tumour necrosis factor (TNF) related receptor,  
 CC TR6. TR6 can be expressed by standard recombinant methodology. The TR6  
 CC polypeptides are useful for treating chronic and acute inflammation,  
 CC rheumatoid arthritis, septicemia, autoimmune diseases (e.g. inflammatory  
 CC bowel disease, psoriasis), transplant rejection, graft vs. host disease,  
 CC infection, stroke, ischemia, acute respiratory disease syndrome, asthma,  
 CC restenosis, brain injury, AIDS (acquired immunodeficiency syndrome), bone  
 CC diseases, cancer, atherosclerosis, and Alzheimer's disease. These may  
 CC also be used to inhibit production of TNF-alpha and eicosanoids, as  
 CC research reagents and materials for discovering treatments and  
 CC diagnostics to animal and human diseases. The polypeptides may further be  
 CC used as immunogens to produce antibodies immunospecific for the TR6  
 CC polypeptides. The polynucleotides may also be used as hybridization  
 CC probes for cDNA and genomic DNA, for isolating full-length cDNAs and  
 CC genomic clones encoding TR6 and of other genes having high sequence  
 CC similarity to TR6 gene, and for chromosome identification.  
 CC  
 XX Sequence 411 AA;  
 SQ

Query Match 3.4%; Score 8; DB 22; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 SPENCRCRC 102  
 |||||||  
 Db 149 spencrcrc 156

RESULT 50  
 AAB48352  
 ID AAB48352 standard; Protein: 424 AA.  
 XX  
 AC AAB48352;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE TR6-Ig fusion protein sequence.  
 XX  
 KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human;  
 KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;  
 KW antisthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;  
 KW neurotropic; neuroprotective; antiarthritic; antineumatic; antischismic;  
 KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; fusion protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..53  
 FT /note="leader sequence"  
 FT Protein 1..184  
 FT /note="TR6 receptor"  
 FT Cleavage-site 187..190

```

FT      /note="factor Xa protease cleavage site"
FT      Protein
FT      191..424
FT      /note="IgG-gamma1 hinge Fc region"
XX
XX      WO200077191-A1.
XX
XX      21-DEC-2000.
XX
XX      12-JUN-2000; 2000WO-US16134.
XX
XX      15-JUN-1999; 99US-0333593.
XX
XX      (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX      Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
XX      WPI; 2001-112223/12.
XX
XX      New tumor necrosis factor related receptor TR6 polynucleotides and
XX      polypeptides useful for e.g. for treating chronic and acute
XX      inflammation, arthritis, septicemia, autoimmune diseases, infection,
XX      cancer, bone diseases
XX
XX      Claim 28; Page 17; 47pp; English.
XX
XX      The invention relates to a human tumour necrosis factor (TNF) related
XX      receptor, TR6. TR6 can be expressed by standard recombinant methodology.
XX      The TR6 polypeptides are useful for treating chronic and acute
XX      inflammation, rheumatoid arthritis, septicemia, autoimmune diseases
XX      (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft
XX      vs. host disease, infection, stroke, ischaemia, acute respiratory disease
XX      syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
XX      atherosclerosis, and Alzheimer's disease. These may also be used to
XX      inhibit production of TNF-alpha and eicosanoids, as research reagents and
XX      materials for discovering treatments and diagnostics to animal and human
XX      diseases. The polypeptides may further be used as immunogens to produce
XX      antibodies immunospecific for the TR6 polypeptides. The polynucleotides
XX      may also be used as hybridization probes for cDNA and genomic DNA, for
XX      isolating full-length cDNAs and genomic clones encoding TR6 and of other
XX      genes having high sequence similarity to TR6 gene, and for chromosome
XX      identification. The present sequence represents a TR6-Ig fusion protein
XX      sequence where the N-terminal amino acids (1-184) of TR6 is fused to a
XX      factor Xa protease cleavage site and the hinge Fc region of a human
XX      IgG-gamma1 heavy chain.
XX
XX      Sequence 424 AA;
XX
XX      Query Match 3.4%; Score 8; DB 22; Length 424;
XX      Best Local Similarity 100.0%; Pred. No. 8.2;
XX      Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 95 SPEMCRKC 102
XX      |
XX      DB 149 SPEMCRKC 156

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Search completed: August 13, 2002, 08:37:59  
 Job time: 388 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:35:56 ; Search time 19.29 Seconds  
(without alignments)  
1160.644 Million cell updates/sec

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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

word size : 5

Total number of hits satisfying chosen parameters: 8656

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

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Database : PIR_71:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	3.4	464	2	D72058	transcription term
2	8	3.4	464	2	G86566	transcription term
3	8	3.4	491	2	AC1185	B. subtilis ydb p
4	8	3.4	494	2	AB1543	B. subtilis ydb p
5	8	3.4	685	2	G82022	methionine-tRNA l
6	8	3.4	801	2	T29018	hypothetical proteol
7	7	3.0	155	2	S71358	major latex proteol
8	7	3.0	165	2	T21313	hypothetical proteol
9	7	3.0	184	2	H90386	hypothetical proteol
10	7	3.0	199	2	H72242	flagellar V-ring p
11	7	3.0	201	2	D70519	probable lppc prot
12	7	3.0	219	2	E75477	hypothetical proteol
13	7	3.0	255	2	T05958	cold acclimation p
14	7	3.0	256	2	H82517	hypothetical proteol
15	7	3.0	256	2	B82661	hypothetical proteol
16	7	3.0	256	2	B82648	hypothetical proteol
17	7	3.0	262	2	T01505	hypothetical proteol
18	7	3.0	263	2	T15453	hypothetical proteol
19	7	3.0	266	2	T46853	yibq protein limpo
20	7	3.0	268	2	T06802	cold acclimation p
21	7	3.0	283	2	S27708	daunorubicin resist
22	7	3.0	313	2	T45537	moab protein limpo
23	7	3.0	365	2	C81050	cytochrome c oxida
24	7	3.0	365	2	F81826	probable cytochrom
25	7	3.0	366	2	T01169	phosphate transpor
26	7	3.0	374	2	T50265	probable phosphate
27	7	3.0	390	2	A53773	La/SS-B homolog D-
28	7	3.0	390	2	A53781	ribonucleoprotein
29	7	3.0	397	2	H71116	hypothetical proteol

103	6	2.6	104	2	H90197	hypothetical prote
104	6	2.6	105	2	AH1551	hypothetical prote
105	6	2.6	106	2	S67941	Ig heavy chain var
106	6	2.6	107	2	A87676	SUGC protein [limp
107	6	2.6	108	2	PH1668	Ig heavy chain V r
108	6	2.6	109	2	T42436	FMFamide-like pep
109	6	2.6	110	1	RBV722	60s acidic ribosom
110	6	2.6	111	2	PH1669	Ig heavy chain V r
111	6	2.6	112	2	T37490	ribosomal protein
112	6	2.6	113	2	T6537	FMFamide-like pep
113	6	2.6	114	2	E72524	probable ribosomal
114	6	2.6	115	2	EB6141	protein T25K16.9 [
115	6	2.6	116	2	S54462	probable membrane
116	6	2.6	117	1	A45252	P1LV variable regi
117	6	2.6	118	2	HVH0HG	Ig heavy chain pre
118	6	2.6	119	2	S31680	Ig heavy chain V r
119	6	2.6	120	2	S18551	Ig heavy chain V r
120	6	2.6	121	2	G72772	hypothetical prote
121	6	2.6	122	2	A97730	hypothetical prote
122	6	2.6	123	2	T17003	dormancy-associate
123	6	2.6	124	2	S31999	Ig heavy chain V r
124	6	2.6	125	2	S20783	Ig heavy chain V r
125	6	2.6	126	2	H71086	hypothetical prote
126	6	2.6	127	2	C84953	mutator mult prote
127	6	2.6	128	2	H70101	gIpe protein (gIpe
128	6	2.6	129	2	I44151	Ig heavy chain V r
129	6	2.6	130	2	C71730	hypothetical prote
130	6	2.6	131	2	S46393	Ig heavy chain V r
131	6	2.6	132	2	B97706	hypothetical prote
132	6	2.6	133	2	E72763	immunoglobulin lam
133	6	2.6	134	2	A26986	hypothetical prote
134	6	2.6	135	2	C82297	DNA polymerase III
135	6	2.6	136	2	S49530	anti-Sm antibody V
136	6	2.6	137	2	C81436	biopolymer transpo
137	6	2.6	138	2	AB1127	hypothetical prote
138	6	2.6	139	2	AG1487	hypothetical prote
139	6	2.6	140	2	S78306	photosystem I ferr
140	6	2.6	141	2	AB1938	probable membrane
141	6	2.6	142	2	A32124	photosystem I chal
142	6	2.6	143	2	C83529	hypothetical prote
143	6	2.6	144	2	A32483	Ig heavy chain V r
144	6	2.6	145	2	T48769	hypothetical prote
145	6	2.6	146	2	G81048	biopolymer transpo
146	6	2.6	147	2	B70111	V-type ATPase, sub
147	6	2.6	148	2	C84053	sodium-glutamate/a
148	6	2.6	149	2	S58488	DNA polymerase III
149	6	2.6	150	2	T10641	carbonic anhydrase
150	6	2.6	151	2	A82110	bacterioferritin c
151	6	2.6	152	2	AC1172	hypothetical prote
152	6	2.6	153	2	AE1529	hypothetical prote
153	6	2.6	154	2	C86206	hypothetical prote
154	6	2.6	155	2	AB2717	conserved hypotet
155	6	2.6	156	2	T35610	whle protein II -
156	6	2.6	157	2	D84987	smg protein [impor
157	6	2.6	158	2	AG2775	protein-export mem
158	6	2.6	159	2	D81820	hypothetical prote
159	6	2.6	160	2	G75059	hypothetical prote
160	6	2.6	161	2	E97555	hypothetical prote
161	6	2.6	162	2	E90497	hypothetical prote
162	6	2.6	163	2	A86941	conserved hypotet
163	6	2.6	164	2	S43476	histone-like DNA-b
164	6	2.6	165	2	H75384	osmotically induci
165	6	2.6	166	2	T32120	hypothetical prote
166	6	2.6	167	2	AB1684	hypothetical prote
167	6	2.6	168	2	T38617	zinc finger protei
168	6	2.6	169	2	JE0305	propanediol denydr
169	6	2.6	170	2	T18921	hypothetical prote
170	6	2.6	171	2	B64505	hypothetical prote
171	6	2.6	172	2	S24960	gene C98 protein -
172	6	2.6	173	1	S32238	ribosomal protein
173	6	2.6	174	2	B64615	hypothetical prote
174	6	2.6	175	2	E97498	outer membrane ser
175	6	2.6	190	2	E64775	probable lipoprote
176	6	2.6	190	2	C90692	glycoprotein/polys
177	6	2.6	191	2	G85542	glycoprotein/polys
178	6	2.6	192	2	AE0492	probable membrane
179	6	2.6	193	2	AF0082	conserved hypotet
180	6	2.6	194	2	T14746	hypothetical prote
181	6	2.6	195	2	A97351	hypothetical secre
182	6	2.6	196	1	M0BPM1	lysozyme (EC 3.2.1
183	6	2.6	197	2	S34993	nitrite reductase
184	6	2.6	198	2	D70637	hypothetical prote
185	6	2.6	199	1	S41182	phage-related repl
186	6	2.6	200	2	S52798	hypothetical prote
187	6	2.6	201	2	A10970	probable YecR-famI
188	6	2.6	202	2	AF1887	hypothetical prote
189	6	2.6	203	2	B83717	NADP-dependent alc
190	6	2.6	204	2	D83997	hypothetical prote
191	6	2.6	205	2	T20407	hypothetical prote
192	6	2.6	206	2	T02247	photosystem I chal
193	6	2.6	207	2	T26846	hypothetical prote
194	6	2.6	208	1	R3RT8	ribosomal protein
195	6	2.6	209	2	S42110	ribosomal protein
196	6	2.6	210	2	S25022	ribosomal protein
197	6	2.6	211	2	A87269	hypothetical prote
198	6	2.6	212	2	JX0266	hypothetical prote
199	6	2.6	213	2	C70665	platelet aggregati
200	6	2.6	214	2	D69529	probable urea prot
201	6	2.6	215	2	A1SP2	conserved hypotet
202	6	2.6	216	2	AB1407	photosystem I chal
203	6	2.6	217	2	AB1783	ribulose-phosphate
204	6	2.6	218	2	T11966	ribulose-phosphate
205	6	2.6	219	2	T36448	lipoate biosynthes
206	6	2.6	220	1	A40181	probable methyltra
207	6	2.6	221	2	H84084	23K integral membr
208	6	2.6	222	2	H84340	hypothetical prote
209	6	2.6	223	1	XMECAD	circadian regulato
210	6	2.6	224	2	A98029	deda protein - Esc
211	6	2.6	225	2	B85873	hypothetical prote
212	6	2.6	226	2	AE0802	hypothetical prote
213	6	2.6	227	2	T04082	deda protein (dsq-
214	6	2.6	228	2	T04088	probable ribosomal
215	6	2.6	229	2	S44651	ribosomal protein
216	6	2.6	230	2	A27270	f42h10.4 protein -
217	6	2.6	231	2	E89567	myosin light chain
218	6	2.6	232	1	A64599	protein T08A9.3 [i
219	6	2.6	233	2	S69635	hydrogenase (EC 1.
220	6	2.6	234	2	B28456	hypothetical prote
221	6	2.6	235	2	G89662	histone H1.11L - c
222	6	2.6	236	2	S46353	protein E01G6.2 [i
223	6	2.6	237	2	E86326	nef protein - siml
224	6	2.6	238	2	T35236	protein F18014.3 [
225	6	2.6	239	2	H86940	hypothetical prote
226	6	2.6	240	2	T41834	probable membrane
227	6	2.6	241	2	G72861	OVV-E25 P25 orF94
228	6	2.6	242	2	T32999	occlusion-derived
229	6	2.6	243	2	T18613	hypothetical prote
230	6	2.6	244	2	I50467	hypothetical prote
231	6	2.6	245	2	T03678	MHC class II beta
232	6	2.6	246	2	S73912	plasma membrane pr
233	6	2.6	247	2	T02984	5-guanylate kinase
234	6	2.6	248	2	AG1571	myb-related protei
235	6	2.6	249	2	T68673	gene X123 protein
236	6	2.6	250	2	AG2203	glucose inhibited
237	6	2.6	251	2	A71847	carbonic anhydrase
238	6	2.6	252	2	T21406	synaptogyrin homol
239	6	2.6	253	2	T43324	hypothetical prote
240	6	2.6	254	2	AG1571	cobalamin (5'-phos
241	6	2.6	255	2	T40405	hypothetical prote
242	6	2.6	256	2	T35285	probable integral
243	6	2.6	257	2	G95361	probable ABC trans
244	6	2.6	258	2	T10185	MADS-box protein C
245	6	2.6	259	2	A87582	conjugal transfer
246	6	2.6	260	2	T10376	hypothetical prote
247	6	2.6	261	2	AE0285	conserved hypotet
248	6	2.6	262	2	G70453	indole-3-glycerol
249	6	2.6	263	2	T12092	G-box-binding prot

249	6	2.6	258	2	AD2531
250	6	2.6	260	2	T10642
251	6	2.6	261	2	E70957
252	6	2.6	261	2	AB3070
253	6	2.6	262	2	AB0715
254	6	2.6	264	2	C97402
255	6	2.6	264	2	AC2620
256	6	2.6	266	2	AE0979
257	6	2.6	268	2	AH1646
258	6	2.6	269	1	C69651
259	6	2.6	269	2	T21407
260	6	2.6	270	2	G90595
261	6	2.6	270	2	A43711
262	6	2.6	270	2	S28682
263	6	2.6	270	2	E87649
264	6	2.6	271	2	S12783
265	6	2.6	273	2	H71212
266	6	2.6	274	2	T12791
267	6	2.6	275	2	A32057
268	6	2.6	275	2	C69808
269	6	2.6	275	2	A97226
270	6	2.6	276	2	A12292
271	6	2.6	279	2	AG0421
272	6	2.6	279	2	T51515
273	6	2.6	280	2	H75194
274	6	2.6	281	2	A41400
275	6	2.6	281	2	F84313
276	6	2.6	283	2	G84458
277	6	2.6	284	2	T39544
278	6	2.6	284	2	H72370
279	6	2.6	287	2	T42085
280	6	2.6	290	2	S64312
281	6	2.6	292	2	T18584
282	6	2.6	294	2	S71642
283	6	2.6	294	2	D70525
284	6	2.6	296	2	T46617
285	6	2.6	297	2	F86839
286	6	2.6	297	2	A45335
287	6	2.6	297	2	S38477
288	6	2.6	299	2	T12505
289	6	2.6	299	2	D98238
290	6	2.6	300	2	AH1357
291	6	2.6	300	2	AH1727
292	6	2.6	301	2	A87445
293	6	2.6	307	2	JC5927
294	6	2.6	308	2	H65035
295	6	2.6	308	2	H64409
296	6	2.6	308	2	T17248
297	6	2.6	310	2	S65966
298	6	2.6	310	2	B83331
299	6	2.6	311	2	B69191
300	6	2.6	312	1	Q0B63L
301	6	2.6	312	1	H91237
302	6	2.6	312	2	D90504
303	6	2.6	312	2	H81432
304	6	2.6	312	2	H78664
305	6	2.6	312	2	D86085
306	6	2.6	313	2	B69588
307	6	2.6	315	1	S63990
308	6	2.6	315	2	JC5201
309	6	2.6	316	2	A11935
310	6	2.6	317	2	T20302
311	6	2.6	318	2	AG1084
312	6	2.6	318	2	AG1441
313	6	2.6	318	2	AB0476
314	6	2.6	318	2	B95844
315	6	2.6	319	2	E98330
316	6	2.6	319	2	AH2952
317	6	2.6	319	2	H98216
318	6	2.6	320	2	C95970
319	6	2.6	324	2	S05396
320	6	2.6	325	2	T02117
321	6	2.6	326	2	AE0658

hypothetical prote  
 carbonic anhydrase  
 probable lprf prot  
 conserved hypochet  
 aminoglycoside-res  
 probable acyltrans  
 1-acyl-sn-glycerol  
 probable transcrip  
 hypothetical prote  
 AH1646  
 prolipoprotein dia  
 conserved hypochet  
 replication protei  
 replication protei  
 hypothetical prote  
 OX40 antigen precu  
 hypothetical prote  
 hypothetical prote  
 nitrogemase (EC 1.  
 transporter homolo  
 uncharacterized co  
 hypothetical prote  
 sugar transport sy  
 syntaxin homolog F  
 hypothetical prote  
 myristylated alani  
 hypothetical prote  
 probable protein p  
 suppressor protein  
 conserved hypochet  
 MPR4 protein homol  
 hypothetical prote  
 f15c11.2 - Caemorph  
 dolichyl phosphate  
 probable beta-1 -  
 probable chemotaxi  
 phosphate ABC tran  
 cytochrome-c oxida  
 lytic enzyme lysa  
 hypothetical prote  
 helix-turn-helix d  
 hypothetical prote  
 integral membrane  
 syntaxin 16 - huma  
 hypothetical prote  
 succinate--CoA lig  
 catechol 1,2-dioxy  
 conserved hypochet  
 hypothetical prote  
 conserved hypochet  
 conserved hypochet  
 probable membrane  
 conserved hypochet  
 probable membrane  
 hypothetical prote  
 hypothetical prote  
 hypothetical prote  
 L-arabinose transp  
 thioredoxin reduct  
 chemoreceptor TB56  
 hypothetical prote  
 phosphoglycerate d  
 phosphoglycerate d  
 phosphoglycerate d  
 probable periplasm  
 probable sugar ABC  
 hypothetical prote  
 hypothetical prote  
 hypothetical prote  
 probable sugar upt  
 bifunctional cycla  
 hypothetical prote  
 psp operon transcr

322	6	2.6	326	2	S74844
323	6	2.6	327	2	S49619
324	6	2.6	327	2	T50744
325	6	2.6	328	2	S32369
326	6	2.6	329	2	G82900
327	6	2.6	329	2	A10574
328	6	2.6	330	2	C64792
329	6	2.6	330	2	C95844
330	6	2.6	330	2	D90707
331	6	2.6	330	2	H85357
332	6	2.6	332	2	A89837
333	6	2.6	333	2	G95915
334	6	2.6	339	2	C83335
335	6	2.6	339	2	H64348
336	6	2.6	341	2	T16091
337	6	2.6	343	2	E64363
338	6	2.6	343	2	T50179
339	6	2.6	344	2	F72524
340	6	2.6	345	2	H90515
341	6	2.6	347	2	A75537
342	6	2.6	347	2	A46567
343	6	2.6	348	2	T35968
344	6	2.6	348	2	AD0654
345	6	2.6	349	2	H97006
346	6	2.6	350	2	B82777
347	6	2.6	353	2	A75027
348	6	2.6	353	2	D75328
349	6	2.6	353	2	S38080
350	6	2.6	355	2	T05390
351	6	2.6	356	2	S42388
352	6	2.6	357	2	H83388
353	6	2.6	357	2	D86707
354	6	2.6	359	2	E86706
355	6	2.6	362	2	S37220
356	6	2.6	362	2	S40092
357	6	2.6	364	2	I46604
358	6	2.6	364	2	J01488
359	6	2.6	366	2	A60363
360	6	2.6	366	2	I46603
361	6	2.6	369	2	T30592
362	6	2.6	369	2	T05013
363	6	2.6	370	2	A75371
364	6	2.6	371	2	D96771
365	6	2.6	372	1	Q0B888
366	6	2.6	372	2	E43674
367	6	2.6	372	2	C96771
368	6	2.6	372	2	S67770
369	6	2.6	372	2	A83714
370	6	2.6	372	2	B98331
371	6	2.6	372	2	AC2952
372	6	2.6	374	2	T10165
373	6	2.6	375	2	F75467
374	6	2.6	378	2	B99469
375	6	2.6	380	2	T23546
376	6	2.6	380	2	H96731
377	6	2.6	381	2	T40341
378	6	2.6	382	2	T24963
379	6	2.6	383	1	ALR20C
380	6	2.6	388	2	JC6543
381	6	2.6	391	2	C84268
382	6	2.6	391	2	A42973
383	6	2.6	392	2	E75042
384	6	2.6	392	2	E96707
385	6	2.6	395	2	S73531
386	6	2.6	396	2	T26967
387	6	2.6	399	1	D64327
388	6	2.6	400	2	AD3293
389	6	2.6	401	2	H69833
390	6	2.6	405	2	S23260
391	6	2.6	408	2	A46712
392	6	2.6	409	2	AD0646
393	6	2.6	411	2	D82524
394	6	2.6	413	2	AB3174

lmbp protein - Syn  
 crta protein - Rho  
 sperulidene monoox  
 gamma-SNAP protein  
 aspartate-ammonia  
 ferric enterobacti  
 ferric enterobacti  
 probable sugar ABC  
 ferric enterobacti  
 ferric enterobacti  
 hypothetical prote  
 hypothetical prote  
 probable sugar ABC  
 probable oxidoredu  
 hypothetical prote  
 hypothetical prote  
 acidc ribosomal p  
 yeast bud pattern  
 probable acidc ri  
 lipote-protein 11  
 hypothetical prote  
 tetracycline resis  
 conserved hypochet  
 probable protease  
 probable permease,  
 conserved hypochet  
 oligopeptide trans  
 conserved hypochet  
 hypothetical prote  
 probable cysteine  
 torso-like protein  
 ABC transporter pe  
 hypothetical prote  
 fiber protein - hu  
 MHC PD14 transplan  
 bradykinin B2 rece  
 MHC class I histoc  
 MHC PD14 transpla  
 conserved hypochet  
 hypothetical prote  
 threonine 3-dehydr  
 unknown protein FI  
 glycoprotein I pre  
 u57 protein - huma  
 unknown protein FI  
 probable membrane  
 Iron (III) transpo  
 probable transamin  
 aspartate aminotra  
 site-specific DNA-  
 probable lipoprote  
 glycosyltransferas  
 hypothetical prote  
 hypothetical prote  
 hypothetical prote  
 alpha-amylase (EC  
 p2X4 receptor - hu  
 aspartate aminotra  
 serum protein MSE5  
 transporter (major  
 hypothetical prote  
 CDP-diacylglycerid  
 hypothetical prote  
 H+-transporting tw  
 opgc protein [limp  
 conserved hypochet  
 hypothetical prote  
 glycoprotein ita -  
 aminotripeptidase  
 transcription term  
 aminotransferase,

355	6	2.6	413	2	AC3614	dtudp-4-dehydrorham	468	6	2.6	476	2	D87386	sodium-dicarboxyla
356	6	2.6	414	1	C70859	probable hexosyltr	469	6	2.6	476	2	S59339	proline oxidase -
397	6	2.6	417	2	E95327	conserved hypotnet	470	6	2.6	478	2	T33942	hypothetical prote
398	6	2.6	419	2	D49917	transcription term	471	6	2.6	480	2	C75614	probable xanthine
399	6	2.6	419	2	F82991	transcription term	472	6	2.6	481	2	F87715	transcription term
400	6	2.6	419	2	F81927	transcription term	473	6	2.6	484	2	T33504	hypothetical prote
401	6	2.6	419	2	F81667	transcription term	474	6	2.6	484	2	F71317	probable antigen,
402	6	2.6	419	2	F81177	transcription term	475	6	2.6	487	2	B96815	hypothetical prote
403	6	2.6	419	2	S74329	hypothetical prote	476	6	2.6	491	2	S61715	clathrin-associate
404	6	2.6	420	2	JW0076	sorbitol oxidase (	477	6	2.6	491	2	AH1140	transmembrane prot
405	6	2.6	420	2	B64060	transcription term	478	6	2.6	491	2	A86824	sensor protein kin
406	6	2.6	420	2	D71833	preprotein transio	479	6	2.6	492	2	C82217	conserved hypotnet
407	6	2.6	420	2	D64682	preprotein transio	480	6	2.6	493	2	AC1856	diaminobutyrate--p
408	6	2.6	421	2	G97698	transcription term	481	6	2.6	493	2	JC5621	lymphocyte growth f
409	6	2.6	421	2	AH2924	transcription term	482	6	2.6	494	1	A29079	glymphocyte surface
410	6	2.6	421	2	AF3252	transcription term	483	6	2.6	494	2	E75486	hypothetical prote
411	6	2.6	421	2	T35515	hypothetical prote	484	6	2.6	495	2	A44489	GT box-binding pro
412	6	2.6	422	2	JC6035	transcription term	485	6	2.6	497	1	MZBE83	host shutoff vario
413	6	2.6	422	2	T24865	hypothetical prote	486	6	2.6	497	2	JC2054	complement regulat
414	6	2.6	423	2	T38056	nicotinic acetylch	487	6	2.6	497	2	F82747	conserved hypotnet
415	6	2.6	423	2	E84122	transcription term	488	6	2.6	498	1	VGXPLM	surface glycoprote
416	6	2.6	423	2	A81769	transcription term	489	6	2.6	498	1	VGXPLM	surface glycoprote
417	6	2.6	423	2	AG1393	transcription term	490	6	2.6	498	2	G97062	glycerol kinase, G
418	6	2.6	427	2	A47051	transcription term	491	6	2.6	500	2	F86845	glycerol kinase,
419	6	2.6	428	2	S10013	transcription term	492	6	2.6	501	2	AC0939	H+-transporting AT
420	6	2.6	429	1	A31950	alpha-amylase (EC	493	6	2.6	502	1	K1ECGL	glycerol kinase (I
421	6	2.6	429	1	AG3150	leucine dehydrogen	494	6	2.6	502	2	C91235	glycerol kinase (E
422	6	2.6	431	2	C82219	hypothetical prote	495	6	2.6	502	2	T18562	hypothetical prote
423	6	2.6	433	2	T36609	probable secreted	496	6	2.6	503	2	T64086	glycerol kinase (E
424	6	2.6	434	2	S12775	alpha-amylase (EC	497	6	2.6	504	2	A83901	hypothetical prote
425	6	2.6	434	2	B72328	conserved hypotnet	498	6	2.6	505	2	C82422	glycerol kinase VC
426	6	2.6	435	2	T39719	beta transducin -	499	6	2.6	505	2	H83196	glycerol kinase PA
427	6	2.6	436	2	T39299	probable proteosom	500	6	2.6	507	2	JG0165	LMT1 protein - hum
428	6	2.6	439	2	C84981	hypothetical prote	501	6	2.6	507	2	T33024	hypothetical prote
429	6	2.6	440	2	H97705	hypothetical prote	502	6	2.6	508	2	A33378	fasciclin III prec
430	6	2.6	442	2	C69785	cellobiose phospho	503	6	2.6	508	2	T29988	hypothetical prote
431	6	2.6	445	1	S54140	D-serine permease	504	6	2.6	509	2	C86082	hypothetical prote
432	6	2.6	445	2	AD0962	DsdX permease (Imp	505	6	2.6	510	2	S57808	glycerol kinase (I
433	6	2.6	445	2	C69596	branched-chain ami	506	6	2.6	510	2	A95134	cellulase (EC 3.2.
434	6	2.6	446	2	E85691	probable tail comp	507	6	2.6	517	2	A10510	probable crotonobe
435	6	2.6	448	2	A69747	ABC transporter (p	508	6	2.6	518	2	T10621	hypothetical prote
436	6	2.6	449	2	T30982	hypothetical prote	509	6	2.6	519	2	C71346	hypothetical prote
437	6	2.6	449	2	S49904	cyclin - common to	510	6	2.6	521	2	E98002	probable transcrip
438	6	2.6	450	2	F71351	probable preprotei	511	6	2.6	522	2	H90633	conserved hypotnet
439	6	2.6	453	2	D84018	two-component resp	512	6	2.6	522	2	S40558	probable crotonobe
440	6	2.6	453	2	S73800	probable protoporp	513	6	2.6	522	2	H85484	probable carnitine
441	6	2.6	455	2	A55972	nicotinic acetylch	514	6	2.6	525	2	B48058	RNA-binding protei
442	6	2.6	455	2	S51116	nicotinic acetylch	515	6	2.6	526	2	D75391	Algp-related prote
443	6	2.6	457	2	E71656	transcription term	516	6	2.6	526	2	T39445	probable transcrip
444	6	2.6	457	2	E98213	hypothetical prote	517	6	2.6	535	2	S78598	probable transcrip
445	6	2.6	457	2	AD3073	hypothetical prote	518	6	2.6	536	2	A99199	D-ribulokinase (EC
446	6	2.6	458	2	E65068	hypothetical prote	519	6	2.6	536	2	AH3087	D-ribulokinase (EC
447	6	2.6	458	2	A85938	probable invasion	520	6	2.6	537	2	A46611	ribitol kinase (Im
448	6	2.6	458	2	E91092	probable invasion	521	6	2.6	539	2	F75497	myosin-binding pro
449	6	2.6	458	2	G97794	transcription term	522	6	2.6	542	2	E90604	probable arginine
450	6	2.6	461	2	B64992	acetosuccinate metab	523	6	2.6	543	2	T50905	hypothetical prote
451	6	2.6	461	2	S60253	set-12 protein - C	524	6	2.6	543	2	E93403	protochlorophyllid
452	6	2.6	462	1	DEECXB	NAD(P)+ transhydro	525	6	2.6	544	2	AF1900	probable extracell
453	6	2.6	462	1	C71296	glycine--trRNA liga	526	6	2.6	544	2	C42653	hydrogenase chain
454	6	2.6	462	2	A85766	NAD(P)+ transhydro	527	6	2.6	544	2	A71260	dhidriolipoamide S
455	6	2.6	462	2	D90917	NAD(P)+ transhydro	528	6	2.6	546	2	D86811	hypothetical prote
456	6	2.6	463	2	S27491	hypothetical prote	529	6	2.6	547	1	S52489	mannosyl-glycopro
457	6	2.6	464	2	A33523	nicotinic acetylch	530	6	2.6	547	2	H83018	choline oxidase (E
458	6	2.6	464	2	A71509	probable transcrip	531	6	2.6	547	2	A47178	dhidriolipoamide a
459	6	2.6	466	2	AD3550	NAD(P) transhydrog	532	6	2.6	547	2	A10990	methvl-accepting c
460	6	2.6	466	2	S16333	nicotinic acetylch	533	6	2.6	547	2	A32803	luciferin 1,4-alpha-m
461	6	2.6	466	2	AB2540	two-component sens	534	6	2.6	549	2	B45154	SMF2 protein - yea
462	6	2.6	468	2	A69468	ammonium transport	535	6	2.6	551	2	F83015	hypothetical prote
463	6	2.6	470	2	F85164	hypothetical prote	536	6	2.6	551	2	S05667	glucan 1,4-alpha-m
464	6	2.6	471	2	S01037	flavonol 3-O-glucos	537	6	2.6	551	2	T49900	2-oxoglutarate/mal
465	6	2.6	473	2	T04482	ribophorin I homol	538	6	2.6	561	2	T06075	hypothetical prote
466	6	2.6	473	2	A54691	octamer-binding pr	539	6	2.6	564	2	T23269	hypothetical prote
467	6	2.6	474	2	D75285	hira difunctional	540	6	2.6	564	2	A38271	serotonin receptor

541	6	2.6	564	2	A48141	614	2.6	725	2	T33498	hypothetical prote
542	6	2.6	567	2	F87594	615	2.6	726	2	T47700	delta-1-pyrroline-
543	6	2.6	567	2	A71619	616	2.6	726	2	T50684	pyrroline-5-carbox
544	6	2.6	573	2	H82257	617	2.6	729	2	UC7501	oligopeptide trans
545	6	2.6	573	2	F86663	618	2.6	735	2	SS4147	alpha adducin - ra
546	6	2.6	575	1	WQECPI	619	2.6	753	2	F69338	pyruvate,water dik
547	6	2.6	575	1	WQEBPI	620	2.6	758	2	A29253	finger protein hun
548	6	2.6	575	1	H91039	621	2.6	764	2	A40077	thylotropin recept
549	6	2.6	575	2	C85864	622	2.6	764	2	A47456	down-regulated in
550	6	2.6	575	2	AC0364	623	2.6	772	2	T13078	KRAM092 protein -
551	6	2.6	578	2	T51230	624	2.6	778	2	B86218	protein T2767.20 l
552	6	2.6	585	2	T20979	625	2.6	778	2	B70667	hypothetical prote
553	6	2.6	592	2	T21536	626	2.6	800	2	A84293	helicase [imported
554	6	2.6	598	2	T48822	627	2.6	803	2	T46179	hypothetical prote
555	6	2.6	603	2	G82738	628	2.6	809	2	T40574	guanine nucleotide
556	6	2.6	608	2	B87282	629	2.6	814	2	T00953	hypothetical prote
557	6	2.6	610	1	S30234	630	2.6	827	1	A31642	villin [validated]
558	6	2.6	613	2	B91024	631	2.6	829	2	E87305	TonB-dependent rec
559	6	2.6	613	2	D64999	632	2.6	835	2	I55603	reduced hepatic gl
560	6	2.6	613	2	C85868	633	2.6	836	2	E89453	protein F35H12.3 l
561	6	2.6	616	2	C82641	634	2.6	839	2	F75518	hypothetical prote
562	6	2.6	620	2	F90969	635	2.6	849	2	C90834	tail length tape m
563	6	2.6	620	2	E85742	636	2.6	853	1	TLBPHL	minor tail protein
564	6	2.6	631	2	B98137	637	2.6	853	2	S49876	gamma-adaptin - sm
565	6	2.6	635	1	WMBEW6	638	2.6	859	1	VCLJST	env polypotein pr
566	6	2.6	638	2	T36309	639	2.6	859	2	B90768	probable tail leng
567	6	2.6	643	2	T30746	640	2.6	859	2	B85718	probable tail comp
568	6	2.6	643	2	B25817	641	2.6	865	1	S02196	DNA-directed RNA p
569	6	2.6	648	2	A71342	642	2.6	865	1	S53098	envelope polypote
570	6	2.6	648	2	E98216	643	2.6	872	2	T30237	hypothetical prote
571	6	2.6	648	2	AD3070	644	2.6	876	1	A57988	regulatory protein
572	6	2.6	650	2	AB0585	645	2.6	877	2	S72541	nitrate reductase
573	6	2.6	650	2	B70766	646	2.6	881	2	T28013	hypothetical prote
574	6	2.6	658	2	T41309	647	2.6	883	2	C86729	hypothetical prote
575	6	2.6	660	1	Q0BE3	648	2.6	885	1	VGBESA	hypothetical prote
576	6	2.6	662	2	S55274	649	2.6	885	1	JC4732	beta-N-acetylhexos
577	6	2.6	662	2	T16845	650	2.6	887	2	C86453	COS protein F9L1.
578	6	2.6	664	2	H83962	651	2.6	889	2	H84506	probable retroelem
579	6	2.6	664	2	H83962	652	2.6	889	2	H71558	probable translati
580	6	2.6	665	1	VCWVVR	653	2.6	892	2	T13029	beta-adaptin homol
581	6	2.6	665	1	VCWVVR	654	2.6	894	2	T13029	probable toxR-regu
582	6	2.6	669	1	VCWVVR	655	2.6	898	2	T42131	hypothetical prote
583	6	2.6	669	1	VCWVVR	656	2.6	900	2	T32827	hypothetical prote
584	6	2.6	671	2	A46295	657	2.6	910	2	F83257	conserved hypotet
585	6	2.6	673	2	C82346	658	2.6	923	2	AC2705	hypothetical prote
586	6	2.6	673	2	G85095	659	2.6	923	2	C97487	hypothetical prote
587	6	2.6	677	2	E95417	660	2.6	923	2	T41350	meiotic recombinat
588	6	2.6	682	2	T47473	661	2.6	925	2	T22388	hypothetical prote
589	6	2.6	682	2	F70421	662	2.6	943	2	B83068	probable oxidoredu
590	6	2.6	684	2	G69015	663	2.6	946	2	B87316	TonB-dependent rec
591	6	2.6	685	2	A81246	664	2.6	948	2	S52739	H-transporing Ar
592	6	2.6	685	2	T06334	665	2.6	965	2	S55658	tegment protein 6
593	6	2.6	686	2	S33475	666	2.6	970	2	F64230	spore germination
594	6	2.6	687	2	T02459	667	2.6	972	2	T22488	hypothetical prote
595	6	2.6	688	2	A43491	668	2.6	980	2	G75523	probable cell divi
596	6	2.6	689	2	B43491	669	2.6	981	2	T32707	hypothetical prote
597	6	2.6	693	2	T19598	670	2.6	983	2	A87063	conserved large me
598	6	2.6	693	2	T47474	671	2.6	986	2	S71750	import intermediat
599	6	2.6	694	2	A53978	672	2.6	999	1	IJH0G3	desmoglein 3 precu
600	6	2.6	700	2	A42599	673	2.6	1008	2	S72698	transport protein
601	6	2.6	703	1	ALBSX1	674	2.6	1024	2	H87599	TonB-dependent rec
602	6	2.6	707	2	S43297	675	2.6	1025	2	H86250	hypothetical prote
603	6	2.6	708	2	A56163	676	2.6	1027	2	T46481	hypothetical prote
604	6	2.6	710	2	T22377	677	2.6	1031	2	C81302	probable type I si
605	6	2.6	710	2	S72497	678	2.6	1033	2	T31084	RNA-directed DNA p
606	6	2.6	712	1	VCLUS4	679	2.6	1047	2	T114897	probable ATPase (E
607	6	2.6	714	2	C90100	680	2.6	1049	2	C95883	probable efflux pr
608	6	2.6	716	2	T03695	681	2.6	1057	2	H83273	ribonuclease E PA2
609	6	2.6	717	2	T50685	682	2.6	1061	2	H97361	hypothetical prote
610	6	2.6	717	2	S66637	683	2.6	1061	2	AT2579	conserved hypotet
611	6	2.6	719	2	T12258	684	2.6	1067	2	T28663	hypothetical prote
612	6	2.6	719	2	T05384	685	2.6	1091	2	S33556	protein-tyrosine k
613	6	2.6	723	2	T30094	686	2.6	1099	2	A56155	tumor suppressor p

687	6	2.6	1111	2	T29070	hypothetical prote
688	6	2.6	1135	1	GNVUH7	M polypeptin - Ha
689	6	2.6	1135	1	GNVUH7	M polypeptin - Ha
690	6	2.6	1135	2	J02163	hypothetical 126.5
691	6	2.6	1135	2	J50605	M polypeptin - Ha
692	6	2.6	1141	2	A44093	cGMP-inhibited CAM
693	6	2.6	1150	2	S58775	myl protein - smu
694	6	2.6	1166	2	S37692	probable tumor sup
695	6	2.6	1169	2	S38181	flocculation prote
696	6	2.6	1182	2	T29097	pro-pol-dUPase po
697	6	2.6	1188	2	F64367	pyruvate, water dik
698	6	2.6	1203	2	T51029	related to pathway
699	6	2.6	1207	2	H87475	urea amidolyase-re
700	6	2.6	1224	2	F96795	hypothetical prote
701	6	2.6	1233	2	T30989	serine/threonine p
702	6	2.6	1244	2	T19068	hypothetical prote
703	6	2.6	1246	2	G89287	protein H39E23.1 l
704	6	2.6	1271	2	A45555	glutamate rich pro
705	6	2.6	1274	2	S55050	cardiac myosin-b1n
706	6	2.6	1280	2	G96796	hypothetical prote
707	6	2.6	1295	2	B96549	hypothetical prote
708	6	2.6	1299	2	T47182	hypothetical prote
709	6	2.6	1307	2	T21283	hypothetical prote
710	6	2.6	1329	2	E70917	hypothetical glyci
711	6	2.6	1329	2	A64828	cell division prot
712	6	2.6	1342	2	G90750	cell division prot
713	6	2.6	1342	2	E85614	cell division prot
714	6	2.6	1386	2	T00257	hypothetical prote
715	6	2.6	1421	2	T02501	hypothetical prote
716	6	2.6	1477	2	S64616	YOR1 protein - yea
717	6	2.6	1501	2	C84512	probable retroelem
718	6	2.6	1579	2	S25329	carboxypeptidase Y
719	6	2.6	1750	2	E86151	hypothetical prote
720	6	2.6	1816	2	F83901	hypothetical prote
721	6	2.6	1884	2	JC4975	plexin 2 precursor
722	6	2.6	1902	1	B44858	lactocepin (EC 3.4
723	6	2.6	1902	2	B45764	lactocepin (EC 3.4
724	6	2.6	1952	2	T48814	hypothetical prote
725	6	2.6	1957	2	T38077	hypothetical colle
726	6	2.6	1962	2	A32634	lactocepin (EC 3.4
727	6	2.6	2187	2	T30826	nascent polyepid
728	6	2.6	2499	1	A30788	mannose 6-phosphat
729	6	2.6	2747	2	B49132	fat facets (fat) s
730	6	2.6	2783	2	T34416	hypothetical prote
731	6	2.6	2897	2	B48666	cell proliferation
732	6	2.6	3104	2	S20473	fatty-acid synthas
733	6	2.6	3256	2	A48666	cell proliferation
734	6	2.6	3388	1	GNMWP	genome polypeptin
735	6	2.6	3391	1	GNMVA	genome polypeptin
736	6	2.6	3391	1	GNMVA	genome polypeptin
737	6	2.6	3391	1	GNMVA	genome polypeptin
738	6	2.6	3391	1	GNMVA	genome polypeptin
739	6	2.6	3391	1	GNMVA	genome polypeptin
740	6	2.6	3391	1	GNMVA	genome polypeptin
741	6	2.6	3391	1	GNMVA	genome polypeptin
742	6	2.6	3391	1	GNMVA	genome polypeptin
743	6	2.6	3391	1	GNMVA	genome polypeptin
744	6	2.6	3391	1	GNMVA	genome polypeptin
745	6	2.6	3391	1	GNMVA	genome polypeptin
746	6	2.6	3391	1	GNMVA	genome polypeptin
747	6	2.6	3391	1	GNMVA	genome polypeptin
748	6	2.6	3391	1	GNMVA	genome polypeptin
749	6	2.6	3391	1	GNMVA	genome polypeptin
750	6	2.6	3391	1	GNMVA	genome polypeptin
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757	6	2.6	3391	1	GNMVA	genome polypeptin
758	6	2.6	3391	1	GNMVA	genome polypeptin
759	6	2.6	3391	1	GNMVA	genome polypeptin

833	5	2.1	71	2	G83792	hypothetical prote	906	5	2.1	89	2	S03805	hypothetical prote
834	5	2.1	71	2	G98356	hypothetical prote	907	5	2.1	89	2	D97038	probable membrane
835	5	2.1	72	2	S41611	high-potential iro	908	5	2.1	89	2	AC1576	carbon dioxide con
836	5	2.1	72	2	T32629	hypothetical prote	909	5	2.1	89	2	AH1222	carbon dioxide con
837	5	2.1	72	2	T03190	hypothetical prote	910	5	2.1	90	1	WMBPMB	gene m protein - p
838	5	2.1	72	2	T21081	hypothetical prote	911	5	2.1	90	2	D84247	hypothetical prote
839	5	2.1	72	2	A36460	glucocorticoid rec	912	5	2.1	90	2	F69511	hypothetical prote
840	5	2.1	72	2	F95408	hypothetical prote	913	5	2.1	91	1	A46539	monocyte chemotatr
841	5	2.1	73	2	F90556	acyl carrier prote	914	5	2.1	91	1	G71562	ferredoxin [2Fe-2S
842	5	2.1	73	2	T12383	hypothetical prote	915	5	2.1	91	2	G72088	ferredoxin [2Fe-2S
843	5	2.1	74	2	E69028	hypothetical prote	916	5	2.1	91	2	E81715	ferredoxin [2Fe-2S
844	5	2.1	74	2	T48037	hypothetical prote	917	5	2.1	91	2	H86701	hypothetical prote
845	5	2.1	75	2	T26916	hypothetical prote	918	5	2.1	91	2	B86536	ferredoxin IV [imp
846	5	2.1	75	2	G97116	probable nucleic a	919	5	2.1	91	2	S34669	hypothetical prote
847	5	2.1	75	2	AD3131	hypothetical prote	920	5	2.1	91	2	F59093	hypothetical prote
848	5	2.1	76	2	A69391	DNA-directed RNA p	921	5	2.1	91	2	F83654	pro sigma K proces
849	5	2.1	76	2	S41722	excisionase - Sacc	922	5	2.1	92	2	A84637	hypothetical prote
850	5	2.1	76	2	G84788	hypothetical prote	923	5	2.1	92	2	C75348	hypothetical prote
851	5	2.1	76	2	B75271	hypothetical prote	924	5	2.1	92	2	T45441	hypothetical prote
852	5	2.1	76	2	T45877	hypothetical prote	925	5	2.1	92	2	A40533	cAMP-dependent pro
853	5	2.1	76	2	F83739	hypothetical prote	926	5	2.1	92	2	D71151	hypothetical prote
854	5	2.1	76	2	AC0163	hypothetical prote	927	5	2.1	92	2	B85911	hypothetical prote
855	5	2.1	77	2	S52636	metallothionein -	928	5	2.1	93	2	S77812	probable DNA topoi
856	5	2.1	77	2	S57862	metallothionein 2b	929	5	2.1	93	2	S25466	r-cell receptor al
857	5	2.1	78	2	T12021	acyl carrier prote	930	5	2.1	93	2	S50649	hypothetical prote
858	5	2.1	78	2	PQ0053	hypothetical prote	931	5	2.1	93	2	C86764	hypothetical prote
859	5	2.1	78	2	E61547	p27 protein - huma	932	5	2.1	93	2	F84175	hypothetical prote
860	5	2.1	78	2	AC0694	conserved hypotet	933	5	2.1	93	2	S04152	outer membrane pro
861	5	2.1	78	2	AB1133	hypothetical orf 1	934	5	2.1	93	2	S33842	acyl-CoA thioester
862	5	2.1	79	2	U02128	metallothionein -	935	5	2.1	93	2	AC0592	probable membrane
863	5	2.1	79	2	F90575	hypothetical prote	936	5	2.1	93	2	B86305	FcII.4 protein - A
864	5	2.1	79	2	S08454	hypothetical prote	937	5	2.1	94	2	H70654	hypothetical prote
865	5	2.1	79	2	A97847	hypothetical prote	938	5	2.1	94	2	A69105	hypothetical prote
866	5	2.1	80	2	T10087	metallothionein -	939	5	2.1	94	2	C97181	uncharacterized se
867	5	2.1	80	2	A84528	hypothetical prote	940	5	2.1	95	2	T06905	ribosomal protein
868	5	2.1	80	2	T68668	transcription fact	941	5	2.1	95	2	T25253	hypothetical prote
869	5	2.1	80	2	168256	ORF MSV095 hypot	942	5	2.1	96	1	U00349	11.5K protein - Ch
870	5	2.1	81	2	JN0710	ubiquitin-like pro	943	5	2.1	96	1	ERBP62	gene 6 protein - p
871	5	2.1	82	2	T07076	metallothionein ty	944	5	2.1	96	2	T17865	hypothetical prote
872	5	2.1	82	2	T07114	metallothionein-1i	945	5	2.1	96	2	F97645	hypothetical prote
873	5	2.1	82	2	H90491	conserved hypotet	946	5	2.1	96	2	AD2869	conserved hypotet
874	5	2.1	82	2	A47482	pilin-like coloniz	947	5	2.1	97	2	PH1090	Ig lambda chain V
875	5	2.1	83	2	C81840	hypothetical prote	948	5	2.1	97	2	F65108	hypothetical 10.8
876	5	2.1	83	2	A36505	oxalacetate decar	949	5	2.1	97	2	S60889	hypothetical prote
877	5	2.1	83	2	S76476	hypothetical prote	950	5	2.1	97	2	G72117	conserved hypotet
878	5	2.1	83	2	AE0870	endonuclease fragm	951	5	2.1	97	2	B90725	hypothetical prote
879	5	2.1	84	2	S06077	H+-transporting At	952	5	2.1	97	2	C91136	hypothetical prote
880	5	2.1	84	2	A53578	esculentin-1b prec	953	5	2.1	97	2	B86506	hypothetical prote
881	5	2.1	84	2	T23177	hypothetical prote	954	5	2.1	97	2	F64809	hypothetical prote
882	5	2.1	85	1	IMECE3	immunity protein (	955	5	2.1	97	2	S72866	hypothetical prote
883	5	2.1	85	1	S68906	alpha-toxin Bot XI	956	5	2.1	97	2	T25342	hypothetical prote
884	5	2.1	85	2	S49177	colicin E4 immunit	957	5	2.1	97	2	C85576	hypothetical prote
885	5	2.1	85	2	T30462	hypothetical prote	958	5	2.1	97	2	F85961	hypothetical prote
886	5	2.1	85	2	A10316	sec-independent pr	959	5	2.1	98	2	S55622	hypothetical prote
887	5	2.1	85	2	AD2497	hypothetical prote	960	5	2.1	98	2	H81072	hypothetical prote
888	5	2.1	86	2	S54912	Ig heavy chain V r	961	5	2.1	98	2	S72990	hypothetical prote
889	5	2.1	86	2	T34975	hypothetical prote	962	5	2.1	98	2	S26981	pvs protein 1 - ki
890	5	2.1	86	2	C90666	probable DNA bindi	963	5	2.1	98	2	T29026	hypothetical prote
891	5	2.1	86	2	H75364	hypothetical prote	964	5	2.1	99	2	PH1089	Ig lambda chain V
892	5	2.1	86	2	S37381	chitin-binding ant	965	5	2.1	99	2	S14582	Ig lambda chain V
893	5	2.1	86	2	G85516	probable DNA bindi	966	5	2.1	99	2	S14583	Ig lambda chain V
894	5	2.1	87	2	T17591	hypothetical prote	967	5	2.1	99	2	S14584	Ig lambda chain V
895	5	2.1	87	2	T27890	hypothetical prote	968	5	2.1	99	2	S14585	Ig lambda chain V
896	5	2.1	88	2	S69489	bombyxin B-8 precu	969	5	2.1	99	2	S14586	Ig lambda chain V
897	5	2.1	88	2	S02720	outer membrane pro	970	5	2.1	99	2	E69267	hypothetical prote
898	5	2.1	88	2	S61552	mammary tumor prot	971	5	2.1	99	2	E82707	hypothetical prote
899	5	2.1	88	2	B75116	hypothetical prote	972	5	2.1	100	2	PH1087	Ig lambda chain V
900	5	2.1	88	2	AG0910	conserved hypotet	973	5	2.1	100	2	PH1088	Ig lambda chain V
901	5	2.1	88	2	AC2561	hypothetical prote	974	5	2.1	100	2	AT1298	cobalt transport p
902	5	2.1	88	2	T01863	guanylate kinase-r	975	5	2.1	100	2	T41217	hypothetical prote
903	5	2.1	89	2	154187	small proline-rich	976	5	2.1	100	2	F86836	transcription regu
904	5	2.1	89	2	A46709	probable transcrip	977	5	2.1	100	2	D22848	hypothetical ORF-1
905	5	2.1	89	2	D90802		978	5	2.1	101	2	S07706	T-cell receptor al

979 5 2.1 101 2 D43255 hypothetical prote  
980 5 2.1 101 2 AC3467 sarcosine oxidase  
981 5 2.1 101 2 T26641 hypothetical prote  
982 5 2.1 101 2 B97851 hypothetical prote  
983 5 2.1 102 2 B34770 ORF2 protein - sai  
984 5 2.1 102 2 A37887 apolipoprotein A-I  
985 5 2.1 102 2 B23594 apolipoprotein A-I  
986 5 2.1 102 2 A23594 apolipoprotein A-I  
987 5 2.1 102 2 A24846 apolipoprotein A-I  
988 5 2.1 102 2 I48250 apolipoprotein A-I  
989 5 2.1 102 2 S45406 probable membrane  
990 5 2.1 102 2 T45810 hypothetical prote  
991 5 2.1 102 2 C96595 hypothetical prote  
992 5 2.1 102 2 T49565 hypothetical prote  
993 5 2.1 103 2 T03541 probable cobalt tr  
994 5 2.1 103 2 T34790 hypothetical prote  
995 5 2.1 103 2 E72635 hypothetical prote  
996 5 2.1 103 2 AD3217 conserved hypotne  
997 5 2.1 104 2 ERBP69 early protein gp6  
998 5 2.1 104 2 PH1053 Ig light chain V r  
999 5 2.1 104 2 G75090 hypothetical prote  
1000 5 2.1 104 2 A85838 probable outer mem

## ALIGNMENTS

RESULT 1  
D72058  
transcription termination factor Rho CP0137 [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000  
C:Accession: D72058; H81608  
R:Kalmay, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Ollinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606  
A:Accession: D72058  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-464 <RNA>  
A:Cross-references: GB:AE001645; GB:AE001363; NID:g4376896; PIDN:AD18749.1; PID:g437690  
A:Experimental source: strain CWL029  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Whinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255  
A:Accession: H81608  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-464 <RNA>  
A:Cross-references: GB:AE002175; GB:AE002161; NID:g7189069; PIDN:AF38020.1; PID:g718907  
A:Experimental source: strain AR39, HL cells  
C:Genetics:  
A:Gene: rho; CP0137  
C:Superfamily: transcription termination factor rho  
C:Keywords: transcription termination

Query Match 3.4%; Score 8; DB 2; Length 464;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 IVLIVLLI 230  
|||||  
DB 248 IVLIVLLI 255

RESULT 2  
G86566  
transcription termination factor [imported] - Chlamydia pneumoniae (strain J138)  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: G86566  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20330349  
A:Accession: G86566  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-464 <SNO>  
A:Cross-references: GB:BA000008; NID:g8978982; PIDN:BA98817.1; GSPDB:GN00142  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: rho  
C:Superfamily: transcription termination factor rho  
C:Keywords: transcription termination

Query Match 3.4%; Score 8; DB 2; Length 464;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 IVLIVLLI 230  
|||||  
DB 248 IVLIVLLI 255

RESULT 3  
AC1185  
B. subtilis ydbB protein homolog lmo0883 [imported] - Listeria monocytogenes (strain  
C:Species: Listeria monocytogenes  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AC1185  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Eshti,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.;  
Ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla  
A:Title: Comparative genomes of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AC1185  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-491 <GTA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC98961.1; PID:g16410286; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0883  
C:Superfamily: Bacillus subtilis hypothetical protein ydbB

Query Match 3.4%; Score 8; DB 2; Length 491;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVIVL 228  
|||||  
DB 228 GIIVIVL 235

RESULT 4  
AB1543  
B. subtilis ydbB protein homolog lmo0882 [imported] - Listeria innocua (strain C1p11  
C:Species: Listeria innocua  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AB1543  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Eshti,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.;  
Ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla



A>Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AB1543  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-494 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC96114.1; PID:g16413332; GSPDB:GN00178  
A:Experimental source: strain C1p11262  
C:Genetics:  
A:Gene: 11n082  
C:Superfamily: *Bacillus subtilis* hypothetical protein ydbT

Query Match 3.4%; Score 8; DB 2; Length 494;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIVL 228  
|||||||  
DB 231 GIIVLIVL 238

RESULT 5  
G82022  
methionine--tRNA ligase (EC 6.1.1.10) NMA0275 [imported] - *Neisseria meningitidis* (strain C) [Species: *Neisseria meningitidis*]  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: G82022  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holtz, S.; Jørgensen, K.; Leather, S.; Mout, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000  
A>Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A:Reference number: AB1775; MUID:20222556  
A:Accession: G82022  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-685 <PAR>  
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83583.1; PID:g737903  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: metG: NMA0275  
C:Superfamily: methionine--tRNA ligase  
C:Keywords: ligase

Query Match 3.4%; Score 8; DB 2; Length 685;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAEE 155  
|||||||  
DB 561 TPAPAAEE 568

RESULT 6  
T29018  
hypothetical protein ZK84.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C:Accession: T29018  
R:Kirsten, J.  
submitted to the EMBL Data Library, April 1995  
A:Description: The sequence of *C. elegans* cosmid ZK84.  
A:Reference number: Z20553  
A:Accession: T29018  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-801 <KIR>  
A:Cross-references: EMBL:U23181; PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZK84.1  
A:Experimental source: strain Bristol N2; clone ZK84  
C:Genetics:  
A:Gene: CESP:ZK84.1  
A:Map position: 2

A:introns: 22/2; 45/3; 108/1  
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 3.4%; Score 8; DB 2; Length 801;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAAEET 156  
|||||||  
DB 267 PAPAAEET 274

RESULT 7  
S71258  
major latex protein type 3 - *Arabidopsis thaliana*  
C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
C:Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 20-Jun-2000  
C:Accession: S71258  
R:Grellet, F.; Cooke, R.; Laudie, M.; Raynal, M.; Delseny, M.  
submitted to the EMBL Data Library, October 1995  
A:Reference number: S71258  
A:Accession: S71258  
A:Molecule type: mRNA  
A:Residues: 1-155 <GRE>  
A:Cross-references: EMBL:X91961; NID:g1107494; PID:g1107495  
C:Superfamily: wound-induced protein Sn-1

Query Match 3.0%; Score 7; DB 2; Length 155;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 91 RENSPE 97  
|||||||  
DB 123 RENSPE 129

RESULT 8  
T21313  
hypothetical protein F23H12.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T21313  
R:Kershaw, J.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19405  
A:Accession: T21313  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-165 <NLL>  
A:Cross-references: EMBL:Z74472; PIDN:CAA98941.1; GSPDB:GN00023; CESP:F23H12.3  
A:Experimental source: clone F23H12  
C:Genetics:  
A:Gene: CESP:F23H12.3  
A:Map position: 5  
A:introns: 22/3; 56/3; 95/3  
C:Superfamily: *Caenorhabditis elegans* hypothetical protein F23H12.3

Query Match 3.0%; Score 7; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIV 227  
|||||||  
DB 89 GIIVLIV 95

RESULT 9  
H90386  
hypothetical protein SSO2176 [imported] - *Sulfolobus solfataricus*  
C:Species: *Sulfolobus solfataricus*

C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
 C/Accession: H90386  
 R/She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Anayez, M.J.; Chan-  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi Ngoc, H.P.; Redder, H.  
 arrett, R.A.; Ragan, M.A.; SENSEN, C.W.; Van der Oost, J.  
 submitted to Genbank, April 2001  
 A/Description: *Sulfolobus solfataricus* complete genome.  
 A/Reference number: A99139  
 A/Accession: H90386  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-184 <KUR>  
 A/Cross-references: GB:AE006641; NID:g13815473; PIDN:AAK42351.1; GSPDB:GN00155  
 C/Genetics:  
 A/Gene: SS02176

Query Match 3.0%; Score 7; DB 2; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLLIV 231  
 |||||  
 Db 164 LIVLLIV 170

RESULT 10  
 H72242  
 flagellar L-ring protein - Thermotoga maritima (strain MSB8)  
 C/Species: Thermotoga maritima  
 C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
 C/Accession: H72242  
 R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.D.; Haft, D.H.; Hickey  
 Garrett, M.M.; Stewart, A.A.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
 C.M.  
 Nature 399, 323-329, 1999  
 A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
 A/Reference number: A72200; M0ID:99287316  
 A/Accession: H72242  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-199 <ARN>  
 A/Cross-references: GB:AE001800; GB:AE000512; NID:g4982090; PIDN:AAD36607.1; PID:g498210  
 A/Experimental source: strain MSB8  
 C/Genetics:  
 A/Gene: TM1540

Query Match 3.0%; Score 7; DB 2; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 IVLLIVF 232  
 |||||  
 Db 6 IVLLIVF 12

RESULT 11  
 D70519  
 Probable lppc protein - Mycobacterium tuberculosis (strain H37RV)  
 C/Species: Mycobacterium tuberculosis  
 C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C/Accession: D70519  
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 Rajandream, M.A.; Rogers, J.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
 Nature 393, 537-544, 1998  
 A/Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A/Reference number: A70500; M0ID:98295967  
 A/Accession: D70519  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA

A/Residues: 1-201 <COL>  
 A/Cross-references: GB:D97193; GB:AL123456; NID:g3261816; PIDN:CAB10030.1; PID:g32482  
 A/Experimental source: strain H37RV  
 C/Genetics:  
 A/Gene: lppc

Query Match 3.0%; Score 7; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAE 154  
 |||||  
 Db 48 TPAPAAE 54

RESULT 12  
 E75477  
 hypothetical protein - Deinococcus radiodurans (strain R1)  
 C/Species: Deinococcus radiodurans  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C/Accession: E75477  
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.  
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.;  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A/Reference number: A75250; M0ID:20036896  
 A/Accession: E75477  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-219 <WHI>  
 A/Cross-references: GB:AE001932; GB:AE000513; NID:g6458481; PIDN:AAF10355.1; PID:g645  
 A/Experimental source: strain R1  
 C/Genetics:  
 A/Gene: DR0772  
 A/Map position: 1

Query Match 3.0%; Score 7; DB 2; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 GTPAPAA 153  
 |||||  
 Db 205 GTPAPAA 211

RESULT 13  
 T05958  
 cold acclimation protein homolog - barley  
 C/Species: Hordeum vulgare (barley)  
 C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 08-Oct-1999  
 C/Accession: T05958  
 R/Grossi, M.; Gull, M.; Stanca, A.M.; Cattivelli, L.  
 Plant Sci. 105, 71-80, 1995  
 A/Title: Characterization of two barley genes that respond rapidly to dehydration str  
 A/Reference number: Z15371  
 A/Accession: T05958  
 A/Status: preliminary; translated from GB/EMBL/DDBT  
 A/Molecule type: mRNA  
 A/Residues: 1-255 <GRO>  
 A/Cross-references: EMBL:X84056; NID:g642245; PIDN:CAA58875.1; PID:g642246  
 A/Experimental source: cv. Georgie, leaf  
 C/Genetics:  
 A/Gene: paf93

Query Match 3.0%; Score 7; DB 2; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAAEE 155

Db 206 PAPAEE 212

## RESULT 14

H82517 hypothetical protein XF2765 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C/Accession: H82517

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82517

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <SIM>

A:Cross-references: GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF85550.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2765

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 256;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155

Db 65 PAPAEE 71

## RESULT 15

H82661 hypothetical protein XF1591 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C/Accession: H82661

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82661

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <SIM>

A:Cross-references: GB:AE003987; GB:AE003849; NID:g9106634; PIDN:AAF84400.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1591

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 256;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155

Db 65 PAPAEE 71

## RESULT 16

H82648 hypothetical protein XF1697 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C/Accession: H82648

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82648

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <SIM>

A:Cross-references: GB:AE003994; GB:AE003849; NID:g9106756; PIDN:AAF84506.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1697

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 256;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155

Db 65 PAPAEE 71

## RESULT 17

T01305 hypothetical protein T14P8.5 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 14-May-1999

C/Accession: T01305

R:Kitajima, J.; Elliott, G.; Cloud, J.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of A. thaliana T14P8.

A:Reference number: Z14290

A:Accession: T01305  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-262 <KAL>  
A:Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193303  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Map position: 4  
A:Introns: 6/2; 68/3; 121/1; 163/3; 226/1  
A:Note: T14P8.5

Query Match 3.0%; Score 7; DB 2; Length 262;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAAEET 156  
|||  
Db 249 APAAEET 255

RESULT 18  
T13453  
hypothetical protein C08A9.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: T13453  
R:Latreille, P.  
submitted to the EMBL Data Library, December 1995  
A:Description: The sequence of C. elegans cosmid C08A9.  
A:Reference number: Z18353  
A:Accession: T13453  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-263 <LAT>  
A:Cross-references: EMBL:U42844; NID:g1125797; PID:g1125799; PIDN:AAB53817.1; GSPDB:GN04  
A:Experimental source: strain Bristol N2; clone C08A9  
C:Genetics:  
A:Gene: CESP:C08A9.3  
A:Map position: X  
A:Introns: 45/3; 79/3; 128/2

Query Match 3.0%; Score 7; DB 2; Length 263;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLIYVLLI 230  
|||  
Db 116 VLIYVLLI 122

RESULT 19  
T46853  
yibD protein [imported] - Rhodobacter sphaeroides  
C:Species: Rhodobacter sphaeroides  
C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 21-Jul-2000  
C:Accession: T46853  
R:MacKenzie, C.; Simmons, A.E.; Kaplan, S.  
Genetics 153, 525-538, 1999  
A:Title: Multiple chromosomes in bacteria. The Yin and Yang of trp gene localization in  
A:Reference number: Z24108; MUID:99442363  
A:Accession: T46853  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-266 <MAC>  
A:Cross-references: EMBL:AF108766; NID:g4185542; PIDN:AAD09126.1; PID: g4185554  
A:Experimental source: strain 2.4.1  
C:Genetics:  
A:Gene: yibQ  
A:Map position: I

Query Match 3.0%; Score 7; DB 2; Length 266;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAAEE 155  
|||  
Db 37 PAPAAEE 43

RESULT 20  
T06802  
cold acclimation protein WCOR410b - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 08-Oct-1999  
C:Accession: T06802  
R:Danyluk, J.; Sarhan, F.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z15826  
A:Accession: T06802  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-268 <DAN>  
A:Cross-references: EMBL:U73210; NID:g1657842; PIDN:AAB18201.1; PID:g1657843  
A:Experimental source: cv. Norstar; seedling; shoot  
C:Genetics:  
A:Gene: Wcor410b

Query Match 3.0%; Score 7; DB 2; Length 268;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAAEE 155  
|||  
Db 219 PAPAAEE 225

RESULT 21  
S27708  
daunorubicin resistance protein - Streptomyces peucetius  
C:Species: Streptomyces peucetius  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
C:Accession: S27708  
R:Guilloule, P.G.; Hutchinson, C.R.  
submitted to the EMBL Data Library, August 1991  
A:Description: A bacterial analog of the mdr gene of mammalian tumor cells is present  
A:Reference number: S27706  
A:Accession: S27708  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-283 <GUI>  
A:Cross-references: EMBL:M73758; NID:g153228; PIDN:AA74718.1; PID:g153231  
C:Superfamily: Streptomyces peucetius daunorubicin resistance protein  
C:Keywords: transmembrane protein

Query Match 3.0%; Score 7; DB 2; Length 283;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 172 MTTSPTG 178  
|||  
Db 1 MTTSPTG 7

RESULT 22  
T45537  
moab protein [imported] - Agrobacterium tumefaciens plasmid pT115955  
C:Species: Agrobacterium tumefaciens  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 21-Jul-2000  
C:Accession: T45537  
R:Lyti, S.M.; Jafri, S.; Winaas, S.C.  
Mol. Microbiol. 31, 339-347, 1999

A>Title: Mannopinic acid and agropinic acid catabolism region of the octopine-type T1 p  
A:Reference number: Z23002; M0ID:99141607  
A:Accession: T45537  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1313 <LTY>  
A:Cross-references: EMBL:AF03413; NID:92665704; PIDN:AB88473.1; PID:92665713  
A:Experimental source: strain 15955  
C:Genetics:  
A:Gene: moab  
A:Genome: plasmid pT15955  
C:Superfamily: oligopeptide permease protein oppb

Query Match 3.0%; Score 7; DB 2; Length 313;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 IVLLIVF 232  
|||  
Db 149 IVLLIVF 155

RESULT 23  
C81050  
cytochrome c oxidase, chain III NMB1723 [imported] - Neisseria meningitidis (strain MC58)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: C81050  
R:Nettelin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignanl, V.; Pizze, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; Ve  
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: AB1000; M0ID:20157555  
A:Accession: C81050  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-365 <TET>  
A:Cross-references: GB:AE002522; GB:AE002098; NID:97226972; PIDN:AAF42068.1; PID:9722697  
C:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1723

Query Match 3.0%; Score 7; DB 2; Length 365;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAE 154  
|||  
Db 321 TPAPAAE 327

RESULT 24  
F81826  
probable cytochrome c NMA1977 [imported] - Neisseria meningitidis (strain Z2491 serogrou  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: F81826  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jørgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: AB1775; M0ID:20222556  
A:Accession: F81826  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-365 <PAR>  
A:Cross-references: GB:AL162757; GB:AL157959; NID:97380371; PIDN:CAB85197.1; PID:9738066  
C:Experimental source: serogroup A, strain Z2491  
C:Genetics:

A:Gene: NMA1976; NMA1977

Query Match 3.0%; Score 7; DB 2; Length 365;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAE 154  
|||  
Db 321 TPAPAAE 327

RESULT 25  
T01169  
phosphate transport protein, mitochondrial - maize  
C:Species: Zea mays (maize)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 20-Jun-2000  
C:Accession: T01169  
R:Takabatake, R.; Hata, S.; Taniguchi, M.; Kouchi, H.; Sugiyama, T.; Izui, K.  
submitted to the EMBL Data Library, July 1998  
A:Description: Isolation and Characterization of cDNAs Encoding Mitochondrial Phospha  
A:Reference number: Z14251  
A:Accession: T01169  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-366 <TAK>  
A:Cross-references: EMBL:AB016064; PIDN:BAA31583.1  
A:Experimental source: strain H84; root  
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
C:Keywords: mitochondrion

Query Match 3.0%; Score 7; DB 2; Length 366;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAE 154  
|||  
Db 353 TPAPAAE 359

RESULT 26  
T50265  
probable phosphate/phosphoenolpyruvate translocator protein - fission yeast (Schizos  
C:Species: Schizosaccharomyces pombe  
C:Date: 09-Jun-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000  
C:Accession: T50265; T38158  
R:Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, December 1999  
A:Reference number: Z25052  
A:Accession: T50265  
A:Molecule type: DNA  
A:Residues: 1-258 <SAU>  
A:Cross-references: EMBL:AL13498; PIDN:CAB63500.1; GSPDB:GN00066; SPDB:SPAC890.09  
A:Experimental source: strain 972h-?; cosmid c890  
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z21775  
A:Accession: T38158  
A:Molecule type: DNA  
A:Residues: 229-374 <DEV>  
A:Cross-references: EMBL:Z70043; NID:91220275; PIDN:CAA93888.1; GSPDB:GN00066; SPDB:S  
A:Experimental source: strain 972h-?; cosmid c22E12  
C:Genetics:  
A:Gene: SPAC22E12.01; SPDB:SPAC890.09  
A:Map position: 1

Query Match 3.0%; Score 7; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 IVLLIVL 228

Db 52 IIVLVL 58

# RESULT 27

A53773  
la/SS-B homolog D-1a - fruit fly (Drosophila melanogaster)  
C/Species: Drosophila melanogaster  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jul-2000  
C/Accession: A53773  
R/Bai, C.; Li, Z.; Tolias, P.P.  
Mol. Cell. Biol. 14, 5123-5129, 1994  
A/Title: Developmental characterization of a Drosophila RNA-binding protein homologous to  
A/Reference number: A53773; MUID:94309632  
A/Accession: A53773  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-390 <BAI>  
A/Cross-references: GB:U07652; NID:g464019; PIDN:AAA20518.1; PID:g464020  
C/Genetics:  
A/Gene: FlyBase:La  
A/Cross-references: FlyBase:FBgn0011638  
C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology  
C/Keywords: leucine zipper; RNA binding

Query Match 3.0%; Score 7; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
Db 36 PAPAEE 42

# RESULT 28

A53781  
ribonucleoprotein la - fruit fly (Drosophila melanogaster)  
C/Species: Drosophila melanogaster  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 20-Sep-1999  
C/Accession: A53781  
R/Yoo, C.J.; Molin, S.L.  
Mol. Cell. Biol. 14, 5412-5424, 1994  
A/Title: la proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast  
A/Reference number: A53781; MUID:94309661  
A/Accession: A53781  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-390 <YOO>  
A/Cross-references: GB:U32988; NID:g488469; PID:g488470  
C/Genetics:  
A/Gene: FlyBase:La  
A/Cross-references: FlyBase:FBgn0011638  
C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology  
C/Keywords: RNA binding

Query Match 3.0%; Score 7; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
Db 36 PAPAEE 42

# RESULT 29

H7116  
hypothetical protein PH0703 - Pyrococcus horikoshii  
C/Species: Pyrococcus horikoshii  
C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000  
C/Accession: H7116  
R/Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Hainawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu  
DNA Res. 5, 55-76, 1998  
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A/Reference number: A71000; MUID:98344137  
A/Accession: H7116  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-397 <RAM>  
A/Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29794.1; PID:g3257111  
A/Experimental source: strain OT3  
A/Note: this accession replaces an interim accession for a sequence replaced by Genba  
C/Genetics:  
A/Gene: PH0703

Query Match 3.0%; Score 7; DB 2; Length 397;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 227 VLLIVFV 233  
Db 133 VLLIVFV 139

# RESULT 30

S64704  
ornithine decarboxylase (EC 4.1.1.17) - Jimsonweed  
C/Species: Datura stramonium (Jimsonweed; common thornapple)  
C/Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 08-Sep-2000  
C/Accession: S64704; S57484  
R/Michael, A.J.; Furze, J.M.; Rhodes, M.J.C.; Burtin, D.  
Biochem. J. 314, 241-248, 1996  
A/Title: Molecular cloning and functional identification of a plant ornithine decarbo  
A/Reference number: S64704; MUID:96195135  
A/Accession: S64704  
A/Molecule type: mRNA  
A/Residues: 1-431 <MIC>  
A/Cross-references: EMBL:X87847; NID:g871007; PIDN:CAA61121.1; PID:g871008  
C/Superfamily: ornithine decarboxylase  
C/Keywords: carbon-carbon lyase; carboxy-lyase; phosphoprotein; polyamine biosynthesi  
F;94/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 3.0%; Score 7; DB 2; Length 431;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAE 154  
Db 25 TPAPAE 31

# RESULT 31

T21515  
hypothetical protein F28G4.4 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C/Accession: T21515  
R/Mall, M.  
submitted to the EMBL Data Library, March 1997  
A/Reference number: Z19433  
A/Accession: T21515  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-450 <MTL>  
A/Cross-references: EMBL:Z93381; PIDN:CAB07607.1; GSPDB:GN00023; CESP:F28G4.4  
A/Experimental source: clone F28G4  
C/Genetics:  
A/Gene: CESP:F28G4.4  
A/Map position: 5  
A/Introns: 28/3; 52/3; 74/3; 104/3; 233/3; 293/3

Query Match 3.0%; Score 7; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 LIVLIV 230  
|||  
Db 11 LIVLIV 17

## RESULT 32

S12591  
beta-1-adrenergic receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Jun-2000  
C:Accession: S12591; S40185; A36618  
R:Shimomura, H.; Terada, A.  
Nucleic Acids Res. 18, 4591, 1990  
A:Title: Primary structure of the rat beta-1 adrenergic receptor gene.  
A:Reference number: S12591; MUID:90356399  
A:Accession: S12591  
A:Molecule type: DNA  
A:Residues: 1-464 <SH1>  
R:Shimomura, H.; Terada, A.  
Submitted to the EMBL Data Library, July 1991  
A:Reference number: S40185  
A:Accession: S40185  
A:Molecule type: DNA  
A:Residues: 1-25, 'A', 26-174, 'R', 175-464 <SH2>  
A:Cross-references: EMBL:D00634; NID:g220670; PIDN:BAA0057.1; PID:g220671  
R:Michida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Tester, B.; Neve, K.A.; Teal, J. Biol. Chem. 265, 12960-12965, 1990  
A:Title: Molecular cloning and expression of the rat beta-1-adrenergic receptor gene.  
A:Reference number: A36618; MUID:90330633  
A:Accession: A36618  
A:Molecule type: DNA  
A:Residues: 1-26, 'A', 27-160, 'L', 162-174, 'R', 175-264, 'T', 266-464 <MAC>  
A:Cross-references: GB:J05561; NID:g203073; PIDN:AAA40792.1; PID:g203074  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

Query Match 3.0%; Score 7; DB 2; Length 464;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
|||  
Db 66 LIVLIV 72

## RESULT 33

S36794  
beta-1-adrenergic receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 09-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 13-Aug-1999  
C:Accession: S36794  
R:Jasper, J.R.; Link, R.E.; Chruschinski, A.J.; Kobilka, B.K.; Benstein, D.  
Biochim. Biophys. Acta 1178, 307-309, 1993  
A:Title: Primary structure of the mouse beta(1)-adrenergic receptor gene.  
A:Reference number: S36794; MUID:93372116  
A:Accession: S36794  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-466 <UAS>  
A:Cross-references: EMBL:L10084; NID:g293278; PIDN:AAA02929.1; PID:g293279  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

Query Match 3.0%; Score 7; DB 2; Length 466;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
|||  
Db 67 LIVLIV 73

## RESULT 34

S08325  
flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele BzMcC2) - maize  
N:Alternate names: UDPglucose flavonoid glucosyl-transferase  
C:Species: Zea mays (maize)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S08325  
R:Futtek, D.; Schiefelbein, J.W.; Johnston, F.; Nelson Jr., O.E.  
Plant Mol. Biol. 11, 473-481, 1988  
A:Title: Sequence comparisons of three wild-type Bronze-1 alleles from Zea mays.  
A:Reference number: S08324  
A:Accession: S08325  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-471 <FUR>  
A:Cross-references: EMBL:X13501; NID:g22361; PIDN:CAA31856.1; PID:g295854  
C:Genetics:  
A:Gene: Bz1  
A:Introns: 175/1  
C:Superfamily: flavonol O3-glucosyltransferase  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 3.0%; Score 7; DB 1; Length 471;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEET 156  
|||  
Db 83 APAEET 89

## RESULT 35

S01052  
flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele Bz-Mcc) - maize  
N:Alternate names: UDPglucose flavonoid glucosyltransferase  
C:Species: Zea mays (maize)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 18-Jun-1999  
C:Accession: S01052; S08324  
R:Raiston, E.J.; English, J.J.; Dooner, H.K.  
Genetics 119, 185-197, 1988  
A:Title: Sequence of three bronze alleles of maize and correlation with the genetic f  
A:Reference number: S01037; MUID:88284304  
A:Accession: S01052  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-471 <RAL>  
A:Cross-references: EMBL:X07940; NID:g22204; PIDN:CAA30761.1; PID:g22205  
R:Futtek, D.; Schiefelbein, J.W.; Johnston, F.; Nelson Jr., O.E.  
Plant Mol. Biol. 11, 473-481, 1988  
A:Title: Sequence comparisons of three wild-type Bronze-1 alleles from Zea mays.  
A:Reference number: S08324  
A:Accession: S08324  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-471 <FUR>  
A:Cross-references: EMBL:X13500; NID:g22364; PIDN:CAA31855.1; PID:g1030071  
C:Genetics:  
A:Gene: Bz1  
A:Map position: 9  
A:Introns: 175/1  
C:Superfamily: flavonol O3-glucosyltransferase  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 3.0%; Score 7; DB 2; Length 471;  
Best Local Similarity 100.0%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEET 156  
|||||||  
Db 83 APAEET 89

RESULT 36  
ORF01  
beta-1-adrenergic receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 22-Jan-1993 #sequence\_revision 18-Aug-1995 #text\_change 22-Jun-1999  
C:Accession: A39911  
R:Fielle, T.; Collins, S.; Daniel, K.W.; Caron, M.G.; Lefkowitz, R.J.; Kobilka, B.K.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7920-7924, 1987  
A:Title: Cloning of the cDNA for the human beta-1-adrenergic receptor.  
A:Reference number: A39911; MUID:88068509  
A:Accession: A39911  
A:Molecule type: mRNA  
A:Residues: 1-477 <FRI>  
A:Cross-references: GB:J03019; NID:g178199; PIDN:AAA51667.1; PID:g178200  
C:Genetics:  
A:Gene: GDB:ADRB1; ADRB1R  
A:Cross-references: GDB:119654; OMIM:109630  
A:Map position: 10q25-10q25  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F:58-84/Domain: transmembrane #status predicted <TM1>  
F:94-121/Domain: transmembrane #status predicted <TM2>  
F:133-154/Domain: transmembrane #status predicted <TM3>  
F:177-199/Domain: transmembrane #status predicted <TM4>  
F:224-245/Domain: transmembrane #status predicted <TM5>  
F:325-346/Domain: transmembrane #status predicted <TM6>  
F:358-377/Domain: transmembrane #status predicted <TM7>  
F:15/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.0%; Score 7; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLIV 231  
|||||||  
Db 67 LIVLIV 73

RESULT 37  
I53053  
beta 1 adrenergic receptor - rhesus macaque  
C:Species: Macaca mulatta (rhesus macaque)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C:Accession: I53053  
R:Searles, R.P.; Nipper, V.J.; Machida, C.A.  
DNA Seq. 4, 231-241, 1994  
A:Title: The rhesus macaque beta 1-adrenergic receptor gene: structure of the gene and  
A:Reference number: I53053; MUID:95078456  
A:Accession: I53053  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-480 <RES>  
A:Cross-references: EMBL:X75540; NID:g510532; PIDN:CAA53228.1; PID:g510533  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: neurotransmitter receptor

Query Match 3.0%; Score 7; DB 2; Length 480;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLIV 231  
|||||||  
Db 67 LIVLIV 73

RESULT 38  
F95238  
PTS system, membrane component, probable [imported] - Streptococcus pneumoniae (strain  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
C:Accession: F95238  
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: F95238  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-485 <KUR>  
A:Cross-references: GB:AE005672; PIDN:AAK76103.1; PID:g14973548; GSPDB:GN00164; TIGR:  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP2038

Query Match 3.0%; Score 7; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLIVF 232  
|||||||  
Db 358 IVLIVF 364

RESULT 39  
G98102  
hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
C:Accession: G98102  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.  
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: G98102  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-508 <KUR>  
A:Cross-references: GB:AE007317; PIDN:AAU00652.1; PID:g15459539; GSPDB:GN00174  
C:Genetics:  
A:Gene: PTS-EII

Query Match 3.0%; Score 7; DB 2; Length 508;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLIVF 232  
|||||||  
Db 381 IVLIVF 387

RESULT 40  
JC7391  
Ca2+-binding protein, DD4 - prawn  
N:Alternate names: DD4 protein  
C:Species: Marsupenaeus japonicus  
C>Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 18-Jul-2001  
C:Accession: JC7391  
R:Endo, H.; Persson, P.; Watanabe, T.  
Biochem. Biophys. Res. Commun. 276, 286-291, 2000



A:Title: Molecular cloning of the crustacean Dp4 cDNA encoding a Ca<sup>2+</sup>-binding protein.  
A:Reference number: JG7391; MUID:20462952; PMID:11006119  
A:Accession: JG7391  
A:Molecule type: mRNA  
A:Residues: 1-542 <END>  
C:Comment: This protein, acidic and proline-rich, is involved in the calcification process.  
C:Genetics:  
A:Gene: dd4  
C:Keywords: calcium binding

Query Match 3.0%; Score 7; DB 2; Length 542;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 TVERPAA 138  
|||||  
Db 13 TVERPAA 19

## RESULT 41

hypothetical protein SSO3099 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C:Accession: D90493  
R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Anayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: D90493  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-548 <KUR>  
A:Cross-references: GB:AE006641; NID:913816517; PIDN:AAK43203.1; GSPDB:GN00155  
C:Genetics:  
A:Gene: SSO3099

Query Match 3.0%; Score 7; DB 2; Length 548;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIIV 227  
|||||  
Db 530 GIIVLIIV 536

## RESULT 42

hypothetical protein RV0538 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: E70546  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garfield, T.; Churcher, C.; Harris, D.; Gordon, S.  
Rajandream, M.A.; Rogers, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987  
A:Accession: E70546  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-548 <COL>  
A:Cross-references: GB:Z95558; GB:AL123456; NID:93261781; PIDN:CAB08989.1; PID: e316975;  
C:Genetics:  
A:Experimental source: strain H37RV  
A:Gene: RV0538

Query Match 3.0%; Score 7; DB 2; Length 548;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QOTVAPQ 16  
|||||  
Db 517 QOTVAPQ 523

## RESULT 43

T42100  
serine/threonine protein kinase (Ec 2.7.1.-) - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: T42100  
R:Bakal, C.J.; Davies, J.E.  
submitted to the EMBL Data Library, September 1998  
A:Description: Cloning, nucleotide sequence and expression of a serine/threonine prot  
A:Reference number: 222067  
A:Accession: T42100  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-556 <BAK>  
A:Cross-references: EMBL:AF094711; PIDN:AA064406.1  
C:Genetics:  
A:Note: pksc  
C:Superfamily: Synechocystis sp. protein kinase, 58K; protein kinase homology  
C:Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match 3.0%; Score 7; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 GTPAPAA 153  
|||||  
Db 347 GTPAPAA 353

## RESULT 44

T36502  
serine/threonine protein kinase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: T36502  
R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.  
submitted to the EMBL Data Library, July 1999  
A:Reference number: 221608  
A:Accession: T36502  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-556 <SAU>  
A:Cross-references: EMBL:AL096822; PIDN:CAB46944.1; GSPDB:GN00070; SCODB:SCGD3.22  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: pksc; SCODB:SCGD3.22  
C:Superfamily: Synechocystis sp. protein kinase, 58K; protein kinase homology

Query Match 3.0%; Score 7; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 GTPAPAA 153  
|||||  
Db 347 GTPAPAA 353

## RESULT 45

H83085  
conserved hypothetical protein PA4491 [imported] - Pseudomonas aeruginosa (strain PAO  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C;Accession: H83085  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337  
A;Accession: H83085  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-589 <SNO>  
A;Cross-references: GB:AE004862; GB:AE004091; NID:9950716; PIDN:AA07879.1; GSPDB:GN001  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA4491  
C;Superfamily: *Escherichia coli* yfaA protein

Query Match 3.0%; Score 7; DB 2; Length 589;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 147 TPAPAA 153  
|||||||  
Db 12 TPAPAA 18

RESULT 46  
H65057  
sulfite reductase (NADPH) (EC 1.8.1.2) flavoprotein beta chain - *Escherichia coli*  
C;Species: *Escherichia coli*  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 15-Oct-1999  
C;Accession: H65057; B34231; I41185  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shapiro, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of *Escherichia coli* K-12.  
A;Reference number: A64720; MUID:9742617  
A;Accession: H65057  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A;Residues: 1-599 <BIAT>  
A;Cross-references: GB:AE000360; GB:U00096; NID:92367157; PIDN:AA075806.1; PID:91789123;  
A;Experimental source: strain K-12, substrain MG1655  
R;Ostrowski, J.; Barber, M.J.; Rueger, D.C.; Miller, B.E.; Siegel, L.M.; Kredich, N.M.  
J. Biol. Chem. 264, 15796-15808, 1989  
A;Title: Characterization of the flavoprotein moieties of NADPH-sulfite reductase from *S. typhimurium* DT104  
ed from DNA sequence of cyst, and comparison with NADPH-cytochrome P-450 reductase.  
A;Reference number: A92735; MUID:89380164  
A;Accession: B34231  
A:Molecule type: DNA  
A;Residues: 1-155; 'T', 157-267, 'L', 269-507, 'E', 509-599 <OST>  
A;Cross-references: GB:M23008; NID:9145679; PIDN:AAA23650.1; PID:9145680; GB:J05025; GB:R;London, J.A.; Loughlin, R.E.  
Gene 122, 17-25, 1992  
A;Title: Mutagenesis and regulation of the cyst promoter of *Escherichia coli* K-12.  
A;Reference number: I41185; MUID:93083978  
A;Accession: I41185  
A;Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A;Residues: 1-29 <RES>  
A;Cross-references: GB:M65058; NID:9145677; PIDN:AAA23649.1; PID:9145678  
C;Genetics:  
A;Gene: *cysJ*  
C;Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH--ferrithemoprotein F;64-598/Domain: NADPH--ferrithemoprotein reductase homology <FEH>  
F;64-598/Domain: NADPH--ferrithemoprotein reductase homology <FEH>  
F;66-205/Domain: flavodoxin homology <FLX>

Query Match 3.0%; Score 7; DB 1; Length 599;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 148 TPAPAAE 154  
|||||||  
Db 54 TPAPAAE 60

RESULT 47  
C91081  
sulfite reductase (NADPH) beta subunit [imported] - *Escherichia coli* (strain O157:H7,  
C;Species: *Escherichia coli*  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 24-Aug-2001  
C;Accession: C91081  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.  
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and 9  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: C91081  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-599 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA837042.1; PID:913363090; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: EC53619  
C;Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH--ferrithemoprotein  
C;Keywords: flavoprotein

Query Match 3.0%; Score 7; DB 2; Length 599;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 148 TPAPAAE 154  
|||||||  
Db 54 TPAPAAE 60

RESULT 48  
D85926  
sulfite reductase (NADPH) beta subunit [imported] - *Escherichia coli* (strain O157:H7,  
C;Species: *Escherichia coli*  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 27-Nov-2001  
C;Accession: D85926  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallmalis, K.; Apoda  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A;Reference number: A83480; MUID:21074935; PMID:11206351  
A;Accession: D85926  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-599 <SNO>  
A;Cross-references: GB:AE005174; NID:912517225; PIDN:AA057872.1; GSPDB:GN00145; UMGPR:  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: *cysJ*  
C;Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH--ferrithemoprotein  
C;Keywords: flavoprotein

Query Match 3.0%; Score 7; DB 2; Length 599;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 148 TPAPAAE 154  
|||||||  
Db 54 TPAPAAE 60

RESULT 49  
T47484  
receptor like protein kinase - *Arabidopsis thaliana*

N;Alternate names: protein F9K21.20  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 02-Sep-2000  
 C;Accession: T47484  
 R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.  
 submitted to the Protein Sequence Database, February 2000  
 A;Reference number: Z24467  
 A;Accession: T47484  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-669 <JDR>  
 A;Cross-references: EMBL:AL138657  
 A;Experimental source: cultivar Columbia; BAC clone F9K21  
 C;Genetics:  
 A;Map position: 3  
 A;Note: F9K21.20  
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold

Query Match 3.0%; Score 7; DB 2; Length 669;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 VLIIVLI 230  
 |||||  
 Db 287 VLIIVLI 293

## RESULT 50

T12712  
 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Clerodendrum incisum chloroplast  
 C;Species: chloroplast Clerodendrum incisum  
 C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 11-Jan-2000  
 C;Accession: T12712  
 R;Steeane, D.A.; Scotland, R.W.; Mabbertley, D.J.; Wagstaff, S.J.; Reeves, P.A.; Olmstead,  
 submitted to the EMBL Data Library, July 1996  
 A;Description: Phylogenetic relationships of Clerodendrum s.l. (Lamiaceae) inferred from  
 A;Reference number: Z17577  
 A;Accession: T12712  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-694 <STP>  
 A;Cross-references: EMBL:LA9156; NID:q1448957; PID:q1448958; PIDN:AA04624.1  
 C;Genetics:  
 A;Genome: chloroplast  
 A;Note: ndhF  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
 C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 3.0%; Score 7; DB 2; Length 694;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 VGIIVLI 226  
 |||||  
 Db 95 VGIIVLI 101

Search completed: August 13, 2002, 08:38:52  
 Job time: 176 sec



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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:38:01 ; Search time 11.26 Seconds  
(without alignments)  
801.213 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_27\_259  
Perfect score: 233  
Sequence: 1 TTARQEEVPOQTVAPOQQRH.....YLSCIVGIIVLLIVFV 233

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 5

Total number of hits satisfying chosen parameters: 3416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	233	100.0	259	1	T10C_HUMAN
2	14	6.0	386	1	T10D_HUMAN
3	8	3.4	440	1	T10B_HUMAN
4	7	3.0	199	1	FLGH_THEMA
5	7	3.0	205	1	YJ11_MYCTU
6	7	3.0	275	1	TFZD_ARTSF
7	7	3.0	283	1	DRRB_STRPE
8	7	3.0	374	1	YD1L_SCHPO
9	7	3.0	390	1	LA_DROME
10	7	3.0	431	1	DCOR_DATST
11	7	3.0	466	1	BLAR_MOUSE
12	7	3.0	466	1	BLAR_RAT
13	7	3.0	468	1	BLAR_PIG
14	7	3.0	468	1	T10A_HUMAN
15	7	3.0	471	1	UF01_MAIZE
16	7	3.0	471	1	UF02_MAIZE
17	7	3.0	473	1	BLAR_CANFA
18	7	3.0	474	1	BLAR_FELCA
19	7	3.0	477	1	BLAR_HUMAN
20	7	3.0	480	1	BLAR_MACMU
21	7	3.0	584	1	PARF_PARTE
22	7	3.0	598	1	CYSJ_ECOLI
23	7	3.0	1036	1	YANZ_SCHPO
24	7	3.0	1177	1	DP3A_STRCO
25	7	3.0	1179	1	DP3A_STRCO
26	7	3.0	1184	1	DP3A_MYCTU
27	7	3.0	1637	1	MRSP_STRAU
28	7	3.0	1835	1	CCAI_RAT
29	7	3.0	1856	1	MGA_HUMAN
30	6	2.6	50	1	RS14_METHN
31	6	2.6	54	1	TATA_RICPR
32	6	2.6	62	1	Y416_ARCFU
33	6	2.6	89	1	IAPP_FELCA

34	6	2.6	95	1	RL25_BUCAI	P57238 buchnera ap
35	6	2.6	110	1	RLA1_ALTPA	P49148 alternaria
36	6	2.6	110	1	RLA2_SCHPO	P08094 schizosacch
37	6	2.6	111	1	RL12_ARPE	O99999 aeropyrum p
38	6	2.6	111	1	RLA2_BRAFL	O01725 brachiosteo
39	6	2.6	117	1	HV1B_HUMAN	P01743 homo sapien
40	6	2.6	124	1	MUTP_BUCAI	P57298 buchnera ap
41	6	2.6	128	1	Y192_RICPR	O99999 rickettsia
42	6	2.6	134	1	TYRT_STRGA	P55047 streptomyce
43	6	2.6	139	1	PSAD_OPOST	P49481 odontella s
44	6	2.6	139	1	PSAD_SKECO	O96800 skeletonema
45	6	2.6	140	1	PSAD_SYNY3	P19569 synchocyst
46	6	2.6	141	1	PSAD_GUTTH	O78502 guillardia
47	6	2.6	144	1	EXBD_NEIMA	O06434 neisseria g
48	6	2.6	144	1	EXBD_NEIMA	P95376 neisseria m
49	6	2.6	157	1	SMG_BUCAI	P57562 buchnera ap
50	6	2.6	157	1	WH16_STRCO	P23157 streptomyce
51	6	2.6	183	1	OLEC_BRANA	P29526 brassica na
52	6	2.6	185	1	RL10_STRGR	P36213 streptomyce
53	6	2.6	189	1	RL6_SULAC	O05637 sulfolobus
54	6	2.6	190	1	YBAY_ECOLI	P77171 escherichia
55	6	2.6	190	1	B3G1_MOUSE	O99999 m galactosy
56	6	2.6	202	1	LYCA_BPAV1	P33486 lactococcus
57	6	2.6	204	1	RS8_GRIYA	O92556 griffithsia
58	6	2.6	205	1	PSAD_HORVU	P36213 hordeum vul
59	6	2.6	207	1	RS8_HUMAN	P09058 homo sapien
60	6	2.6	210	1	RS8_ARATH	O99999 arabidopsis
61	6	2.6	211	1	YREF_MYCTU	P50050 mycobacteri
62	6	2.6	211	1	YREF_MYCTU	O28047 archaeglob
63	6	2.6	212	1	PSAD_SPTOL	P12353 spinachia ol
64	6	2.6	214	1	LIPIB_CYACA	O19898 cyanidium c
65	6	2.6	218	1	IM23_SCHYA	P27591 schistosoma
66	6	2.6	219	1	DEDA_ECOLI	P09548 escherichia
67	6	2.6	220	1	RS8_ORYSA	P49199 oryza sativ
68	6	2.6	221	1	MR_DROME	P18432 drosophila
69	6	2.6	221	1	RS8_DROME	O08009 zea mays (m
70	6	2.6	221	1	RS8_MAIZE	O01361 prunus arme
71	6	2.6	221	1	YL24_CAEEL	P34417 caenorhabdi
72	6	2.6	224	1	H11L_CHICK	P08287 gallus gall
73	6	2.6	228	1	VP25_NPVAC	P14483 onchophora
74	6	2.6	230	1	YF23_CAEEL	O09282 caenorhabdi
75	6	2.6	239	1	KGDA_MYCPN	P73536 mycoplasma
76	6	2.6	245	1	X123_HUMAN	O15884 homo sapien
77	6	2.6	247	1	SNGL_CAEEL	O76735 caenorhabdi
78	6	2.6	250	1	YC97_HUMAN	O09355 homo sapien
79	6	2.6	252	1	AROD_SALEN	O99999 salmonella
80	6	2.6	252	1	AROD_SALEN	P58667 salmonella
81	6	2.6	252	1	CAH_NETGO	O50940 neisseria g
82	6	2.6	256	1	Y107_NPVOP	O10346 oryza pseu
83	6	2.6	257	1	TRPC_AOUAE	O67657 aquilex aeo
84	6	2.6	261	1	LPRE_MYCTU	P71798 mycobacteri
85	6	2.6	266	1	FEA2_RAT	O63558 rattus norv
86	6	2.6	269	1	LGT_BACSU	O34752 bacillus su
87	6	2.6	270	1	FEA2_HUMAN	P15927 homo sapien
88	6	2.6	270	1	FEA2_MOUSE	O62193 mus musculu
89	6	2.6	271	1	TNR4_RAT	P15725 rattus norv
90	6	2.6	275	1	NH3_AZOVI	P16269 azotobacter
91	6	2.6	279	1	STX_ARATH	O39233 arabidopsis
92	6	2.6	280	1	MACS_CHICK	P16577 gallus gall
93	6	2.6	290	1	YGLD_YEAST	P53212 saccharomyc
94	6	2.6	293	1	YFIE_ECOLI	P33634 escherichia
95	6	2.6	294	1	DPM1_USYMA	O94816 mus musculu
96	6	2.6	295	1	MTLS_MOUSE	P32667 escherichia
97	6	2.6	301	1	YJIE_ECOLI	O58280 methanococ
98	6	2.6	308	1	YB80_METJA	P39667 dictyostell
99	6	2.6	310	1	SUCA_DICDI	P81127 bos taurus
100	6	2.6	312	1	SNAG_BOVIN	P03208 epstein-bar
101	6	2.6	312	1	VMEW_EBV	P52223 clostridium
102	6	2.6	315	1	TRXB_CLOLI	O13667 homo sapien
103	6	2.6	317	1	O2F1_HUMAN	O95006 homo sapien
104	6	2.6	317	1	O2F2_HUMAN	P16500 streptomyce
105	6	2.6	324	1	CYRK_STRVN	O14662 homo sapien
106	6	2.6	324	1	STXF_HUMAN	

107	6	2.6	330	1	FEPG_ECOLI	P23877	escherichia	180	504	1	TPM5_DROME	P49456	drosophila
108	6	2.6	334	1	B3G1_HUMAN	O3P247	homo sapien	181	505	1	GLPK_PSEAE	O01390	pseudomonas
109	6	2.6	334	1	B3G1_RAT	O3P2789	r galactosy	182	507	1	LAT1_HUMAN	O01630	homo sapien
110	6	2.6	338	1	RLA0_HUMAN	P54049	methanococc	183	508	1	FAS3_DROME	P15278	drosophila
111	6	2.6	339	1	Y392_MERJA	O57837	methanococc	184	508	1	BAE2_HUMAN	O93520	homo sapien
112	6	2.6	344	1	RLA0_AERPE	O57968	aeropyrum p	185	519	1	RHO_TREPA	O83281	treponema p
113	6	2.6	347	1	YK21_YEAST	P14551	streptomyces	186	522	1	CAIC_ECOLI	P31552	escherichia
114	6	2.6	353	1	TKR_STRIM	O02209	saccharomyc	187	525	1	NAB2_YEAST	P32505	saccharomyc
115	6	2.6	356	1	TSU_DROME	P40689	drosophila	188	537	1	MYPH_CHICK	O05633	gallus gall
116	6	2.6	357	1	TF35_HUMAN	O00303	homo sapien	189	543	1	BCHB_RHOGE	O91993	rhodocyclus
117	6	2.6	362	1	FIIBP_ADR09	P36846	human adeno	190	544	1	ODP2_ACHTA	P35499	achtolepiasm
118	6	2.6	366	1	DHLE_BACE	O39194	dacillus ce	191	547	1	Y966_TREPA	O83932	treponema p
119	6	2.6	367	1	BRB2_RABIT	O28612	oryctolagus	192	547	1	MCPC_SALTU	O02755	salmonella
120	6	2.6	372	1	BRB2_CAYPO	O70526	cavia porce	193	547	1	ODP2_PSEAE	O59638	pseudomonas
121	6	2.6	372	1	VGLI_HSV23	P06746	herpes simp	194	548	1	AMT4_PSEAE	P13507	pseudomonas
122	6	2.6	372	1	VGLI_HSV2H	P13291	herpes simp	195	549	1	SMF2_YEAST	P38778	saccharomyc
123	6	2.6	374	1	MTEF_NEIGO	O59606	neisseria g	196	551	1	AMT4_PSESA	P22963	saccharomyc
124	6	2.6	377	1	DHLE_BACST	P13154	dacillus st	197	554	1	SHT1_DROME	P20905	drosophila
125	6	2.6	381	1	VATC_MERJA	O37672	methanococc	198	554	1	ACH3_CAEEL	P54244	caenorhabd1
126	6	2.6	383	1	AMC1_ORYSA	P27940	oryza sativ	199	564	1	FRP1_SCHPO	O04800	schizosacch
127	6	2.6	385	1	TGT_PASMU	P57831	pasteurella	200	569	1	SOT1_SPIOL	O41364	splinacla ol
128	6	2.6	388	1	P2X4_HUMAN	O95571	homo sapien	201	575	1	PTI_ECOLI	P08839	escherichia
129	6	2.6	391	1	MSEB_HUMAN	P30411	homo sapien	202	575	1	PTI_SALTU	P51254	escherichia
130	6	2.6	391	1	MSEB_HUMAN	O00557	homo sapien	203	599	1	RP2P_DROST	P24629	drosophila
131	6	2.6	395	1	CDSA_MTCPN	P75160	m putative	204	604	1	VE1_HPV38	O80909	human papil
132	6	2.6	408	1	LMP1_BOVIN	O05204	bos taurus	205	606	1	SP2_HUMAN	O02086	homo sapien
133	6	2.6	410	1	NEUS_HUMAN	O99574	homo sapien	206	610	1	POUC_BRARE	P13167	brachydanio
134	6	2.6	410	1	NEUS_MOUSE	O35684	mus musculu	207	613	1	MDU1_ECOLI	P33607	escherichia
135	6	2.6	410	1	NEUS_RAT	O91182	rattus norv	208	620	1	MUT1_TREPA	O83325	treponema p
136	6	2.6	415	1	KLIF_MOUSE	O9EPW2	mus musculu	209	635	1	VP40_HSV11	P10210	herpes simp
137	6	2.6	419	1	RHO_NEIGO	O06447	neisseria g	210	637	1	ODP2_AZOVI	P10802	azotobacter
138	6	2.6	419	1	RHO_PSEFL	O26457	pseudomonas	211	640	1	SCAA_RABIT	O97741	oryctolagus
139	6	2.6	420	1	RHO_HAEIN	P44619	haemophilus	212	642	1	PHSA_STRAT	O53632	streptomyces
140	6	2.6	420	1	SECY_HELPT	O92159	helicobacte	213	656	1	YK79_MYCTU	O10667	mycobacteri
141	6	2.6	420	1	SECY_HELPT	O25879	helicobacte	214	660	1	YH11_EBY	P03181	epstein-bar
142	6	2.6	422	1	RHO_RHOSH	P52156	rhodobacter	215	662	1	ABPA_STRLI	P53627	streptomyces
143	6	2.6	427	1	RHO_BACSU	O03222	dacillus su	216	662	1	YRW3_CAEEL	O09353	caenorhabd1
144	6	2.6	428	1	AMV1_ORYSA	P17654	oryza sativ	217	665	1	ATKB_TREAC	P57700	thermoplasm
145	6	2.6	433	1	RHO_CHRYT	P52152	chromatium	218	665	1	ENV_MLVAD	P11268	radiation m
146	6	2.6	434	1	Y830_THEMA	O9wz17	thermotoga	219	665	1	ENV_MLVAK	P31794	radiation m
147	6	2.6	439	1	Y441_BUCAI	P57516	buchnera ap	220	669	1	ENV_MLVAV	P03386	akv murine
148	6	2.6	445	1	DSDX_ECOLI	P08555	escherichia	221	671	1	P5CS_VIGAC	P32286	delta 1-p
149	6	2.6	453	1	Y259_MYCPN	P75419	mycoplasma	222	684	1	P5PSA_METTH	O27180	methanobact
150	6	2.6	455	1	ACHO_CHICK	P43679	gallus gall	223	700	1	FLHA_CAUCR	O03845	caulobacter
151	6	2.6	457	1	RHO_RICPR	O9Zd24	ricketsia	224	703	1	CDGT_BACS2	P31746	caulobacter
152	6	2.6	458	1	ACHO_HUMAN	O05901	homo sapien	225	707	1	PET1_RABIT	P36836	oryctolagus
153	6	2.6	458	1	YGEH_ECOLI	P76139	escherichia	226	708	1	PET1_HUMAN	P46059	homo sapien
154	6	2.6	461	1	ATOC_ECOLI	O06065	escherichia	227	710	1	PET1_RAT	P51574	rattus norv
155	6	2.6	461	1	SE12_CAEEL	P52156	caenorhabd1	228	712	1	ENV_HV2S2	P32536	human immun
156	6	2.6	461	1	Y4SH_RHISN	P55651	rhizobium s	229	716	1	P5CS_ORYSA	O04226	delta 1-p
157	6	2.6	461	1	Y40A_RHISN	O53195	rhizobium s	230	717	1	P5C1_ARATH	P54867	delta 1-p
158	6	2.6	462	1	PNTB_ECOLI	P07002	escherichia	231	719	1	P5CS_MESCR	O54361	delta 1-p
159	6	2.6	462	1	SYG_TREPA	O83678	treponema p	232	722	1	Z211_HUMAN	O9P2P4	homo sapien
160	6	2.6	463	1	YAD4_YEAST	P28003	saccharomyc	233	726	1	P5C2_ARATH	P54888	delta 1-p
161	6	2.6	463	1	YKAA_YEAST	P30267	dacillus ti	234	735	1	ADDA_MOUSE	O99400	rattus norv
162	6	2.6	464	1	ACHO_RAT	P12331	rattus norv	235	735	1	ADDA_MOUSE	O99400	rattus norv
163	6	2.6	466	1	ACHP_CARAV	P18257	carassius a	236	753	1	PPSA_ARCFU	O29548	archaeoglob
164	6	2.6	467	1	B1AR_BOVIN	O9t16	bos taurus	237	757	1	HUNB_DROSE	O62538	drosophila
165	6	2.6	467	1	B1AR_SHEEP	O28927	ovis aries	238	758	1	HUNB_DROME	P05084	drosophila
166	6	2.6	471	1	UEO3_MAIZE	P16157	zea mays (m	239	759	1	CHLD_ARATH	O95161	arabidopsis
167	6	2.6	473	1	PHDK_NOSK	O24723	nocardioides	240	759	1	HUNB_DROYA	O62541	drosophila
168	6	2.6	476	1	P09368	P09368	saccharomyc	241	764	1	DSHA_HUMAN	P40879	homo sapien
169	6	2.6	491	1	APM4_YEAST	O99186	saccharomyc	242	764	1	TRSH_CANFA	P14763	caus fami1
170	6	2.6	491	1	CD5_RAT	P51882	rattus norv	243	767	1	HUNB_DROOR	O62537	drosophila
171	6	2.6	493	1	PBI3_RAT	O35568	rattus norv	244	774	1	AD28_MOUSE	O91166	mus musculu
172	6	2.6	494	1	CD5_MOUSE	P13379	mus musculu	245	778	1	RG12_MOUSE	O61193	mus musculu
173	6	2.6	497	1	PSD3_SCHPO	O42897	schizosacch	246	826	1	VILI_HUMAN	P09337	homo sapien
174	6	2.6	497	1	VHS_HSEVB	P28957	equine herp	247	826	1	VILI_MOUSE	O62468	mus musculu
175	6	2.6	498	1	VGLY_LYCYA	P09991	lymphocytic	248	830	1	SREC_HUMAN	O14016	homo sapien
176	6	2.6	501	1	GLPK_ECOLI	P08859	escherichia	249	836	1	YIAK_CAEEL	O20076	caenorhabd1
177	6	2.6	502	1	GLPK_HAEIN	P44400	haemophilus	250	837	1	GCL2_HUMAN	O92830	homo sapien
178	6	2.6	502	1	GLPK_PASMU	P57944	pasteurella	251	853	1	ADG_USTWA	O99128	ustilago ma
179	6	2.6	503	1	GLPK_PSETO	O87924	pseudomonas	252	853	1	VMTB_LAMBD	P03736	bacterioph

253	6	2.6	859	1	ENV_HV2CA	P24105	human	immun	326	5	2.1	66	1	LHA2_RHOA	P35102	rhodopseudo
254	6	2.6	859	1	ENV_HV2ST	P20872	human	immun	327	5	2.1	66	1	MT3_MALDO	024059	malus domes
255	6	2.6	855	1	RPA1_MERTW	P09846	methanobact		328	5	2.1	67	1	MTB_SPHGR	026496	sphaerecthin
256	6	2.6	876	1	AREA_EMENTI	P17429	emeritella		329	5	2.1	67	1	REF1_STRGC	P47980	streptococc
257	6	2.6	885	1	CHB_SERNA	Q54468	serattia ma		330	5	2.1	67	1	SCL3_LEIOH	P56678	leiturus qui
258	6	2.6	885	1	VGLB_HSV2S	P24994	herpes simp		331	5	2.1	67	1	TATA_NEIMA	P57048	neisseria m
259	6	2.6	892	1	IF2_CHLIR	O84088	chlamydia t		332	5	2.1	68	1	EPUB_STRPN	0003159	streptococc
260	6	2.6	904	1	VGLB_HSV1K	P06437	herpes simp		333	5	2.1	70	1	GBG1_DROME	P80400	droscophila
261	6	2.6	923	1	RELI_SCHPO	O92380	schizosacch		334	5	2.1	70	1	S1FA_SPTOL	P42552	spiniacia ol
262	6	2.6	963	1	CHC1_HUMAN	O9h158	homo sapien		335	5	2.1	72	1	HP11_ECTVA	P3891	ectothiorho
263	6	2.6	970	1	Y277_MYGE	Q49409	mycoplasma		336	5	2.1	75	1	MER1_EUPRA	P10774	euploetes ra
264	6	2.6	999	1	DSG3_HUMAN	P32926	homo sapien		337	5	2.1	75	1	PM22_BOVIN	Q9tq43	mus tauros
265	6	2.6	1002	1	YA37_ANASP	P58612	anabena sp		338	5	2.1	76	1	RPON_ARCFU	Q29135	archaeoglob
266	6	2.6	1008	1	MMLA_MYCLE	Q49619	mycobacteri		339	5	2.1	76	1	S1FA_ARATH	P42552	arabidopsi
267	6	2.6	1080	1	HDC_DROME	O9n288	droscophila		340	5	2.1	77	1	MT2B_ARATH	P38805	arabidopsi
268	6	2.6	1111	1	YTER_HAETN	O57352	haemophilus		341	5	2.1	77	1	MT2_VICRA	Q41657	vicia faba
269	6	2.6	1134	1	VGLM_HANTH	P16433	hantaa vir		342	5	2.1	79	1	MT2_CICAR	Q39493	cicer ariet
270	6	2.6	1135	1	VGLM_HANTV	P16853	hantaan vir		343	5	2.1	79	1	VG8_SPVIR	P15899	spiroplasma
271	6	2.6	1135	1	VGLM_HANTV	P08668	hantaan vir		344	5	2.1	80	1	MT21_BRAJU	P56168	brassica ju
272	6	2.6	1141	1	CN3A_HUMAN	Q14432	homo sapien		345	5	2.1	80	1	MT23_BRAJU	P56170	brassica ju
273	6	2.6	1166	1	L2GL_DROPS	O08470	droscophila		346	5	2.1	80	1	MT25_BRAJU	P56172	brassica ju
274	6	2.6	1169	1	YK82_YEAST	P36170	saccharomyc		347	5	2.1	80	1	MT2_RICCO	P30564	ricinus com
275	6	2.6	1171	1	TR12_STRCO	Q3K909	streptomyc		348	5	2.1	81	1	NED8_HUMAN	Q15843	homo sapien
276	6	2.6	1188	1	PPSA_METJA	Q57962	methanococc		349	5	2.1	81	1	NED8_MOUSE	P29595	mus musculu
277	6	2.6	1244	1	YP83_CABEL	Q09441	caenorhabdi		350	5	2.1	82	1	CEP_VIBCH	Q9K333	vibriio chol
278	6	2.6	1274	1	MYPC_HUMAN	Q14896	homo sapien		351	5	2.1	82	1	DNAT_STRAL	P66457	streptomyc
279	6	2.6	1311	1	AFRX_DROME	O9q9n5	droscophila		352	5	2.1	82	1	MT2B_LYCES	O40158	lycoperisico
280	6	2.6	1329	1	FTSK_ECOLI	P46889	escherichia		353	5	2.1	83	1	OADC_KLEPN	P13155	klebsiella
281	6	2.6	1477	1	YOR1_YEAST	P33049	saccharomyc		354	5	2.1	84	1	ATPL_VIBAL	P12991	vibriio algi
282	6	2.6	1579	1	PEP1_YEAST	P32319	saccharomyc		355	5	2.1	84	1	ES1B_RANES	P40848	rana esculie
283	6	2.6	1902	1	P1P_IACLC	P16271	lactococcu		356	5	2.1	84	1	IMM3_ECOLI	P02994	escherichia
284	6	2.6	1902	1	P2P_IACPA	O02470	lactobacill		357	5	2.1	85	1	SCXE_BURCI	P17254	buthus occi
285	6	2.6	1902	1	P3P_IACIC	P15232	lactococcu		358	5	2.1	86	1	AMP_AMACA	P27275	amaranthus
286	6	2.6	1957	1	YD86_SCIPO	Q10411	schistosach		359	5	2.1	87	1	PTHP_STRBO	Q6KX8	streptococc
287	6	2.6	2499	1	MPRI_BOVIN	P08169	bos taurus		360	5	2.1	88	1	BXB8_BOMMO	P26742	domdyx mori
288	6	2.6	2747	1	FAF_DROME	P55824	droscophila		361	5	2.1	88	1	FXY3_MOUSE	Q61835	mus musculu
289	6	2.6	3256	1	K167_HUMAN	P46013	homo sapien		362	5	2.1	88	1	H82_NEIGO	P11910	neisseria g
290	6	2.6	3388	1	POLG_DEN2P	P12823	d genome po		363	5	2.1	89	1	CORA_HUMAN	P25321	homo sapien
291	6	2.6	3391	1	POLG_DEN26	P29990	d genome po		364	5	2.1	89	1	CORB_HUMAN	P22558	homo sapien
292	6	2.6	3391	1	POLG_DEN27	P29991	d genome po		365	5	2.1	89	1	CORN_MACMU	P25332	macaca mula
293	6	2.6	3391	1	POLG_DEN2J	P07564	d genome po		366	5	2.1	89	1	YCO2_PARDE	P08302	paracoccus
294	6	2.6	3391	1	POLG_DEN2N	P14340	d genome po		367	5	2.1	90	1	VPM_BPYPD	P27369	bacterioph
295	6	2.6	3421	1	TEGU_HSVEB	P28955	equine herp		368	5	2.1	90	1	YK94_ARCFU	O28186	archaeoglob
296	6	2.6	4303	1	PKD1_HUMAN	P98161	homo sapien		369	5	2.1	91	1	XY05_MOUSE	Q92882	mus musculu
297	6	2.6	4473	1	PLEI_CRIGR	O9j155	crictetulus		370	5	2.1	91	1	V179_FOMPV	O91554	fowlpox vir
298	6	2.6	4544	1	LRL1_HUMAN	Q07954	homo sapien		371	5	2.1	92	1	PLM_CANFA	P36513	canis famli
299	6	2.6	4687	1	PLE1_RAT	P30427	rattus norv		372	5	2.1	92	1	PLM_HUMAN	O00168	homo sapien
300	5	2.1	14	1	UHA1_CANFA	P99503	canis famli		373	5	2.1	92	1	PLM_MOUSE	Q82539	mus musculu
301	5	2.1	28	1	MT2_BRANA	Q96353	brassica na		374	5	2.1	92	1	PLM_MOUSE	O08589	rattus norv
302	5	2.1	29	1	CX07_CONGE	P05483	conus geogr		375	5	2.1	93	1	LSM5_YEAST	P40089	saccharomyc
303	5	2.1	30	1	RNP_ODOVI	P19640	odococleus		376	5	2.1	95	1	RR20_CVAPA	PR8140	cyanophora
304	5	2.1	37	1	RSBY_GUTTH	O78433	guillardia		377	5	2.1	96	1	VG6_BPPZA	P06955	bacterioph
305	5	2.1	37	1	RK36_CIVACA	Q9PLN9	cyandidium c		378	5	2.1	96	1	Y11K_BPCHP	P19183	bacterioph
306	5	2.1	38	1	H5_COLLT	P02260	columba liv		379	5	2.1	97	1	Y121_CHLPN	Q92960	chlamydia p
307	5	2.1	38	1	MEFA2_USTMA	P31963	ustillago ma		380	5	2.1	97	1	YBGE_ECOLI	P37343	escherichia
308	5	2.1	39	1	VPU_HVIRH	P12518	human immun		381	5	2.1	97	1	YHBY_ECOLI	P42550	escherichia
309	5	2.1	51	1	MLEV_MOUSE	P09542	mus musculu		382	5	2.1	99	1	NIC1_HUMAN	O92757	homo sapien
310	5	2.1	52	1	LHA1_ECTHL	P80102	ectochlorho		383	5	2.1	101	1	YHGX_ALCEU	P29279	alcaligenes
311	5	2.1	53	1	YBAM_ECOLI	P45807	escherichia		384	5	2.1	102	1	APAZ_MOUSE	P09813	mus musculu
312	5	2.1	54	1	YH11_STRCO	P16248	streptomyc		385	5	2.1	102	1	APAZ_RAT	P04658	rattus norv
313	5	2.1	56	1	SCP2_MESMA	Q9njp7	mesobuthus		386	5	2.1	102	1	COLL_HVSC	P22576	herpesviru
314	5	2.1	56	1	SCP3_MESMA	Q9ubd1	mesobuthus		387	5	2.1	102	1	RS24_AERPE	Q92C90	aeropyrum p
315	5	2.1	60	1	MT_BRARE	P52722	brachydanio		388	5	2.1	102	1	VAM5_MOUSE	Q92Z88	mus musculu
316	5	2.1	60	1	MT_CARAU	P52723	carassius a		389	5	2.1	102	1	Y70A_METJA	PR1311	methanococc
317	5	2.1	61	1	AERC_AEROS	P09165	aeromonas s		390	5	2.1	103	1	YBUI_YEAST	PR8171	saccharomyc
318	5	2.1	61	1	Y106_NPVAC	P41659	autographa		391	5	2.1	103	1	CBIN_RHOCA	O68104	rhodobacter
319	5	2.1	63	1	YFEG_ECOLI	P76571	escherichia		392	5	2.1	104	1	HG15_CHICK	P12902	gallus gall
320	5	2.1	64	1	MT3_PRUAV	O48951	prunus aviu		393	5	2.1	104	1	UGR2_MOUSE	Q92067	mus musculu
321	5	2.1	64	1	PMCH_RAT	P80250	rattus norv		394	5	2.1	104	1	VG6_BPAPH	P03665	bacterioph
322	5	2.1	65	1	LHA2_ECTHL	P80103	ectochlorho		395	5	2.1	105	1	LBG_ANTCR	P22031	anthracidari
323	5	2.1	65	1	LHA3_RHOPA	P5103	retrodopseu		396	5	2.1	105	1	PSBX_GOSHI	P31336	gossypium h
324	5	2.1	65	1	MT3_CARPA	Q96386	carlica papa		397	5	2.1	105	1	R440_CANMA	P27074	candida mal
325	5	2.1	65	1	OMP_LOCM1	P80045	locusta mig		398	5	2.1	105	1	RL44_CANTR	P27075	candida tro

399	5	2.1	105	1	SUGE_CITRER	069279	citrobacter	472	5	2.1	133	1	TRK4_ECOLI	P17910	escherichia
400	5	2.1	105	1	VE7_HPVS30	P36826	human papil	473	5	2.1	134	1	ANP3_RHIDE	P5753	trichophila
401	5	2.1	105	1	YNC8_YEAST	P53967	saccharomyc	474	5	2.1	134	1	CVS1_RHIDE	P42332	arbidopsis
402	5	2.1	106	1	PSIE_ECOLI	P27295	escherichia	475	5	2.1	134	1	E315_ADE03	P13136	human adeno
403	5	2.1	106	1	RLI2_SUSLO	P66040	sulfolobus	476	5	2.1	134	1	E315_ADE07	P15136	human adeno
404	5	2.1	106	1	VATF_HALVO	Q48331	halobacteri	477	5	2.1	135	1	H2A_TRYCR	P35066	trypanosoma
405	5	2.1	108	1	YG16_YEAST	P53205	saccharomyc	478	5	2.1	135	1	VE6_PAPVE	P11331	european el
406	5	2.1	109	1	VATL_MAIZE	Q41773	zea mays (m	479	5	2.1	135	1	V274_BUCAI	P57362	buchnera ap
407	5	2.1	109	1	YPERF_SALTU	O92fuf5	salmonella	480	5	2.1	135	1	YDOA_SCHPO	014202	schistosacch
408	5	2.1	109	1	YQ31_BACAN	O9rn01	bacillus an	481	5	2.1	135	1	YF72_ARCFU	028700	archaeoglob
409	5	2.1	110	1	LV1C_MOUSE	P01725	mus musculus	482	5	2.1	136	1	ATPM_HUMAN	099766	homo sapien
410	5	2.1	110	1	US36_HCWVA	P16842	human cytom	483	5	2.1	136	1	RS8E_AERPE	Q97490	aeropyrum p
411	5	2.1	111	1	RA2A_MAIZE	P46252	zea mays (m	484	5	2.1	136	1	YF09_DEIRA	O97r12	deinococcus
412	5	2.1	111	1	RLAI_CABEL	P91913	caenorhabdi	485	5	2.1	137	1	CPC_CUCSA	P96602	cuncunus sat
413	5	2.1	111	1	RLA2_ARTSA	P02399	artemia sal	486	5	2.1	138	1	GRIM_DROME	Q4570	dtrosophila
414	5	2.1	112	1	RLAI_DROME	P08570	dtrosophila	487	5	2.1	140	1	BW88_PIG	Q29028	scrofa
415	5	2.1	112	1	VG33_BPT4	P13338	bacteriopho	488	5	2.1	141	1	HBAD_CHICK	P02001	gallus gall
416	5	2.1	113	1	CY4C_PSEPU	P09787	pseudomonas	489	5	2.1	141	1	HBAD_MERGA	P81024	melaeagris g
417	5	2.1	113	1	DTLX_HUMAN	Q15763	homo sapien	490	5	2.1	141	1	HBA_STUVU	P01997	sturnus vul
418	5	2.1	113	1	NTRC_PSEST	P4039	pseudomonas	491	5	2.1	141	1	YEDD_SALTU	Q06399	salmonella
419	5	2.1	113	1	RLI2_HALVO	P41197	halobacteri	492	5	2.1	142	1	RK40_SPIOL	P27668	splincia ol
420	5	2.1	113	1	Y465_AOUAE	O66767	aquifex aeo	493	5	2.1	143	1	RK2_SOYBN	P18663	glycine max
421	5	2.1	114	1	ET3_RABIT	P19998	oryctolagus	494	5	2.1	144	1	SODI_HALME	O08461	halobacteri
422	5	2.1	114	1	RLAI_HUMAN	P05386	homo sapien	495	5	2.1	144	1	Y100_AOUAE	O58599	methanococ
423	5	2.1	114	1	RLAI_MOUSE	P47955	mus musculu	496	5	2.1	146	1	HBH_BRATR	P14526	bradyus tr
424	5	2.1	114	1	VL03_FOWPV	P19944	rattus norv	497	5	2.1	146	1	HBH_ERIEU	P02059	erinaeacus e
425	5	2.1	114	1	VL03_FOWPV	O9j5b7	fowlpox vir	498	5	2.1	146	1	HBE_RABIT	P02103	oryctolagus
426	5	2.1	115	1	RA2B_ARATH	P51407	arabidopsis	499	5	2.1	146	1	SOD2_HALME	O08460	halobacteri
427	5	2.1	115	1	RUBR_SYNY3	P73068	synechocyst	500	5	2.1	146	1	Y142_AOUAE	O66557	aquifex aeo
428	5	2.1	116	1	LV1A_MOUSE	P01722	mus musculu	501	5	2.1	146	1	YB99_MERJA	O58599	methanococ
429	5	2.1	116	1	NU3M_MACRO	P92666	macropus ro	502	5	2.1	146	1	YG56_YEAST	P53311	saccharomyc
430	5	2.1	116	1	VAM5_HUMAN	O95183	homo sapien	503	5	2.1	147	1	HV1C_HUMAN	P01744	homo sapien
431	5	2.1	116	1	YJG7_YEAST	P40367	saccharomyc	504	5	2.1	147	1	PSAE_HORPI	PJ3194	hordeum vul
432	5	2.1	117	1	LV2A_MOUSE	P01728	mus musculu	505	5	2.1	147	1	UCRH_YEAST	P00127	saccharomyc
433	5	2.1	118	1	ATPZ_SYNP6	P08443	synechococc	506	5	2.1	147	1	Y1F3_MOUSE	O88784	mus musculu
434	5	2.1	118	1	CBIN_STRCO	O54189	streptomyce	507	5	2.1	148	1	GP22_LITCA	O01443	littomosoid
435	5	2.1	118	1	VPML_HAEIN	P44234	haemophilus	508	5	2.1	148	1	YEES_ECOLI	P76362	escherichia
436	5	2.1	119	1	ID3_HUMAN	Q02535	homo sapien	509	5	2.1	150	1	LSPA_LACIC	Q48729	lactococcus
437	5	2.1	119	1	ORNT_ORNMO	P56409	ornithodor	510	5	2.1	150	1	YTR1_AZOB	P69694	azospirillum
438	5	2.1	119	1	RNP_CHESE	P04061	chelydra se	511	5	2.1	151	1	YVB2_RHIME	Q92391	rhizobium m
439	5	2.1	119	1	YPX3_BLYJ	P03414	bovine leuk	512	5	2.1	152	1	YCF8_YEAST	P25565	saccharomyc
440	5	2.1	120	1	CU19_ARADI	P80515	arateneus dia	513	5	2.1	153	1	HEMA_MUMPS	P33460	mumps virus
441	5	2.1	120	1	NU3C_NEPOL	O9TKx9	nephroselini	514	5	2.1	154	1	YAI6_ARCFU	O92946	archaeoglob
442	5	2.1	120	1	RBFa_BUCAI	P57457	buchnera ap	515	5	2.1	154	1	YGG9_YEAST	P53162	saccharomyc
443	5	2.1	120	1	Y041_UREPA	O9Prt4	ureaplasma	516	5	2.1	155	1	COX4_YEAST	P40407	saccharomyc
444	5	2.1	120	1	YD42_MYCTU	Q11012	mycoplasma	517	5	2.1	155	1	NU6M_ALBCO	O89922	albilaria c
445	5	2.1	121	1	GSP1_ERMCA	P31588	erwinia car	518	5	2.1	155	1	RL21_PYST	P49667	pyrua stolo
446	5	2.1	122	1	RBS2_HYDMR	O59461	hydrogenovi	519	5	2.1	156	1	BCCP_PSEAE	P37789	pseudomonas
447	5	2.1	122	1	RL7_DEIRA	O9RSIO	deinococcus	520	5	2.1	157	1	BSAA_BACHD	O92947	bacillus ha
448	5	2.1	123	1	RP14_HUMAN	O95059	homo sapien	521	5	2.1	157	1	FLIN_PSEAE	O51466	pseudomonas
449	5	2.1	124	1	CMGG_BACSU	P25959	bacillus su	522	5	2.1	159	1	RL21_MOUSE	P02080	rattus norv
450	5	2.1	124	1	HYPA_MERJA	O57667	methanococc	523	5	2.1	159	1	RL21_MOUSE	P43334	caenorhabd1
451	5	2.1	125	1	RL7_RICCN	O92j87	rickettsia	524	5	2.1	160	1	RL21_CABEL	P17637	bacteriopho
452	5	2.1	126	1	ACTR_PAPHA	O28928	papio hamad	525	5	2.1	161	1	VP12_BPREO	P33154	arabidopsis
453	5	2.1	126	1	CU24_ARADI	P80516	arateneus dia	526	5	2.1	161	1	PRI_ARATH	P44275	haemophilus
454	5	2.1	126	1	PLAS_STNY3	P21697	synechocyst	527	5	2.1	161	1	YG22_HAEIN	P42725	haemophilus
455	5	2.1	127	1	Y55B_MYCGE	P00708	columba liv	528	5	2.1	162	1	XYLB_AMPSP	P54271	ampliarief
456	5	2.1	127	1	LYC_COLDI	O9Zb81	mycoplasma	529	5	2.1	162	1	YDYA_SCHPO	O13669	schistosacch
457	5	2.1	127	1	Y55B_MYCGE	P75041	mycoplasma	530	5	2.1	162	1	Y227_MERJA	O60266	methanococc
458	5	2.1	129	1	DYIA_CHIRE	O39591	chlamydomon	531	5	2.1	164	1	VATL_LYCES	O24011	lysoferisico
459	5	2.1	129	1	LV1B_MOUSE	P01724	mus musculu	532	5	2.1	164	1	VATL_PHAU	O22532	piaseolius a
460	5	2.1	129	1	LV1D_MOUSE	P01726	mus musculu	533	5	2.1	165	1	RS16_GAOCR	P80142	caulobacter
461	5	2.1	129	1	LV1E_MOUSE	P01727	mus musculu	534	5	2.1	165	1	SSB_PSEAE	P04947	pseudomonas
462	5	2.1	129	1	LV2B_MOUSE	P01729	mus musculu	535	5	2.1	165	1	VATL_ARATH	O39039	arabidopsis
463	5	2.1	129	1	RT16_DROME	O9v6v3	dtrosophila	536	5	2.1	165	1	VATL_AVSRA	P23957	avena sativ
464	5	2.1	130	1	CHB1_ANTPO	P02848	antheraea p	537	5	2.1	165	1	VATL_BETVU	Q39457	beta vulgar
465	5	2.1	130	1	RS22_AGABI	P46792	agarticus bi	538	5	2.1	165	1	VATL_GOSHI	Q03434	gossypium h
466	5	2.1	130	1	TAT_HVNZ	P05909	human immun	539	5	2.1	165	1	VATL_KALDA	Q06473	kalanchoe d
467	5	2.1	130	1	TAT_HVZRO	P04605	human immun	540	5	2.1	165	1	VATL_ORYSA	Q04055	oryza sativ
468	5	2.1	131	1	CHHB_BOOMO	P05688	bombyx mori	541	5	2.1	165	1	VATL_TOBAC	Q04055	nicotiana t
469	5	2.1	132	1	IMEP_STRNI	P01077	streptomyce	542	5	2.1	165	1	Y051_HAEIN	P44484	haemophilus
470	5	2.1	132	1	YJW_ECOLI	P39394	escherichia	543	5	2.1	166	1	YREP_BUCTS	O31289	buchnera ap
471	5	2.1	133	1	TAT_HVZCA	P24109	human immun	544	5	2.1	166	1	HES5_RAT	O03082	rattus norv



545	5	2.1	166	1	RS5_ECOLI	P02356	escherichia	618	5	2.1	190	1	APOM_MOUSE	Q921r3	mus musculus
546	5	2.1	166	1	P542_MYCPN	P75270	mycoplasma	619	5	2.1	190	1	APOM_RAT	P14630	rattus norv
547	5	2.1	167	1	HES5_MOUSE	P70120	mus musculus	620	5	2.1	190	1	CAN2_FLALI	P45630	flavescens
548	5	2.1	167	1	MB12_MYCLE	O49771	mycobacteri	621	5	2.1	190	1	CC42_COIGL	O94103	colletotric
549	5	2.1	167	1	NU6M_MTXGL	O992w7	myxine glut	622	5	2.1	190	1	ESS1_YEAST	P22566	saccharomyc
550	5	2.1	167	1	YREP_BUCPP	O92ae4	buchnera ap	623	5	2.1	190	1	LEPW_BACST	P54506	bacillus su
551	5	2.1	168	1	ATPD_RAT	P35434	rattus norv	624	5	2.1	190	1	MAF_BACHD	O9K8h3	bacillus ha
552	5	2.1	168	1	VA34_VACCC	P21057	vaccinia vi	625	5	2.1	190	1	YREG_STRCO	P39595	strptomyc
553	5	2.1	168	1	VA34_VACCV	P24761	vaccinia vi	626	5	2.1	191	1	CBP2_ARATH	P30187	arabidopsis
554	5	2.1	168	1	VA34_VARV	P33851	vaccinia vi	627	5	2.1	191	1	FGHD_BOVIN	O02853	bos taurus
555	5	2.1	168	1	VA40_VACCC	P21053	vaccinia vi	628	5	2.1	191	1	TF2D_BOVIN	P4627d	acetabulari
556	5	2.1	168	1	VA40_VACCV	P24765	vaccinia vi	629	5	2.1	192	1	CSR2_HUMAN	O16537	homo sapien
557	5	2.1	168	1	Y22_MYCTU	O50706	mycobacteri	630	5	2.1	192	1	CSR2_RAT	O62908	rattus norv
558	5	2.1	169	1	GP38_CANFA	O95152	canis fami	631	5	2.1	192	1	MLEF_MOUSE	P09541	mus musculus
559	5	2.1	169	1	GPO_SYNY3	P74280	synecocyst	632	5	2.1	192	1	RHOI_DRONE	P48188	drosophila
560	5	2.1	169	1	HUPJ_BRAJA	P483d1	bradyrhizob	633	5	2.1	192	1	RHOI_CAEEL	Q22038	caenorhabd1
561	5	2.1	169	1	VPL_BPP2	P25475	bacterioph	634	5	2.1	192	1	RHO_APLCA	P01122	aplysia cal
562	5	2.1	171	1	IF3_BACSV	P16808	human cytom	635	5	2.1	192	1	RHO_DISOM	P22122	discopyge o
563	5	2.1	171	1	IR10_HCMVA	O26142	methanobact	636	5	2.1	192	1	Y678_AOUAE	O66906	aquilex aeo
564	5	2.1	171	1	RS4_MERTH	O26142	escherichia	637	5	2.1	192	1	YBCC_RHOCA	P26166	rhodobacter
565	5	2.1	171	1	SFME_ECOLI	P37926	salmonella	638	5	2.1	193	1	CSR2_CHICK	P50460	gallus gall
566	5	2.1	172	1	FIME_SALTY	O62011	mus musculu	639	5	2.1	193	1	CSR2_COTJA	O05138	coturnix co
567	5	2.1	172	1	GP38_MOUSE	O60830	homo sapien	640	5	2.1	193	1	H5_ANSAN	P00258	anser anser
568	5	2.1	172	1	IM7B_HUMAN	P00272	pseudomonas	641	5	2.1	193	1	H5_CAIMO	P06513	california mos
569	5	2.1	172	1	RUB2_PSEOL	O61597	mus musculu	642	5	2.1	193	1	MP70_MYCTU	O50769	mycobacteri
570	5	2.1	173	1	CRGC_MOUSE	P08209	bos taurus	643	5	2.1	193	1	RHOA_CANFA	P24406	canis fami
571	5	2.1	173	1	CRGD_BOVIN	P04342	mus musculu	644	5	2.1	193	1	RHOA_HUMAN	P06749	homo sapien
572	5	2.1	173	1	CRGD_MOUSE	P10067	rattus norv	645	5	2.1	193	1	RHOA_MOUSE	Q9qu10	mus musculu
573	5	2.1	173	1	CRGD_RAT	P20821	bos taurus	646	5	2.1	193	1	RHOA_HUMAN	P08134	homo sapien
574	5	2.1	173	1	GCSH_BOVIN	O42570	drosophila	647	5	2.1	193	1	RHOA_MOUSE	O62159	mus musculu
575	5	2.1	174	1	PLD_DROME	O92b51	raistrionia s	648	5	2.1	193	1	VA57_VACCC	P21074	vaccinia vi
576	5	2.1	174	1	POPB_RALSO	P55668	rhizobium s	649	5	2.1	193	1	VA57_VACCV	O01230	vaccinia vi
577	5	2.1	174	1	Y4TN_RHISN	P09002	homo sapien	650	5	2.1	193	1	VIN3_BPP4	P13302	bacterioph
578	5	2.1	174	1	Y4TN_HUMAN	P21688	pantoea ana	651	5	2.1	194	1	HL_SALTR	P02284	salmo trutt
579	5	2.1	175	1	CRT2_PANAN	P43664	salmonella	652	5	2.1	195	1	AANT_HVSV1	P25883	hepatitis d
580	5	2.1	175	1	LPFE_SALTY	O10620	hallothis z	653	5	2.1	195	1	IRX3_HUMAN	P78412	homo sapien
581	5	2.1	175	1	O5E6_NEPVZ	P03643	bacterioph	654	5	2.1	196	1	AMEL_MOUSE	P45559	mus musculu
582	5	2.1	175	1	VGG_BPPIX	O91kx7	bacterioph	655	5	2.1	196	1	RHOB_HUMAN	P01121	homo sapien
583	5	2.1	176	1	VGL1_BPMU	O06235	mycobacteri	656	5	2.1	197	1	CYCL_BACSV	O34577	bacillus su
584	5	2.1	176	1	YLAO_MYCTU	P52036	neisseria m	657	5	2.1	197	1	Y392_PSEAE	P25254	pseudomonas
585	5	2.1	177	1	GPXA_NEIMA	P52036	neisseria m	658	5	2.1	197	1	Y075_ANASP	P58632	anabena sp
586	5	2.1	178	1	HPRT_ECOLI	P56766	escherichia	659	5	2.1	198	1	RHO1_CANAL	O42825	candida alb
587	5	2.1	178	1	YE57_HAEIN	O57201	haemophilus	660	5	2.1	198	1	TTK_ECOLI	P06969	escherichia
588	5	2.1	180	1	BST2_HUMAN	O10589	homo sapien	661	5	2.1	199	1	CYCY_RHOCA	O05389	rhodobacter
589	5	2.1	180	1	GEHF_HELAN	O23968	heliandus	662	5	2.1	199	1	YPHA_BACSV	P16409	rattus norv
590	5	2.1	180	1	NEF_HVZMZ	P05860	human immun	663	5	2.1	199	1	YPHA_BACSV	P50741	bacillus su
591	5	2.1	181	1	GSPH_ERICH	P24687	erwinia chr	664	5	2.1	200	1	DSBA_VIBCH	P32557	vibrio chol
592	5	2.1	182	1	ARL3_RAT	P37936	rattus norv	665	5	2.1	200	1	RK22_MEDSA	P49143	medicago sa
593	5	2.1	182	1	CASK_HUMAN	P07458	homo sapien	666	5	2.1	200	1	TF21_ARATH	P28147	arabidopsis
594	5	2.1	182	1	FTN_DROME	P35554	drosophila	667	5	2.1	200	1	TF21_MATZE	P50158	zea mays (m
595	5	2.1	182	1	PTHG_ERWAM	O32521	erwinia amy	668	5	2.1	200	1	TF22_ARATH	P28148	arabidopsis
596	5	2.1	183	1	BTUE_ECOLI	P06610	escherichia	669	5	2.1	200	1	TF22_MATZE	P50159	zea mays (m
597	5	2.1	183	1	H81_NEICO	P07211	neisseria g	670	5	2.1	200	1	TF2D_MESCR	P48511	mesembryant
598	5	2.1	183	1	H8_NEIMA	P57025	neisseria m	671	5	2.1	200	1	TF2D_SOLTU	P26357	solanum tub
599	5	2.1	183	1	H8_NEIMB	P57026	neisseria m	672	5	2.1	200	1	TF2D_SOYBN	O42648	glycine max
600	5	2.1	183	1	H8_NEIMC	P07212	neisseria m	673	5	2.1	200	1	TF2D_TOBAC	P93348	nicotiana t
601	5	2.1	183	1	YGIL_ECOLI	P39834	escherichia	674	5	2.1	200	1	YORI_COYMY	P02820	comeliina y
602	5	2.1	184	1	VP50_BPAP5	O91i88	bacterioph	675	5	2.1	201	1	TF22_WHEAT	O09289	tritricum ae
603	5	2.1	185	1	AAC6_CITDI	P10051	citrobacter	676	5	2.1	201	1	TRL_PONIE	P05547	pontastacus
604	5	2.1	185	1	SPP2_YEAST	O02521	saccharomyc	677	5	2.1	202	1	RHO1_SCHPO	O58914	schizosach
605	5	2.1	186	1	MLE1_MUGCA	P82159	mugil capit	678	5	2.1	202	1	YE42_MERTJA	O09837	methanococc
606	5	2.1	186	1	VNSC_MEASA	P35977	measles vir	679	5	2.1	203	1	CLP1_MYXXA	O30612	myxococcus
607	5	2.1	186	1	VNSC_MEASE	P03494	measles vir	680	5	2.1	203	1	KGUA_PSEAE	O9ht82	pseudomonas
608	5	2.1	186	1	VNSC_MEASI	P26035	measles vir	681	5	2.1	204	1	RRA2_HUMAN	P17082	homo sapien
609	5	2.1	186	1	VALD_TRYBB	P17962	trypanosoma	682	5	2.1	205	1	KGUA_LACTA	O9cees3	lactococcus
610	5	2.1	187	1	FMK1_ECOLI	P04740	escherichia	683	5	2.1	205	1	NEF_HV104	P24741	human immun
611	5	2.1	188	1	APOM_HUMAN	O95445	homo sapien	684	5	2.1	205	1	Y585_MERTJA	O58005	methanococc
612	5	2.1	188	1	RL11_LEICH	P42922	leishmania	685	5	2.1	206	1	COX3_BACFI	O04402	bacillus fi
613	5	2.1	188	1	RL11_LEIMA	P48181	leishmania	686	5	2.1	206	1	DCTM_PARDY	O56347	parcoccus
614	5	2.1	188	1	RNFB_PSEAE	O9hyv9	pseudomonas	687	5	2.1	206	1	HL_ONCMY	P06330	oncorhynch
615	5	2.1	188	1	TRE1_ECOLI	P08322	escherichia	688	5	2.1	206	1	RHTB_ECOLI	P27887	escherichia
616	5	2.1	188	1	TRE2_ECOLI	P10514	escherichia	689	5	2.1	206	1	S3AF_BACSV	P49783	bacillus su
617	5	2.1	189	1	Y006_CHLTR	O84009	chlamydia t	690	5	2.1	207	1	MGMT_HUMAN	P16445	homo sapien

691	5	2.1	207	1	UCRI_CARVI	O31214	chromatium	764	5	2.1	228	1	UL09_HCMVA	P16745	human cytom
692	5	2.1	208	1	BCRB_BACLI	P42333	bacillus 1i	765	5	2.1	228	1	VATE_MOUSE	P05018	mus musculus
693	5	2.1	208	1	KTHY_AERPE	O9448	aeropyrum 1i	766	5	2.1	228	1	YTUB_ERWHE	O47826	erwinia her
694	5	2.1	209	1	HIS2_BUCAP	O9zhe0	buchnera ap	767	5	2.1	229	1	CLCB_HUMAN	P09497	homo sapien
695	5	2.1	209	1	PAAD_PSRAP	O9hx08	pseudomonas	768	5	2.1	229	1	SOML_CYCLU	P45640	cyctolpterus
696	5	2.1	209	1	RHO1_YEAST	P06780	saccharomyc	769	5	2.1	229	1	UNG_CHLMU	G9PJ42	chlamydia m
697	5	2.1	209	1	UPE_BACHD	O9k6g5	bacillus ha	770	5	2.1	229	1	VG14_BPPH8	P14814	bacterioph
698	5	2.1	210	1	COX2_TRYBB	P04372	trypanosoma	771	5	2.1	229	1	Y127_TREPA	P31824	treponema p
699	5	2.1	210	1	SODM_PENCH	O75007	penicillium	772	5	2.1	230	1	COX2_CYPCA	P24987	oncorhynch
700	5	2.1	211	1	RLA_MYCGE	P47398	mycoplasma	773	5	2.1	230	1	COX2_ONCMY	P48171	oncorhynch
701	5	2.1	211	1	TIM3_HUMAN	P35625	homo sapien	774	5	2.1	230	1	COX2_SALSA	O37677	salmo salar
702	5	2.1	211	1	YFB0_YEAST	P43582	saccharomyc	775	5	2.1	230	1	Y4NF_RHISM	P35578	thizobium s
703	5	2.1	212	1	COAT_CYMW	P16486	clover yell	776	5	2.1	230	1	Y636_YEAST	P53274	saccharomyc
704	5	2.1	212	1	IF3_DEIRA	O9sm7	deinococcus	777	5	2.1	230	1	YJ02_MERTH	O27934	methanobact
705	5	2.1	212	1	KAD_STRPY	P82549	streptococc	778	5	2.1	231	1	ATMG_SALTU	P20992	salmonella
706	5	2.1	212	1	KTHY_YERPE	O69169	yersinia pe	779	5	2.1	231	1	SOML_PAROL	P79894	spartus aura
707	5	2.1	212	1	Y440_CHLPN	O928a3	chlamydia p	780	5	2.1	231	1	SOML_SCIOC	P20362	paratichthy
708	5	2.1	213	1	KITH_RHOST	O9ziq2	rhodothermu	781	5	2.1	231	1	Y236_CAMJE	O9ygr7	sciaenops o
709	5	2.1	213	1	Y851_STRPN	O94916	streptococc	782	5	2.1	231	1	YEDJ_ECOLI	O9PJ48	campylobact
710	5	2.1	214	1	ACH2_LONAC	P36605	lonomila ach	783	5	2.1	231	1	6PGL_CAUCR	P46144	escherichia
711	5	2.1	214	1	ET3_MOUSE	P48299	mus musculu	784	5	2.1	232	1	HXB9_XENLA	O9a6n1	caulobacter
712	5	2.1	214	1	H11_HUMAN	O02539	homo sapien	785	5	2.1	232	1	YPRH_ECOLI	P31272	xenopus lae
713	5	2.1	214	1	NADD_MYCLE	O9cbx8	mycobacteri	786	5	2.1	232	1	ASH1_RAT	P76561	escherichia
714	5	2.1	214	1	RI9A_ARATH	O9str2	arabidopsis	787	5	2.1	233	1	BCL2_CHICK	P19359	rattus norv
715	5	2.1	214	1	RM06_YEAST	P32904	saccharomyc	788	5	2.1	233	1	Y081_HUMAN	O00709	gallus gall
716	5	2.1	215	1	FLA1_METVA	P95316	methanococc	789	5	2.1	233	1	G038_RAT	O14696	homo sapien
717	5	2.1	215	1	PTH_DEIRA	O9rrw3	deinococcus	790	5	2.1	234	1	MAUM_MERFL	P35897	rattus norv
718	5	2.1	216	1	CSGD_ECOLI	P52106	escherichia	791	5	2.1	234	1	POIN_RHDV3	O50423	methyllobact
719	5	2.1	216	1	CSGD_SALTU	O54294	salmonella	792	5	2.1	234	1	RNH2_XYLF	P27411	rabbit hemo
720	5	2.1	216	1	HYFE_ECOLI	P77524	escherichia	793	5	2.1	234	1	H47_STELP	O6pe17	xyella fas
721	5	2.1	216	1	LEF2_NPYLD	P36869	lymantiria d	794	5	2.1	235	1	HK29_MOUSE	O41348	stellaria 1
722	5	2.1	217	1	D1P_HUMAN	O9nyk4	homo sapien	795	5	2.1	235	1	RS4E_THEVO	O70594	mus musculu
723	5	2.1	217	1	FLA2_METVA	O58302	methanococc	796	5	2.1	235	1	Y332_MYCPN	O97bw4	thermoplasm
724	5	2.1	217	1	RL6_CAEEL	P47991	caenorhabdi	797	5	2.1	235	1	YAEB_ECOLI	P73306	mycoplasma
725	5	2.1	217	1	YL02_ARCFU	O28178	archaeoglob	798	5	2.1	235	1	ALDC_LACTA	P98634	escherichia
726	5	2.1	218	1	HLIR_CHICK	P08288	gallus gall	799	5	2.1	236	1	ALDC_LACTC	P95676	lactococcus
727	5	2.1	218	1	KTHY_CAEEL	O22018	caenorhabdi	800	5	2.1	236	1	PGSA_MYCGE	P77880	lactococcus
728	5	2.1	218	1	RRAS_HUMAN	P10301	homo sapien	801	5	2.1	236	1	PLLI_BOVIN	P97360	mycoplasma
729	5	2.1	218	1	RRAS_MOUSE	P10833	mus musculu	802	5	2.1	236	1	PLI_SHEEP	P09611	bos taurus
730	5	2.1	218	1	Y364_MYCPN	P75236	mycoplasma	803	5	2.1	236	1	YIW2_YEAST	P16038	ovis aries
731	5	2.1	219	1	ATP6_ARTRF	O37708	artemia san	804	5	2.1	237	1	NAPC_PARDT	O66352	paracoccus
732	5	2.1	219	1	BASP_RAT	O05175	rattus norv	805	5	2.1	237	1	RU2_METVA	P21479	methanococc
733	5	2.1	219	1	CAV7_PIG	P80015	sus scrofa	806	5	2.1	238	1	KE5C_RAT	P65436	rattus norv
734	5	2.1	220	1	CLD6_MOUSE	O92262	mus musculu	807	5	2.1	238	1	NEUM_HUMAN	P17677	homo sapien
735	5	2.1	220	1	MPB3_MYCTU	O10790	mycobacteri	808	5	2.1	238	1	TE2D_CANAL	O31373	candida alb
736	5	2.1	220	1	VLVS_BPPH6	P07582	bacterioph	809	5	2.1	238	1	Y457_CHLTR	O84463	chlamydia t
737	5	2.1	220	1	WM02_VARY	P34017	variola vir	810	5	2.1	238	1	Y573_CHLPP	O92770	chlamydia p
738	5	2.1	221	1	EP1B_BOMMO	P29522	bombux mori	811	5	2.1	238	1	Y742_CHLMU	O9PJ45	chlamydia m
739	5	2.1	221	1	NCE3_YEAST	P53615	saccharomyc	812	5	2.1	238	1	YIGB_ECOLI	P23306	escherichia
740	5	2.1	221	1	RANI_ARATH	P41916	arabidopsis	813	5	2.1	238	1	YRN7_CAEEL	O09421	caenorhabdi
741	5	2.1	222	1	AMVB_SECC	P30271	secale cere	814	5	2.1	238	1	NEUM_BOVIN	P16836	bos taurus
742	5	2.1	222	1	EMBP_MOUSE	O61878	mus musculu	815	5	2.1	239	1	TE2D_YEAST	P13323	saccharomyc
743	5	2.1	223	1	GSHU_BRUMA	P35665	brugia mala	816	5	2.1	239	1	Y247_MYCPN	P75428	mycoplasma
744	5	2.1	223	1	GSHU_WUCBA	P35666	wuchereria	817	5	2.1	239	1	Y332_MYCGE	P47574	mycoplasma
745	5	2.1	223	1	KCY_BORBR	O9rnde	bordeletia	818	5	2.1	239	1	YG1P_YEAST	P53223	saccharomyc
746	5	2.1	223	1	YB23_PYRHO	O58960	pyrococcus	819	5	2.1	240	1	8512_TRYCR	P10222	trypanosoma
747	5	2.1	223	1	YB43_YEAST	P38343	saccharomyc	820	5	2.1	240	1	CD48_RAT	P10222	rattus norv
748	5	2.1	224	1	Y088_MYCTU	O10885	mycobacteri	821	5	2.1	240	1	MEF_HYD22	P15829	human immun
749	5	2.1	224	1	Y364_MYCGE	P47604	mycoplasma	822	5	2.1	240	1	T341_ECOLI	P11257	escherichia
750	5	2.1	224	1	YB50_MYCPN	P75036	mycoplasma	823	5	2.1	240	1	YDFB_SCHPO	O10483	schizosacch
751	5	2.1	225	1	GDIT_HUMAN	O99819	homo sapien	824	5	2.1	241	1	MLTE_ECOLI	P76009	escherichia
752	5	2.1	226	1	BASP_BOVIN	P80724	bos taurus	825	5	2.1	241	1	NEUM_SERCA	O98967	serlinus can
753	5	2.1	226	1	BASP_HUMAN	P80723	homo sapien	826	5	2.1	242	1	Y956_HELPP	O92k5	helicobacte
754	5	2.1	226	1	I226_ASFB7	P27944	african swi	827	5	2.1	242	1	CYL_EUGER	O25610	helicobacte
755	5	2.1	226	1	NEUM_RAT	P07936	rattus norv	828	5	2.1	243	1	BRM1_STANU	P06639	staphylococ
756	5	2.1	226	1	NU6M_DICDI	O37314	dicyostell	829	5	2.1	243	1	FOL3_HUMAN	P4143	homo sapien
757	5	2.1	226	1	VATE_BOVIN	P11019	bos taurus	830	5	2.1	243	1	SUMT_SYNP7	P2421	synchrochoc
758	5	2.1	227	1	COX2_BUDBE	P06678	bubalus dep	831	5	2.1	244	1	ATP6_BACSU	P33128	escherichia
759	5	2.1	227	1	NEUM_MOUSE	O83554	treponema p	832	5	2.1	246	1	ECPD_ECOLI	O9yan6	aeropyrum p
760	5	2.1	227	1	NEUM_MOUSE	O83554	treponema p	833	5	2.1	246	1	FLA2_AERPE		
761	5	2.1	227	1	Y173_TREPA	P51012	rhodobacter	834	5	2.1	246	1			
762	5	2.1	227	1	Y173_TREPA	P51012	rhodobacter	835	5	2.1	246	1			
763	5	2.1	228	1	RPE_RHOCA			836	5	2.1	246	1			

837	5	2.1	246	1	NIFU_RHOSH	001180	rhodobacter	910	5	2.1	269	1	S3AD_SHITFL	P14511	shigella fl
838	5	2.1	246	1	RS2_PSEAE	082850	pseudomonas	911	5	2.1	269	1	TCF1_HUMAN	P36402	homo sapien
839	5	2.1	246	1	TF2D_TFETH	027850	tetrahymena	912	5	2.1	269	1	TRC1_SPRO	P06814	streptomyce
840	5	2.1	246	1	TRVB_RAT	P32832	rattus norv	913	5	2.1	270	1	CATA_RHOOP	P95607	rhodococcus
841	5	2.1	246	1	YEBE_ECOLI	P24237	escherichia	914	5	2.1	270	1	PSA1_ORYSA	P52428	oryza sativ
842	5	2.1	246	1	YEBE_HAEIN	P44634	haemophilus	915	5	2.1	270	1	REB1_HUMAN	P000124	homo sapien
843	5	2.1	247	1	FLAI_THEVO	P57719	thermoplasma	916	5	2.1	270	1	YDHT_ECOLI	P77147	escherichia
844	5	2.1	247	1	SURE_THEME	P96112	thermotoga	917	5	2.1	271	1	AOP2_HUMAN	P41181	homo sapien
845	5	2.1	247	1	TRV3_RAT	P08426	rattus norv	918	5	2.1	271	1	MT04_SPRO	P09305	streptomyce
846	5	2.1	248	1	TRPC_SULSO	006121	sulfolobus	919	5	2.1	271	1	RK2_SPTLO	P06509	spiniacia ol
847	5	2.1	248	1	Y964_PSEAE	051423	pseudomonas	920	5	2.1	272	1	CY1_RHODU	P23135	rhodospirill
848	5	2.1	249	1	RIB7_KLUMA	09P408	kluveromyc	921	5	2.1	272	1	UL24_HSVEL	P09314	equine herp
849	5	2.1	249	1	RSF2_HUMAN	P28290	homo sapien	922	5	2.1	272	1	UL24_HSVEL	P24432	equine herp
850	5	2.1	250	1	ETV3_HUMAN	P41162	homo sapien	923	5	2.1	272	1	UL24_HSVEL	P28927	equine herp
851	5	2.1	250	1	HXB9_MOUSE	P20615	mus musculu	924	5	2.1	272	1	YTDA_BACSU	P42407	baacillus su
852	5	2.1	250	1	OS35_SOLCO	P50703	solanum com	925	5	2.1	273	1	BAST_MOUSE	P18572	mus musculu
853	5	2.1	250	1	PLSC_BORBU	059188	borrella bu	926	5	2.1	273	1	DAB1_RHTLO	P58210	rhizobium l
854	5	2.1	250	1	RS2_ZYMO	09X567	zymomonas m	927	5	2.1	273	1	FPG_LACIC	P42371	lactococcus
855	5	2.1	251	1	CAP7_HUMAN	P20160	homo sapien	928	5	2.1	273	1	PRIO_CHICK	P27177	gallus gall
856	5	2.1	251	1	FGFN_HUMAN	09GZV9	homo sapien	929	5	2.1	273	1	RK2_HORVU	P41096	hordium vul
857	5	2.1	251	1	TPIS_VIBSA	056738	vibrio sp.	930	5	2.1	273	1	RK2_MAIZE	P17788	zea mays l'm
858	5	2.1	252	1	BTE4_HUMAN	09bXK1	homo sapien	931	5	2.1	273	1	RK2_ORYSA	P17351	oryza sativ
859	5	2.1	252	1	CEA3_HUMAN	P40198	homo sapien	932	5	2.1	273	1	RK2_PEA	P31163	pisum sativ
860	5	2.1	252	1	CRB1_BOVIN	P07318	bos taurus	933	5	2.1	274	1	GRM_MICEC	P24618	micromonosp
861	5	2.1	252	1	RL7_DROME	P32100	drosophila	934	5	2.1	274	1	GRM_MICEC	P24619	micromonosp
862	5	2.1	252	1	Y455_RICPR	09ZD88	ricicetisia	935	5	2.1	274	1	RK2_ARATH	P56791	arabidopsis
863	5	2.1	252	1	YCX3_GUTPH	078431	guillardia	936	5	2.1	274	1	RK2_EPTVI	P30065	epileagus vl
864	5	2.1	253	1	CYSZ_ECOLI	P12610	escherichia	937	5	2.1	274	1	RK2_OENHO	Q9MDU0	oenothera h
865	5	2.1	253	1	CYSZ_SALTY	P12673	salmonella	938	5	2.1	274	1	RK2_SINHL	P27107	sinapis alb
866	5	2.1	253	1	T2D7_RAT	062860	rattus norv	939	5	2.1	274	1	RK2_TOBAC	P06379	nicotiana t
867	5	2.1	253	1	U170_HUMAN	09H7D2	homo sapien	940	5	2.1	274	1	VGLL_MCNVX	P52513	murine cyto
868	5	2.1	254	1	TPIS_CHLPN	09Z676	chlamydia p	941	5	2.1	274	1	VGLL_MCNVX	P52513	murine cyto
869	5	2.1	254	1	VSPA_SOYBN	P15490	glycine max	942	5	2.1	275	1	IAXX_HUMAN	P10313	homo sapien
870	5	2.1	254	1	VSPA_SOYBN	P10743	glycine max	943	5	2.1	275	1	HXA5_HERRR	091423	heterodontu
871	5	2.1	254	1	WAPA_BACST	P42018	baacillus st	944	5	2.1	275	1	NIR2_RHOCA	Q07942	rhodobacter
872	5	2.1	254	1	Y935_MYCPN	P73597	mycoplasma	945	5	2.1	275	1	RK2_CHLVU	P56367	rhodococcus
873	5	2.1	254	1	YABI_ECOLI	P30149	escherichia	946	5	2.1	275	1	RK2_NEPOL	Q9L118	nephrolella y
874	5	2.1	255	1	RS3A_CANAL	P40910	candida alb	947	5	2.1	275	1	RK2_PICAB	0629541	picea abies
875	5	2.1	255	1	GARL_ECOLI	P23532	escherichia	948	5	2.1	275	1	SC65_CANAL	Q14415	candida alb
876	5	2.1	256	1	YOEU_BACSU	P54461	baacillus su	949	5	2.1	276	1	OCCF_AGRTU	P35121	agrobacteri
877	5	2.1	257	1	FCFA_HUMAN	P12319	homo sapien	950	5	2.1	276	1	RK2_MESVI	Q9MUT9	mesostigma
878	5	2.1	257	1	MOTB_HELPJ	09Z129	helicobacte	951	5	2.1	276	1	RK2_PTINT	Q62940	pinus thunb
879	5	2.1	257	1	MOTB_HELPJ	P56427	helicobacte	952	5	2.1	276	1	ULBP_ECOLI	P75820	escherichia
880	5	2.1	258	1	TF2D_ACACA	P26334	acanthamoeb	953	5	2.1	277	1	CLPR_HUMAN	Q16740	homo sapien
881	5	2.1	258	1	VT1_SFVKA	P25946	shope fibro	954	5	2.1	277	1	DGX_MOUSE	Q9GX60	mus musculu
882	5	2.1	258	1	ZW10_MOUSE	O54692	mus musculu	955	5	2.1	277	1	HXB8_NORVI	P1263	notophthalm
883	5	2.1	259	1	CTRI_ANOGA	Q27289	anopheles g	956	5	2.1	277	1	MSMG_SPRMU	Q00751	streptococc
884	5	2.1	259	1	RUBC_CHIRE	Q42695	chlamydomon	957	5	2.1	277	1	RK2_EUGER	P19158	euglena gra
885	5	2.1	259	1	YGFW_ECOLI	Q46813	escherichia	958	5	2.1	277	1	TRPC_PSEPU	P20578	pseudomonas
886	5	2.1	260	1	AG84_MYCTU	P46816	mycobacteri	959	5	2.1	277	1	Y623_CHLPN	Q9Z761	chlamydia p
887	5	2.1	260	1	H11_VOLCA	Q08864	volvox cart	960	5	2.1	277	1	YD81_YEAST	P48568	saccharomyc
888	5	2.1	260	1	HA20_HUMAN	P20036	homo sapien	961	5	2.1	278	1	MA32_MOUSE	Q35658	mus musculu
889	5	2.1	260	1	NEF_HV2CA	P24103	human immun	962	5	2.1	278	1	MA32_MOUSE	Q35766	rattus norv
890	5	2.1	260	1	VP33_APLCA	Q16943	aplysia cal	963	5	2.1	278	1	RCBL_CHRVI	P31762	chironatium
891	5	2.1	261	1	DER3_DERPT	P39675	dermatophag	964	5	2.1	280	1	NUDC_DEIRA	Q9RV62	delinococcus
892	5	2.1	261	1	TRPC_RHOCA	Q02584	rhodobacter	965	5	2.1	280	1	TRY2_DROME	P42280	drosophila
893	5	2.1	261	1	XPSN_XANCP	P29040	xanthomonas	966	5	2.1	281	1	Y747_RICPR	Q9ZC73	ricicetisia
894	5	2.1	262	1	COR4_WHEAT	P46524	tritricum ae	967	5	2.1	281	1	CEBE_HUMAN	P55174	homo sapien
895	5	2.1	262	1	S3AD_KLEPN	P08881	klebsiella	968	5	2.1	281	1	PANC_XYLPA	Q9P948	xytelia fas
896	5	2.1	262	1	YCJT_ECOLI	P51963	escherichia	969	5	2.1	282	1	LPXC_CIVACA	Q50061	arabidopsis
897	5	2.1	263	1	S3AD_ECOLI	P04826	escherichia	970	5	2.1	282	1	RK4_ARATH	P37660	escherichia
898	5	2.1	264	1	HEM4_SYNP7	P42452	synechococc	971	5	2.1	282	1	TAUD_ECOLI	P71887	mycobacteri
899	5	2.1	265	1	LEF5_NPVAC	P41658	autographa	972	5	2.1	282	1	YN25_MYCTU	P71887	mycobacteri
900	5	2.1	265	1	PYRE_CANRU	Q9Hf90	candida rug	973	5	2.1	283	1	CGIC_CHICK	P55138	gallus gall
901	5	2.1	265	1	PYRE_ZYGBA	Q9Hf90	zygosacchar	974	5	2.1	283	1	CGIC_MOUSE	Q62447	mus musculu
902	5	2.1	266	1	TF2D_STRPU	P91809	strongyloce	975	5	2.1	283	1	DAPA_MERTH	Q26892	methanobact
903	5	2.1	266	1	CD82_RAT	Q70332	rattus norv	976	5	2.1	284	1	AROK_HALNI	Q9H040	halobacteri
904	5	2.1	266	1	RK2_NICDE	P21434	nicotiana d	977	5	2.1	285	1	HXA4_MOUSE	P06788	mus musculu
905	5	2.1	267	1	TRPC_MERJA	Q58338	methanococc	978	5	2.1	285	1	STAR_BOVIN	Q28918	bos taurus
906	5	2.1	267	1	CGIC_DROME	P25008	drosophila	979	5	2.1	285	1	WARD_SCHPO	Q59893	schizosacch
907	5	2.1	268	1	TF2D_EMENT	Q12731	emeritella	980	5	2.1	286	1	COX3_TRYBO	Q37355	trypanoplas
908	5	2.1	269	1	HXB5_MOUSE	P09079	mus musculu	981	5	2.1	286	1	FLAI_TREPA	P21990	treponema p
909	5	2.1	269	1	IOD3_RANCA	P49898	rana catesb	982	5	2.1	286	1	MF5A_PHLPR	Q40962	phleum prat

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983 5 2.1 286 1 SYGA_THEME 09wy59 thermotoga
984 5 2.1 287 1 DLX3_HUMAN 060479 homo sapien
985 5 2.1 287 1 DLX3_MOUSE 064205 mus musculu
986 5 2.1 287 1 SCF_CHICK 009108 gallus gall
987 5 2.1 287 1 STX4_CAEEL P91409 caenorhabdi
988 5 2.1 287 1 YCXB_BACSU P40420 bacillus su
989 5 2.1 288 1 BLC3_PSEAE P37322 pseudomonas
990 5 2.1 288 1 BLC4_PSEAE 051355 pseudomonas
991 5 2.1 288 1 BLC6_VIBCH P11781 vibrio chol
992 5 2.1 288 1 BLP1_PSEAE 003170 pseudomonas
993 5 2.1 288 1 BLP4_PSEAE P16897 pseudomonas
994 5 2.1 288 1 EPWO_HUMAN P32856 homo sapien
995 5 2.1 288 1 PCDI_MOUSE Q02242 mus musculu
996 5 2.1 288 1 PE12_YEAST P32854 saccharomyc
997 5 2.1 288 1 SECF_AQUAE 067536 aquifex aeo
998 5 2.1 289 1 SUCD_THERFL P09143 thermus aqu
999 5 2.1 289 1 PTR1_LERITA P42556 leishmania
1000 5 2.1 291 1 DH11_SAISC Q29508 salmmtl scl

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## ALIGNMENTS

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RESULT 1
TLOC_HUMAN STANDARD; PRT; 259 AA.
ID TLOC_HUMAN 014755;
AC 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10C precursor (Decoy
DE receptor 1) (DcR1) (Decoy TRAIL receptor without death domain) (TNF-
DE related apoptosis-inducing ligand receptor 3) (TRAIL receptor-3)
DE (TRAIL-R3) (TRAIL receptor without an intracellular domain)
DE (Lymphocyte inhibitor of TRAIL) (Antagonist decoy receptor for
DE TRAIL/Apo-2L)
GN TNFRSF10C OR DCR1 OR TRAILR3 OR TRID OR LIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RX MEDLINE-97467318; PubMed-9325248;
RA MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T.,
RA Cohen G.M., Alnemri E.S.;
RT "Identification and molecular cloning of two novel receptors for the
RT cytotoxic ligand TRAIL."
RL J. Biol. Chem. 272:25417-25420(1997).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE-Foreskin fibroblast;
RX MEDLINE-97461602; PubMed-9314565;
RA DeWitt-DeBartoli M.A., Smolak P.J., Malczak H., Waugh J., Huang C.-P.,
RA Dubose R.F., Goodwin R.G., Smith C.A.;
RT "Cloning and characterization of TRAIL-R3, a novel member of the
RT emerging TRAIL receptor family."
RL J. Exp. Med. 186:1165-1170(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-97390508; PubMed-9242610;
RA Pan G., Ni J., Wei Y.-F., Yu G.-L., Gentz R., Dixit V.M.;
RT "An antagonist decoy receptor and a death domain-containing receptor
RT for TRAIL."
RL Science 277:815-818(1997).
RN [4]
RP SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
RX MEDLINE-97390509; PubMed-9242611;
RA Sheridan D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA Goddard A.D., Godowski P., Ashkenazi A.;
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT receptors."

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RL Science 277:818-821(1997).
RN [5]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE-Liver, and Spleen;
RX MEDLINE-98039016; PubMed-9373179;
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,
RA Tschoep J.;
RT "Characterization of two receptors for TRAIL."
RL FEBS Lett. 416:329-334(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-98211672; PubMed-9551946;
RA Mongkolsapaya J., Comper A.E., Xu X.-N., Morris G., McMichael A.J.,
RA Bell J.I., Screaton G.R.;
RT "Lymphocyte inhibitor of TRAIL (TNF-related apoptosis-inducing
RT ligand): a new receptor protecting lymphocytes from the death ligand
RT TRAIL."
RL J. Immunol. 160:3-6(1998).
CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a
CC cytoplasmic death domain and hence is not capable of inducing
CC apoptosis. May protect cells against TRAIL mediated apoptosis by
CC competing with TRAIL-R1 and R2 for binding to the ligand.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Higher expressed in normal tissues than in
CC tumor cell lines. Highly expressed in peripheral blood
CC lymphocytes, spleen, skeletal muscle, placenta, lung and heart.
CC -1- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
DR EMBL: AF020502; AAB71413.1; ALT_INIT.
DR EMBL: AF014794; AAC05593.1; ALT_INIT.
DR EMBL: AF012629; AAB67110.1; -.
DR EMBL: AF012536; AAB67104.1; -.
DR EMBL: AF016267; AAB81181.1; -.
DR EMBL: AF033854; AAB87506.1; -.
DR HSSP: P19438; 1EXT.
DR KIM: 603613; -.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 1.
DR SMART: SM00208; TNFR_1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; GPI-anchor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 236
FT PROPEP 237 259
FT REPEAT 69 109
FT REPEAT 110 149
FT DOMAIN 162 236
FT REPEAT 162 176
FT REPEAT 177 191
FT REPEAT 192 206
FT REPEAT 207 221
FT REPEAT 222 236
FT DISULFID 69 85
FT DISULFID 88 101
FT DISULFID 91 109
FT DISULFID 111 125
FT DISULFID 128 141
FT DISULFID 131 149
FT LIPID 236 236
FT CARBOHYD 77 77
FT CARBOHYD 140 140

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TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 10C.
REMOVED IN MATURE FORM (POTENTIAL).
TNFR-CYS 1.
5 X 15 AA TANDEM TAPE REPEATS.
1.
2.
3.
4.
5.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
GPI-ANCHOR (POTENTIAL).
N-LINKED (GLCNAC. . .) (HIGH MANNOSE)
(POTENTIAL).
N-LINKED (GLCNAC. . .) (HIGH MANNOSE)
(POTENTIAL).

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FT FT CARBOHYD 156 156 (POTENTIAL).  
FT FT CONFLICT 119 119 N-LINKED (GLCNAC. . .) (HIGH MANNOSE)  
FT FT SEQUENCE 259 AA; 27395 MM; PE3BF7FCEEA5088 CRC64; (POTENTIAL).  
E -> V (IN REF. 5).  
Query Match 100.0%; Score 233; DB 1; Length 259;  
Best Local Similarity 100.0%; Pred. No. 4.2e-238;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAQEEVPOQTVAPQOORHSFKGECGAGSHRSEHTGACNCPCEGVDTYNASNNPSCF 60  
DB 27 TTAQEEVPOQTVAPQOORHSFKGECGAGSHRSEHTGACNCPCEGVDTYNASNNPSCF 86  
QY 61 PCTVCKSDQKHKSCTMTMDVCOCKEETFRNNSPEMCRCSRCPSGEVOVSNCTSMDD 120  
DB 87 PCTVCKSDQKHKSCTMTMDVCOCKEETFRNNSPEMCRCSRCPSGEVOVSNCTSMDD 146  
QY 121 IQCVEEFGANATVETPAEETMNTSPGTPAPAEETMNTSPGTPA 180  
DB 147 IQCVEEFGANATVETPAEETMNTSPGTPAPAEETMNTSPGTPA 206  
QY 181 PAEETMTTSGTTPAPAEETMTTSPGTPASSHTLCTIVGIIIVLIVFV 233  
DB 207 PAEETMTTSGTTPAPAEETMTTSPGTPASSHTLCTIVGIIIVLIVFV 259

RESULT 2  
T10D\_HUMAN STANDARD; PRT; 386 AA.  
ID T10D\_HUMAN Q9UBN6; Q9Y6Q4;  
AC Q9UBN6; Q9Y6Q4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10D precursor (Decoy receptor 2) (Dcr2) (TNF-related apoptosis-inducing ligand receptor 4) (TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death domain).  
GN TNFRSF10D OR DCR2 OR TRAILR4 OR TRUND.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND VARIANT.  
RC TISSUE=Fetal lung;  
RA MEDLINE=98044290; PubMed=9382840;  
RA Marsters S.A., Sheridan J.P., Pitti R.M., Huang A., Skubatch M., Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P., Ashkenazi A.;  
RA "A novel receptor for Apo2L/TRAIL contains a truncated death domain.", Curr. Biol. 7:1003-1006(1997).  
RL [2]  
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANTS S-35 AND L-310.  
RC TISSUE=Forebrain fibroblast, and Peripheral blood lymphocytes;  
RA MEDLINE=98090091; PubMed=9430226;  
RA Degli-Esposti M.A., Dougall W.C., Smolak P.J., Maugh J.Y., Smith C.A., Goodwin R.G.;  
RA "The novel receptor TRAIL-R4 induces NF-kappaB and protects against TRAIL-mediated apoptosis, yet retains an incomplete death domain.", Immunity 7:813-820(1997).  
RL [3]  
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RP MEDLINE=98196860; PubMed=9537512;  
RA Pan G., Ni J., Yu G.-L., Wei Y.-F., Dixit V.M.;  
RA "TRUND, a new member of the TRAIL receptor family that antagonizes TRAIL signalling.", FEBS Lett. 424:41-45(1998).  
RL [1]  
CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains a truncated death domain and hence is not capable of inducing apoptosis but protects against TRAIL-mediated apoptosis. Reports are contradictory with regards to its ability to induce the NF-

CC kappab pathway (According to ref.1 it cannot but according to ref.2 it can induce the NF-kappab pathway).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Widely expressed, in particular in fetal kidney, lung & liver and in adult testis and liver. Also expressed in peripheral blood leukocytes, colon and small intestine, ovary, prostate, thymus, spleen, pancreas, kidney, lung, placenta and heart.  
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN (TRUNCATED).  
CC -----  
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CC -----  
CC EMBL; AF029761; AAD03477.1; -;  
CC EMBL; AF021232; AAC32765.1; -;  
CC EMBL; AF021233; AAC32766.1; -;  
CC EMBL; AF023849; AAC52053.1; -;  
CC HSSP; P19438; INCF.  
CC MIM; 603614; -;  
CC InterPro: IPR001368; TNFR\_c6.  
CC Pfam: PF00020; TNFR\_c6; 2.  
CC SMART: SM00208; TNFR; 2.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
CC PROSITE; PS00650; TNFR\_NGFR\_2; 2.  
CC Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;  
CC Polymorphism.  
FT FT SIGNAL 1 55  
FT FT CHAIN 56 386  
FT FT TRANSSEM 212 211  
FT FT DOMAIN 233 386  
FT FT REPEAT 98 139  
FT FT REPEAT 140 180  
FT FT DOMAIN 340 366  
FT FT DOMAIN 225 228  
FT FT DOMAIN 246 250  
FT FT DISULFID 99 115  
FT FT DISULFID 118 131  
FT FT DISULFID 121 139  
FT FT DISULFID 141 155  
FT FT DISULFID 158 172  
FT FT CARBOHYD 162 127  
FT FT CARBOHYD 182 182  
FT FT VARIANT 35 35  
FT FT VARIANT 310 310  
FT FT SEQUENCE 386 AA; 41823 MM; 77A93577CAAF2632 CRC64;  
SQ

Query Match 6.0%; Score 14; DB 1; Length 386;  
Best Local Similarity 100.0%; Pred. No. 4.8e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGACNPTCEGVDT 50  
DB 93 TGACNPTCEGVDT 106

RESULT 3  
T10B\_HUMAN STANDARD; PRT; 440 AA.  
ID T10B\_HUMAN O14763; O15531; O15508; O15517; O14720; Q9BVE0;  
AC O14763; O15531; O15508; O15517; O14720; Q9BVE0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10B precursor (Death  
 DE receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL  
 DE receptor-2) (TRAIL-R2)  
 CN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF N-TERMINUS.  
 RC TISSUE=ForeSkin Fibroblast;  
 RX MEDLINE=97459925; PubMed=9311998;  
 RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Rauch J.Y.,  
 RA Bolani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,  
 RA Goodwin R.G., Rauch C.T.;  
 RT "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";  
 RL EMO J. 16:5386-5397(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE  
 RP SPLICING.  
 RX MEDLINE=97431692; PubMed=9285725;  
 RA Screaton G.R., Mongkolsapaya J., Xu X.-N., Compier A.E.,  
 RA McMichael A.J., Bell J.I.;  
 RT "TRICK2, a new alternatively spliced receptor that transduces the  
 RT cytotoxic signal from TRAIL.";  
 RL Curr. Biol. 7:693-696(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.  
 RC TISSUE=Liver, and Spleen;  
 RX MEDLINE=98039016; PubMed=9373179;  
 RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,  
 RA Teschopp J.;  
 RT "Characterization of two receptors for TRAIL.";  
 RL FEBS Lett. 416:329-334(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RC TISSUE=Ovary;  
 RX MEDLINE=97467719; PubMed=9326928;  
 RA Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,  
 RA Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,  
 RA Spiller N.B., Markowitz S., Wu G., el-Deiry W.S.;  
 RT "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor  
 RT gene.";  
 RL Nat. Genet. 17:141-143(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=97390508; PubMed=9242610;  
 RA Pan G., Ni J., Wei Y.-F., Yu G.-T., Gentz R., Dixit V.M.;  
 RT "An antagonist decoy receptor and a death domain-containing receptor  
 RT for TRAIL.";  
 RL Science 277:815-818(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=97467318; PubMed=9325248;  
 RA McFatlaine M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T.,  
 RA Cohen G.M., Alnemri E.S.;  
 RT "Identification and molecular cloning of two novel receptors for the  
 RT cytotoxic ligand TRAIL.";  
 RL J. Biol. Chem. 272:25417-25420(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=9809092; PubMed=9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
 RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:831-830(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=97390509; PubMed=9242611;  
 RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,  
 RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,  
 RA Goddard A.D., Godowski P., Ashkenazi A.;

RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy  
 RT receptors.";  
 RL Science 277:818-821(1997).  
 RN [9]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yusa Y.;  
 RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2  
 RT gene in colorectal carcinoma.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RA Cao X., Zhang W., Wan T.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RA Farrar T., Vu T., Gilbert T., Gross J., O'Hara P.;  
 RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RC TISSUE=Cervix;  
 RA Strausberg R.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
 RX MEDLINE=20017054; PubMed=10549288;  
 RA Hymowitz S.G., Christinger H.W., Fuh G., Utsch M., O'Connell M.,  
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
 RT complex with death receptor 5.";  
 RL Mol. Cell 4:563-571(1999).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
 RX PubMed=10542098;  
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Screaton G.R.;  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates  
 CC apoptosis in a caspase-dependent manner. Can trigger the nuclear  
 CC factor kappaB pathway and can bind the cytoplasmic adapter  
 CC molecule FADD/MORT1 which engages initiator caspases such as  
 CC caspase 8 leading to subsequent activation of effector caspases  
 CC that execute apoptotic death of the cell.  
 CC -1- SUBUNIT: Homotrimer (potential). Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/TRICK2A (SHOWN HERE)  
 CC AND A SHORT FORM/TRICK2B; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
 CC very highly expressed in tumor cell lines such as HeLa S3, K562,  
 CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral  
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
 CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
 CC the intestinal tract; not detectable in brain.  
 CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.  
 CC -1- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell  
 CC carcinoma of the head and neck.  
 CC -1- SIMILARITY: CONTAINS 1 LA-NCRF/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: AF016849; AAC51778.1; -  
 CC EMBL: AF018657; AAB70577.1; -  
 CC EMBL: AF018658; AAB70578.1; -  
 CC EMBL: AF016266; AAB61180.1; -

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DR EMBL: AF022386; AAB71949.1; -
DR EMBL: AF012628; AAB67109.1; -
DR EMBL: AF020501; AAB71412.1; -
DR EMBL: AF016268; AAC01565.1; -
DR EMBL: AF012535; AAB67103.1; -
DR EMBL: AB014718; BAA33723.1; -
DR EMBL: AB014710; BAA33723.1; JOINED.
DR EMBL: AB014711; BAA33723.1; JOINED.
DR EMBL: AB014712; BAA33723.1; JOINED.
DR EMBL: AB014713; BAA33723.1; JOINED.
DR EMBL: AB014714; BAA33723.1; JOINED.
DR EMBL: AB014715; BAA33723.1; JOINED.
DR EMBL: AB014716; BAA33723.1; JOINED.
DR EMBL: AB014717; BAA33723.1; JOINED.
DR EMBL: AF153687; AAF75587.1; -
DR EMBL: AF192548; AAF07175.1; -
DR EMBL: BC001281; AAH01281.1; -
DR MIM: 603612; -
DR MIM: 601400; -
DR PDB: 1D0G; 22-OCT-99.
DR PDB: 1D4V; 01-NOV-99.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death_1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
DR Receptor: Apoptosis; Transmembrane; Repeat; Signal;
KW Alternative splicing; 3D-structure.
FT SIGNAL 1 55
FT CHAIN 56 440
FT DOMAIN 56 210 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSLEM 211 231 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 232 440 POTENTIAL.
FT REPEAT 97 137 CYTOPLASMIC (POTENTIAL).
FT REPEAT 138 178 TNFR-CYS 1.
FT REPEAT 192 206 TNFR-CYS 2.
FT DOMAIN 339 422 TAPE.
FT DOMAIN 250 253 DEATH.
FT DISULEID 81 94 POLY-GLY.
FT DISULEID 97 113
FT DISULEID 116 129
FT DISULEID 119 137
FT DISULEID 139 153
FT DISULEID 156 170
FT DISULEID 160 178

Query Match
Best Local Similarity 3.4%; Score 8; DB 1; Length 440;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RP SEQUENCE FROM N.A.
RC STRAIN-MSB8 / DSM 3109;
RX MEDLINE-99287316; PubMed-10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -1- FUNCTION: ASSEMBLES AROUND THE ROD TO FORM THE I-RING AND PROBABLY
CC PROTECTS THE MOTOR/BASAL BODY FROM SHEARING FORCES DURING
CC ROTATION.
CC -1- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
CC MOUNTED ON A CENTRAL ROD (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE FLGH FAMILY.
CC -----
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CC -----
DR EMBL: AE001800; AAD36607.1; -
DR TIGR: TMI540; -
DR InterPro: IPR000527; Flag_Lring.
DR Pfam: PF02107; FLGH; 1.
DR PRINTS: PR01008; FLAGRINGFLGH.
KW Flagella; Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 25
FT CHAIN 26 199 POTENTIAL.
FT SIGNAL 1 25 FLAGELLAR L-RING PROTEIN.
SQ SEQUENCE 199 AA; 21896 MW; DZA487647F95E22C CRC64;

Query Match
Best Local Similarity 3.0%; Score 7; DB 1; Length 199;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SQ SEQUENCE 283 AA: 30614 MW: EC42F07A4D15C07A CRC64;  
 Query Match 3.0%; Score 7; DB 1; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 8.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 172 MTSPTGT 178  
 |||||  
 DB 1 MTSPTGT 7

RESULT 8  
 YDB1\_SCHPO STANDARD; PRT: 374 AA.  
 AC 010354: 09URX5:  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Hypothetical 42.3 kDa protein G22E12.01 in chromosome I.  
 GN SPAC22E12.01 OR SPAC890.09.  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 ON NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE OF 1-258 FROM N.A.  
 RC STRAIN=972;  
 RA Saunders D., Harris D., McDougall R.C., Rajandream M.A., Barrell B.G.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 229-374 FROM N.A.  
 RC STRAIN=972;  
 RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL: AL133498; CAB63500.1; -.  
 DR EMBL: Z70043; CA93888.1; -.  
 KW Hypothetical protein; Transmembrane.  
 FT TRANSMEM 50 70  
 FT TRANSMEM 151 171 POTENTIAL.  
 FT TRANSMEM 175 195 POTENTIAL.  
 FT TRANSMEM 201 221 POTENTIAL.  
 FT TRANSMEM 238 258 POTENTIAL.  
 FT TRANSMEM 273 293 POTENTIAL.  
 FT TRANSMEM 329 349 POTENTIAL.  
 SQ SEQUENCE 374 AA: 42300 MW: AE504D8322FAFB12 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 222 IIVIVL 228  
 |||||  
 DB 52 IIVIVL 58

RESULT 9  
 LA\_DROME STANDARD; PRT: 390 AA.  
 AC P40796: 024375: Q9YIN2;  
 DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).  
 GN LA OR CG10922.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CANTON-S; TISSUE=Ovary;  
 RX MEDLINE=94309632; PubMed=8035794;  
 RA Bai C., Li Z., Tollas P.P.;  
 RT "Developmental characterization of a Drosophila RNA-binding protein  
 RT homologous to the human systemic lupus erythematosus-associated  
 RT La/SS-B autoantigen."  
 RL Mol. Cell. Biol. 14:5123-5129(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94309661; PubMed=8035818;  
 RA Yoo C.J., Molin S.L.;  
 RT "La proteins from Drosophila melanogaster and Saccharomyces  
 RT cerevisiae: a yeast homolog of the La autoantigen is dispensable for  
 RT growth."  
 RL Mol. Cell. Biol. 14:5412-5424(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceinikher S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
 RA De Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostel A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshnell A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleby J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein K.C., Wu D., Yang S., Yao O.A.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTION TERMINATION BY RNA  
 CC POLYMERASE III BINDS RNA AND DNA. BINDS TO PRECURSORS OF RNA  
 CC POLYMERASE III TRANSCRIPTS. MAY PLAY A SPECIALIZED ROLE DURING FLY  
 CC DEVELOPMENT.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

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CC -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT EMBRYONIC, LARVAL,
CC PUPAL, AND ADULT DEVELOPMENT. EXPRESSION THROUGHOUT THE EMBRYO IS
CC FOLLOWED BY A RESTRICTED PATTERN OF MESODERMAL EXPRESSION THAT IS
CC LATER CONFINED TO THE VISCERAL MESODERM, GONADS, GUT, AND SALIVARY
CC GLANDS.
CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
CC
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CC -----
CC EMBL: U07652; AAA20518.1; -.
CC DR EMBL: L32988; AAA21776.1; -.
CC DR EMBL: AE003666; AAF53885.1; -.
CC DR FLYBASE: FBgn0011638; La.
CC DR InterPro: IPR002344; Lupus_La.
CC DR InterPro: IPR000504; RRM.
CC DR Pfam: PF00076; rrm; 1.
CC DR PRINTS: PR00302; LUPUSLA.
CC DR SMART: SM00360; RRM; 1.
CC DR PROSITE: PS50102; RRM; 1.
CC DR PROSITE: PS00030; RRM_RNP_1; 1.
CC KM DNA-binding: Nuclear protein; DNA-binding.
CC FT DOMAIN 149 234 RNA-BINDING (RRM).
CC FT CONFLICT 169 169 A -> T (IN REF. 1).
CC FT CONFLICT 182 183 KH -> NS (IN REF. 1).
CC FT CONFLICT 283 283 A -> R (IN REF. 1).
CC FT CONFLICT 329 329 K -> N (IN REF. 1).
CC SQ SEQUENCE 390 AA; 44884 MW; A8099288B90446A5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 390;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAAEE 155
Db 36 PAPAAEE 42

RESULT 10
DCOR_DATST STANDARD: PRT: 431 AA.
AC P50134;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Ornithine decarboxylase (EC 4.1.1.17) (ODC).
OS Datura stramonium (Jimsonweed) (Common thornapple).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Datura.
OX NCBI_TaxID=4076;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CV. D15/5; TISSUE=ROOT;
RA MEDLINE=9615135; PubMed=8660289;
RT "Molecular cloning and functional identification of a plant ornithine
RT decarboxylase cDNA."
RL Biochem. J. 314:241-248(1996).
CC -1- CATALYTIC ACTIVITY: L-ornithine = putrescine + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY
CC OF POLYAMINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE
CC DECARBOXYLASES.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X87847; CAA61121.1; -.
CC DR HSSP: P00860; 70DC.
CC DR InterPro: IPR000183; Orn_DAP_Arg_decarboxylase.
CC DR Pfam: PF02784; Orn_Arg_dec_N; 1.
CC DR Pfam: PF00278; Orn_DAP_Arg_dec; 1.
CC DR PRINTS: PR01179; ODACRBXLYASE.
CC DR PROSITE: PS00878; ODR_DC_2_1; 1.
CC DR PROSITE: PS00879; ODR_DC_2_2; 1.
CC KM Lyase; Decarboxylase; pyridoxal phosphate; polyamine biosynthesis;
CC phosphorylation.
CC FT BINDING 94 94 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC FT ACT_SITE 376 376 BY SIMILARITY.
CC SQ SEQUENCE 431 AA; 46659 MW; 8168064D8CC1C9F8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 431;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 TPAPAAE 154
Db 25 TPAPAAE 31

RESULT 11
BIAR_MOUSE STANDARD: PRT: 466 AA.
AC P34971;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Beta-1 adrenergic receptor.
DE ADRB1 OR ADRB1R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=93372116; PubMed=8395893;
RA Jasper J.R., Link R.E., Chruscinski A.J., Koblika B.K., Bernstein D.;
RT "Primary structure of the mouse beta 1-adrenergic receptor gene."
RL Biochim. Biophys. Acta 1178:307-309(1993).
CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
CC APPROXIMATELY EQUAL AFFINITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L10084; AAA02929.1; -.
CC DR PTR: S36794; S36794.
CC DR HSSP: P07700; IDEP.
CC DR GCRDB: GCR_0578; -.

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DR MGD; MGI:87937; Adrb1.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECIP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECIP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 59  
 FT TRANSSEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSSEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSSEM 132 155  
 FT DOMAIN 156 175  
 FT TRANSSEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSSEM 222 245  
 FT DOMAIN 246 314  
 FT TRANSSEM 315 338  
 FT DOMAIN 339 345  
 FT TRANSSEM 346 369  
 FT DOMAIN 370 466  
 FT CARBOHYD 15 15  
 FT DISULFID 131 209  
 FT LIPID 381 381  
 FT MOD\_RES 296 296  
 FT MOD\_RES 301 301  
 FT MOD\_RES 401 401  
 SQ SEQUENCE 466 AA; 50479 MW; 753CD44C42BC9211 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 466;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
 |||||  
 Db 67 LIVLIV 73

RESULT 12  
 ID BIAR\_RAT STANDARD; PRT; 466 AA.  
 AC P18090;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Beta-1 adrenergic receptor.  
 GN ADRB1 OR ADRB1R.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90330633; PubMed=169589;  
 RA Machuga C.A., Bunzow J.R., Searles R.P., van Tol H.H.M., Tester B.,  
 RA Neve K.A., Teal P., Nipper V., Civelli O.,  
 RT "Molecular cloning and expression of the rat beta 1-adrenergic  
 RT receptor gene."  
 RL J. Biol. Chem. 265:12960-12965(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90356399; PubMed=2167473;  
 RA Shimomura H., Terada A.;  
 RT "Primary structure of the rat beta-1 adrenergic receptor gene."  
 RL Nucleic Acids Res. 18:4591-4591(1990).  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 CC INDUCED ACTIVATION OF ADENYLYL CYCLASE THROUGH THE ACTION OF G  
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 CC APPROXIMATELY EQUAL AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: J05561; AAA40792.1; -;  
 DR EMBL: D00634; BAA00527.1; -;  
 DR PIR: A36618; A36618.  
 DR PIR: S12591; S12591.  
 DR HSSP: P07700; IDEP.  
 DR GCRDB: GCR\_0126; -;  
 DR GCRDB: GCR\_0127; -;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECIP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECIP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 59  
 FT TRANSSEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSSEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSSEM 132 155  
 FT DOMAIN 156 175  
 FT TRANSSEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSSEM 222 245  
 FT DOMAIN 246 314  
 FT TRANSSEM 315 338  
 FT DOMAIN 339 345  
 FT TRANSSEM 346 369  
 FT DOMAIN 370 466  
 FT CARBOHYD 15 15  
 FT DISULFID 131 209  
 FT LIPID 381 381  
 FT MOD\_RES 296 296  
 FT MOD\_RES 301 301  
 FT MOD\_RES 401 401  
 FT CONFLICT 162 162  
 FT CONFLICT 267 267  
 SQ SEQUENCE 466 AA; 50471 MW; 2955CB02494A12B CRC64;

Query Match 3.0%; Score 7; DB 1; Length 466;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
 |||||  
 Db 67 LIVLIV 73

RESULT 13  
 ID BIAR\_PIG STANDARD; PRT; 468 AA.  
 AC Q28998; Q46575;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Beta-1 adrenergic receptor.  
 GN ADRB1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

CC NCBL\_TaxID=9823;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=98318327; PubMed=9655595;  
 CC Cao H., Bidwell C.A., Williams S.K., Liang W., Mills S.E.;  
 CC "Nucleotide sequence of the coding region for the porcine beta1-  
 CC adrenergic receptor gene.";  
 CC J. Anim. Sci. 76:1720-1721(1998).  
 CC [2]  
 CC SEQUENCE OF 101-468 FROM N.A.  
 CC TISSUE=Heart;  
 CC McNeil R.L., Mersmann H.J.;  
 CC Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 CC INDUCED ACTIVATION OF ADENYLYL CYCLASE THROUGH THE ACTION OF G  
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 CC APPROXIMATELY EQUAL AFFINITY (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PFM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 CC EMBL: AF042454; AAB97525.1; -  
 CC DR EMBL: U56425; AAC06330.1; -  
 CC DR HSSP: P07700; IDEP.  
 CC DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 CC Pfm: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR00237; GPCRHHODPSN.  
 CC DR PROSITE: PS00237; G-PROTEIN\_RECPEP\_FL\_1; 1.  
 CC DR PROSITE: PS50262; G-PROTEIN\_RECPEP\_FL\_2; 1.  
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 CC Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 CC FT DOMAIN 1 59  
 CC EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSSEM 60 83  
 CC CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 84 96  
 CC CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSSEM 97 121  
 CC EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSSEM 122 132  
 CC EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSSEM 133 153  
 CC CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 154 176  
 CC CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSSEM 177 197  
 CC EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 198 223  
 CC EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSSEM 224 244  
 CC CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 245 315  
 CC CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSSEM 316 336  
 CC EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 337 347  
 CC EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSSEM 348 368  
 CC CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 369 468  
 CC CYTOPLASMIC (POTENTIAL).  
 CC FT CARBOHYD 15 15  
 CC N-LINKED (GLUCNA. . .) (POTENTIAL).  
 CC FT DISULFID 131 208  
 CC BY SIMILARITY.  
 CC FT LIPID 131 208  
 CC PALMITATE (BY SIMILARITY).  
 CC FT CONFLICT 173 173  
 CC A -> AR (IN REF. 2).  
 CC FT CONFLICT 316 316  
 CC L -> V (IN REF. 2).  
 CC FT CONFLICT 326 328  
 CC CWL -> WWV (IN REF. 2).  
 CC FT CONFLICT 448 448  
 CC R -> A (IN REF. 2).  
 CC FT CONFLICT 458 458  
 CC T -> S (IN REF. 2).  
 CC FT CONFLICT 463 464  
 CC AS -> SF (IN REF. 2).  
 CC SO SEQUENCE 468 AA; 50098 MW; 93C3AE7BB703225 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 225 LIVLLIV 231

Db 67 LIVLLIV 73  
 RESULT 14  
 ID T10A\_HUMAN STANDARD; PRT; 468 AA.  
 AC 000220;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10A precursor (Death  
 DE receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL  
 DE receptor-1) (TRAIL-R1).  
 GN TNFRSF10A OR DR4 OR TRAILR1 OR APO2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 CC NCBL\_TaxID=9606;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=97238921; PubMed=9082980;  
 CC Pan G., O'Rourke K., Chinnaiyan A.M., Gentz R., Edner R., Ni J.,  
 CC Dixit V.M.;  
 CC "The receptor for the cytotoxic ligand TRAIL.";  
 CC Science 276:111-113(1997).  
 CC [2]  
 CC FUNCTION.  
 CC MEDLINE=98090092; PubMed=9430227;  
 CC Chaudhary P.M., Bdy M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 CC "Death receptor 5, a new member of the TNFR family, and DR4 induce  
 CC FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 CC Immunity 7:821-830(1997).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates  
 CC apoptosis in a caspase-dependent manner. Can trigger the nuclear  
 CC factor kappaB-pathway and can bind the cytoplasmic adapter  
 CC molecule FADD/MORT1 which engages initiator caspases such as  
 CC caspase 8 leading to subsequent activation of effector caspases  
 CC that execute apoptotic death of the cell.  
 CC -1- SUBUNIT: Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Widely expressed. High levels are found in  
 CC spleen, peripheral blood leukocytes, small intestine and thymus,  
 CC but also in K562 erythroleukemia cells, MCF7 breast carcinoma  
 CC cells and activated T-cells.  
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: U90875; AAC51226.1; -  
 CC DR HSSP: P19438; IEXT.  
 CC DR MIM: 603611; -  
 CC DR InterPro: IPR000488; Death.  
 CC DR InterPro: IPR001368; TNFR\_c6.  
 CC Pfm: PF00531; death; 1.  
 CC DR Pfm: PF00020; TNFR\_c6; 2.  
 CC DR SMART: SM00005; DEATH; 1.  
 CC DR SMART: SM00208; TNFR; 2.  
 CC DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 CC DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 CC DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 CC KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.  
 CC FT SIGNAL 1 23  
 CC TUMOR NECROSIS FACTOR RECEPTOR  
 CC CHAIN 24 468  
 CC SUPRAFAMILY MEMBER 10A.  
 CC FT DOMAIN 24 239  
 CC EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 240 262 POTENTIAL.  
CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 263 468  
FT REPEAT 147 188 TNER-CYS 1.  
FT REPEAT 189 229 TNER-CYS 2.  
FT DOMAIN 365 448 DEATH.  
FT DOMAIN 29 32 POLY-ALA.  
FT DISULFID 132 145 POTENTIAL.  
FT DISULFID 148 164 POTENTIAL.  
FT DISULFID 167 180 POTENTIAL.  
FT DISULFID 170 188 POTENTIAL.  
FT DISULFID 190 204 POTENTIAL.  
FT DISULFID 207 221 POTENTIAL.  
FT DISULFID 211 229 POTENTIAL.  
FT CARBOHYD 156 156 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 468 AA; 50025 MW; 1E5DCC2C8760F7 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 468;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YTNASN 55  
| | | | |  
Db 154 YTNASN 160

RESULT 15  
UFO2\_MAIZE STANDARD; PRT; 471 AA.  
ID UFO2\_MAIZE  
AC P16165;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (UDP-glucose flavonoid  
3-O-glucosyltransferase) (Bronze-1) (Bz-MC2 allele).  
GN BZ1 OR UGT71A1.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_Taxid=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Furtak D., Schiefelbein J.W., Johnston F., Nelson O.E. Jr.;  
RT "Sequence comparisons of 3 wild-type bronze-1 alleles from Zea mays.";  
RL Plant Mol. Biol. 11:473-481(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-88284304; PubMed-3396861;  
RA Raiston E.J., English J.J., Dooner H.K.;  
RT "Sequence of three bronze alleles of maize and correlation with the  
RT genetic fine structure.";  
RL Genetics 119:185-197(1988).  
CC -!- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS  
CC GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN  
CC PIGMENTS.  
CC -!- CATALYTIC ACTIVITY: UDP-glucose + a flavonol = UDP + flavonol  
CC 3-O-D-glucoside.  
CC -!- PATHWAY: Anthocyanin biosynthesis.  
CC -!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
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CC -----  
CC EMBL: X13500; CAA31855.1; -  
CC EMBL: X07940; CAA30761.1; -  
CC PIR: S01052; S01052.  
CC PIR: S08324; S08324.

DR MaizeDB; 13885; -  
DR InterPro; IPR002213; UDPGT.  
DR Pfam; PF00201; UDPGT; 2.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase.  
SQ SEQUENCE 471 AA; 48769 MW; 6234FD59219AF534 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 471;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEET 156  
| | | | |  
Db 83 APAEET 89

RESULT 16  
UFO2\_MAIZE STANDARD; PRT; 471 AA.  
ID UFO2\_MAIZE  
AC P16165;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (UDP-glucose flavonoid  
3-O-glucosyltransferase) (Bronze-1) (Bz-MC2 allele).  
GN BZ1 OR UGT71A1.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_Taxid=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Furtak D., Schiefelbein J.W., Johnston F., Nelson O.E. Jr.;  
RT "Sequence comparisons of 3 wild-type bronze-1 alleles from Zea mays.";  
RL Plant Mol. Biol. 11:473-481(1988).  
CC -!- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS  
CC GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN  
CC PIGMENTS.  
CC -!- CATALYTIC ACTIVITY: UDP-glucose + a flavonol = UDP + flavonol  
CC 3-O-D-glucoside.  
CC -!- PATHWAY: Anthocyanin biosynthesis.  
CC -!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
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CC -----  
CC EMBL: X13501; CAA31856.1; -  
CC PIR: S08325; S08325.  
CC MaizeDB; 13885; -  
DR InterPro; IPR002213; UDPGT.  
DR Pfam; PF00201; UDPGT; 2.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase.  
SQ SEQUENCE 471 AA; 48621 MW; 81B897410A361299 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 471;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEET 156  
| | | | |  
Db 83 APAEET 89

RESULT 17

BLAR\_CANFA STANDARD: PRT: 473 AA.

ID BLAR\_CANFA STANDARD: PRT: 473 AA.

AC P79148: 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Beta-1 adrenergic receptor.

GN ADRB1.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OC NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=97364078; PubMed=9220370;

RA Huang R.-R.C., Rapoport D., Schaeffer M.-T., Cascleri M.A.,

RA Fong I.M.,

RT "Molecular cloning of the dog beta 1 and beta 2 adrenergic receptors."

RL J. Recept. Signal Transduct. Res. 17:599-607(1997).

CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATELY EQUAL AFFINITY.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: U73207; AAB93648.1; -

DR HSSP: P07700; IDEP.

DR GCRDB: GCR.1183; -

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_Rhodopsn.

DR PROSITE: PS00237; G-PROTEIN\_RECPT\_F1\_1; 1.

DR PROSITE: PS50262; G-PROTEIN\_RECPT\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multi-gene family; Phosphorylation; Lipoprotein; Palmitate.

KM Multi-gene family: Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 59 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 60 83 1 (POTENTIAL).

FT TRANSSEM 84 96 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 97 120 2 (POTENTIAL).

FT TRANSSEM 121 131 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 132 155 3 (POTENTIAL).

FT TRANSSEM 156 175 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 176 199 4 (POTENTIAL).

FT TRANSSEM 200 221 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 222 245 5 (POTENTIAL).

FT TRANSSEM 246 322 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 323 346 6 (POTENTIAL).

FT TRANSSEM 347 353 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 354 377 7 (POTENTIAL).

FT TRANSSEM 378 473 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 15 15 N-LINKED (GLCNAc. . .) (PROBABLE).

FT DISULFID 131 209 N-LINKED (GLCNAc. . .) (PROBABLE).

FT MOD\_RES 309 309 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT LIPID 389 389 PALMITATE (BY SIMILARITY).

SO SEQUENCE 473 AA; 50060 MW; 361357F7DF9BDB7E CRC64;

OY 225 LIVELIV 231

Db 67 LIVELIV 73

RESULT 18

BLAR\_FELCA STANDARD: PRT: 474 AA.

ID BLAR\_FELCA STANDARD: PRT: 474 AA.

AC O92876: 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Beta-1 adrenergic receptor.

GN ADRB1.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OC NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RA Cully D.F., Trembl G., Zachwieja S.;

RT "Feline domestic beta adrenergic receptor subtype 1.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATELY EQUAL AFFINITY (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: AF192344; AAF04303.1; -

DR HSSP: P07700; IDEP.

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_Rhodopsn.

DR PROSITE: PS00237; G-PROTEIN\_RECPT\_F1\_1; 1.

DR PROSITE: PS50262; G-PROTEIN\_RECPT\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multi-gene family; Phosphorylation; Lipoprotein; Palmitate.

KM Multi-gene family: Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 59 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 60 83 1 (POTENTIAL).

FT TRANSSEM 84 96 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 97 120 2 (POTENTIAL).

FT TRANSSEM 121 131 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 132 155 3 (POTENTIAL).

FT TRANSSEM 156 175 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 176 199 4 (POTENTIAL).

FT TRANSSEM 200 221 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 222 245 5 (POTENTIAL).

FT TRANSSEM 246 321 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 322 345 6 (POTENTIAL).

FT TRANSSEM 346 352 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 353 376 7 (POTENTIAL).

FT TRANSSEM 377 474 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 15 15 N-LINKED (GLCNAc. . .) (PROBABLE).

FT DISULFID 131 209 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT MOD\_RES 308 308 PALMITATE (BY SIMILARITY).

FT LIPID 388 388 PALMITATE (BY SIMILARITY).

SO SEQUENCE 474 AA; 50532 MW; 2FC97EDEACFB7C3F CRC64;

Query Match 3.0%; Score 7; DB 1; Length 473;

Best Local Similarity 100.0%; Pred. NO. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3.0%; Score 7; DB 1; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVILLIV 231  
 |||||  
 Db 67 LIVILLIV 73

RESULT 19  
 BIAR\_HUMAN STANDARD; PRT; 477 AA.  
 AC P08588; Q90K8; Q90K7;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-1 adrenergic receptor.  
 GN ADRB1 OR ADRB1R OR B1AR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA MEDLINE=88068509; PubMed=2825170;  
 RA Fietelle T., Collins S., Daniel K.W., Caron M.G., Lefkowitz R.J.,  
 RA Koblika B.K.;  
 RT "Cloning of the cDNA for the human beta 1-adrenergic receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7920-7924(1987).  
 RN [2]  
 RP VARIANT ARG-389.  
 RX MEDLINE=99230291; PubMed=10212248;  
 RA Mason D.A., Moore J.D., Green S.A., Liggett S.B.;  
 RT "A gain-of-function polymorphism in a G-protein coupling domain of the  
 human beta1-adrenergic receptor.";  
 RL J. Biol. Chem. 274:12670-12674(1999).  
 RN [3]  
 RP VARIANTS GLY-49 AND ARG-389.  
 RX MEDLINE=99407229; PubMed=10477438;  
 RA Moore J.D., Mason D.A., Green S.A., Hsu J., Liggett S.B.;  
 RT "Racial differences in the frequencies of cardiac beta(1)-adrenergic  
 receptor polymorphisms: analysis of c145A>G and c165G>C.";  
 RL Hum. Mutat. 14:271-271(1999).  
 RN [4]  
 RP VARIANT GLY-49.  
 RX MEDLINE=20507547; PubMed=11052857;  
 RA Borjesson M., Magnusson Y., Hjalmarsson A., Andersson B.;  
 RT "A novel polymorphism in the gene coding for the beta(1)-adrenergic  
 receptor associated with survival in patients with heart failure.";  
 RL Eur. Heart J. 21:1853-1858(2000).  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
 PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 APPROXIMATIVELY EQUAL AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL: J03019; AAA51667.1; -;  
 DR EMBL: AF169006; AAD53696.1; -;  
 DR EMBL: AF169007; AAD53697.1; -;  
 DR PIR: A39911; A39911.  
 DR HSSP: P07700; IDEP.

DR GCRDb; GCR\_0048; -;  
 DR MIM; 109630; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECCEP\_FL\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECCEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate;  
 KW polymorphism.  
 FT DOMAIN 1 59  
 FT TRANSSEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSSEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSSEM 132 155  
 FT DOMAIN 136 175  
 FT TRANSSEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSSEM 222 245  
 FT DOMAIN 246 325  
 FT TRANSSEM 326 349  
 FT DOMAIN 350 356  
 FT TRANSSEM 357 380  
 FT DOMAIN 381 477  
 FT CARBOHYD 15 15  
 FT DISULFID 131 209  
 FT MOD\_RES 312 312  
 FT MOD\_RES 412 412  
 FT LIPID 392 392  
 FT VARIANT 49 49  
 FT VARIANT 49 49  
 FT VARIANT 389 389  
 FT SEQUENCE 477 AA; 51223 MW; 1D15E6350B5364B8 CRC64;  
 G -> R (ENHANCED BINDING TO G PROTEINS).  
 /FT1d-VAR\_009880.  
 Query Match 3.0%; Score 7; DB 1; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVILLIV 231  
 |||||  
 Db 67 LIVILLIV 73

RESULT 20  
 BIAR\_MACMU STANDARD; PRT; 480 AA.  
 AC P47899;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Beta-1 adrenergic receptor.  
 GN ADRB1.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95078456; PubMed=7987008;  
 RA Seattles R.P., Nipper V.J., Machuga C.A.;  
 RT "The rhesus macaque beta 1-adrenergic receptor gene: structure of the  
 RT gene and comparison of the flanking sequences with the rat beta 1-  
 RT adrenergic receptor gene.";  
 RL DNA Seq. 4:231-241(1994).  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
 PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 APPROXIMATIVELY EQUAL AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- PWM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL: X75540; CA53228.1; -  
 DR HSSP: P07700; IDEP.  
 DR GCRDb: GCR\_1746; -  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECPT\_FL\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECPT\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 59  
 FT TRANSSEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSSEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSSEM 132 155  
 FT DOMAIN 156 175  
 FT TRANSSEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSSEM 222 245  
 FT DOMAIN 246 328  
 FT TRANSSEM 329 352  
 FT DOMAIN 353 359  
 FT TRANSSEM 360 383  
 FT DOMAIN 384 480  
 FT TRANSSEM 480 516  
 FT CARBOXYD 131 209  
 FT DISULFID 315 315  
 FT MOD\_RES 415 415  
 FT LIPID 395 395  
 FT SEQUENCE 480 AA; 51608 MW; 25CB18FA03128084 CRC64;  
 SQ  
 Query Match 3.0%; Score 7; DB 1; Length 480;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 225 LIVLLIV 231  
 Db 67 LIVLLIV 73  
 RESULT 21  
 PARE\_PARTE STANDARD; PRT; 584 AA.  
 AC P47244;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Parafusin.  
 OS Paramecium tetraurelia.  
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Penicillida;  
 OC Paramecium.  
 OX NCBI\_TaxID=5886;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RC STRAIN-STOCK 51;  
 RX MEDLINE=95024055; PubMed=7937900;  
 RA Subramanian S.V., Myroba E., Andersen A.P., Satir B.H.;  
 RT "Cloning and sequencing of parafusin, a calcium-dependent exocytosis-  
 related phosphoglycoprotein.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:9832-9836(1994).  
 RN [2]  
 RP REVISIONS TO 69-70.  
 RA Satir B.H.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=93087514; PubMed=1333606;  
 RA Subramanian S.V., Satir B.H.;  
 RT "Carbohydrate cycling in signal transduction: parafusin, a  
 phosphoglycoprotein and possible Ca(2+)-dependent transducer molecule  
 in exocytosis in Paramecium."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11297-11301(1992).  
 CC -1- FUNCTION: MAY BE INVOLVED IN MEMBRANE FUSION IN EXOCYTOSIS.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PWM: PHOSPHORYLATED VIA A CALCIUM-DEPENDENT PROTEIN KINASE.  
 CC -1- PWM: O-GLYCOSYLATED WITH A SHORT CHAIN OF MANNOSE RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L12471; AAB05649.2; -  
 DR HSSP: P00949; 3PMG.  
 DR InterPro: IPR001485; PGM\_PMM.  
 DR Pfam: PF00408; PGM\_PMM; 1.  
 DR Pfam: PF02878; PGM\_PMM\_I; 1.  
 DR Pfam: PF02879; PGM\_PMM\_II; 1.  
 DR Pfam: PF02880; PGM\_PMM\_III; 1.  
 DR PRINTS: PR00509; PGM\_PMM.  
 DR PROSITE: PS00710; PGM\_PMM; 1.  
 KW Phosphorylation.  
 FT ACT\_SITE 138  
 FT SEQUENCE 584 AA; 65312 MW; D96ED7D815D25A22 CRC64;  
 SQ  
 Query Match 3.0%; Score 7; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 208 TPASSHY 214  
 Db 112 TPASSHY 118  
 RESULT 22  
 CYSJ\_ECOLI STANDARD; PRT; 598 AA.  
 AC P38038; P14782;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)  
 DE (STR-PP)  
 GN CYSJ OR B2764.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-B;  
 RX MEDLINE=89380164; PubMed=2550423;  
 RA Ostrowski J., Barber M.J., Rueger D.C., Miller B.E., Siegel L.M.,  
 RA Kredich N.M.;  
 RT "Characterization of the flavoprotein moieties of NADPH-sulfite  
 reductase from Salmonella typhimurium and Escherichia coli."





```

RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mangall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jajels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrett B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + [DNA] (N).
CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
CC DIMERIZATION TO FORM THE POLIIT' COMPLEX. POLIIT' ASSOCIATES WITH
CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
CC AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: AL049478; CAB39586.1; -.
DR EMBL: AL583921; CAC31588.1; -.
DR Leproma; ML1207; -.
DR InterPro: IPR004013; PHP_C.
DR InterPro: IPR003141; PHP_N.
DR InterPro: IPR002309; tRNA-synt_2.
DR Pfam: PF02811; PHP_C; 1.
DR Pfam: PF02231; PHP_N; 1.
DR Pfam: PF01336; tRNA_ant1; 1.
DR SMART: SM00481; POLIITAC; 1.
DR SMART: SM00481; POLIITAC; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KM Complete proteome.
SQ SEQUENCE 1177 AA; 128971 MW; E53599FE950DDB6B CRC64;

Query Match 3.0%; Score 7; DB 1; Length 1177;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 CPSEGEVQ 111
Db 154 CPSEGEVQ 160

RESULT 25
DP3A_STRCO STANDARD; PRT; 1179 AA.
AC Q92618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA polymerase III alpha subunit (EC 2.7.7.7).
GN DNAB OR SC46.33C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M145;

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RX MEDLINE=99157597; PubMed=10048037;
RA Flett F., Jungmann-Campello D., Mersinias V., Koh S.L.-M., Godden R.,
RA Smith C.P.;
RT "A 'Gram-negative-type' DNA polymerase III is essential for
RT replication of the linear chromosome of Streptomyces coelicolor
RT A3(2).";
RL Mol. Microbiol. 31:949-958(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2).
RA Seeger K.J., Harris D., Bentley S.D., Parkhill J., Barrett B.G.,
RA Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + [DNA] (N).
CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
CC DIMERIZATION TO FORM THE POLIIT' COMPLEX. POLIIT' ASSOCIATES WITH
CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
CC AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF108191; AAD16978.1; -.
DR EMBL: AL096884; CAB51456.1; -.
DR InterPro: IPR004013; PHP_C.
DR InterPro: IPR003141; PHP_N.
DR InterPro: IPR002309; tRNA-synt_2.
DR Pfam: PF02811; PHP_C; 1.
DR Pfam: PF02231; PHP_N; 1.
DR Pfam: PF01336; tRNA_ant1; 1.
DR SMART: SM00481; POLIITAC; 1.
DR SMART: SM00481; POLIITAC; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication.
FT VARIANT 802 802 E->K (IN MUTANT T5-38).
SQ SEQUENCE 1179 AA; 130795 MW; 7E4B58675B634CD3 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 1179;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 CPSEGEVQ 111
Db 154 CPSEGEVQ 160

RESULT 26
DP3A_MYCTU STANDARD; PRT; 1184 AA.
AC Q10779;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA polymerase IIT alpha subunit (EC 2.7.7.7).
GN DNAB OR DNAB1 OR RV1547 OR M1598 OR M1598 OR M1598 OR M1598.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1773;
RN [1]

```

RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornby T., Jags K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTISUBUNIT ENZYME  
 CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.  
 CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.  
 CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate  
 CC + (DNA)(N).  
 CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA  
 CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE,  
 CC DIMERIZATION TO FORM THE POLIIT' COMPLEX. POLIIT' ASSOCIATES WITH  
 CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,  
 CC AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE  
 CC SUBFAMILY.  
 CC  
 CC -----  
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 CC -----  
 CC EMBL: Z74020; CAA98315.1; -;  
 DR EMBL: AE007026; AAK45865.1; -;  
 DR TIGR: MT1598; -;  
 DR Tuberculist: RV1547; -;  
 DR InterPro: IPR004013; PHP\_C;  
 DR InterPro: IPR003141; PHP\_M;  
 DR InterPro: IPR002309; tRNA-synt\_2.  
 DR Pfam: PF02811; PHP\_C; 1.  
 DR Pfam: PF02231; PHP\_N; 1.  
 DR Pfam: PF01336; tRNA\_anti; 1.  
 DR SMART: SM00481; POLIITAC; 1.  
 KW Transferrase; DNA-directed DNA polymerase; DNA replication;  
 KW Complete proteome.  
 SQ SEQUENCE 1184 AA; 129322 MW; A87AB7F0F2E08909 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 1184;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 CPSEGEVQ 111  
 |||||  
 Db 158 CPSEGEVQ 164

RESULT 27  
 MRSP\_STAAU STANDARD; PRT; 1637 AA.  
 ID MRSP\_STAAU  
 AC P80546; O92F62;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Methicillin-resistant surface protein precursor.  
 GN PLS.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ISOLATE 1061;  
 RA Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;  
 RT "Pis, a large repeat-rich surface protein of methicillin resistant  
 RT Staphylococcus aureus.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 624-628; 676-682; 938-948; 1156-1168; 1176-1185;  
 RP 1199-1205 AND 1217-1224.  
 RC STRAIN-ISOLATE 1061;  
 RX MEDLINE=96270743; PubMed=8665912;  
 RA Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P.;  
 RT "Purification and characterisation of a plasmin-sensitive surface  
 RT protein of Staphylococcus aureus.";  
 RL Eur. J. Biochem. 236:904-910(1996).  
 CC  
 CC -----  
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 CC -----  
 CC EMBL: AF115379; AAD09131.1; -;  
 DR InterPro: IPR001899; Gram\_pos\_anchor.  
 DR Pfam: PF00746; Gram\_pos\_anchor; 1.  
 DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; FALSE\_NEG.  
 KW Cell wall; Transmembrane; Antibiotic resistance; Glycoprotein; Repeat;  
 KW Signal.  
 FT SIGNAL 49 48  
 FT CHAIN 1 1637 POTENTIAL.  
 FT DOMAIN 1301 1582 METHICILLIN-RESISTANT SURFACE PROTEIN.  
 FT DOMAIN 1598 1603 141 X 2 AA TANDEM REPEATS OF D-[SAG].  
 FT PROTEINS.  
 SQ SEQUENCE 1637 AA; 174573 MW; 75BE9AD8469BD309 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 1637;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAAEET 156  
 |||||  
 Db 183 APAAEET 189

RESULT 28  
 CCAL\_RAT STANDARD; PRT; 1835 AA.  
 ID CCAL\_RAT  
 AC O92078;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Voltage-dependent T-type calcium channel alpha-1I subunit (CAVT.3).  
 GN CACNA1I.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

CC	NCHI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX	MEDLINE=99165796; PubMed=10066244;
RA	Lee J.-H., Daud A.N., Gibbs L.L., Lacerda A.E., Pereverzev A.,
RA	Kloechner U., Schneider T., Perez-Reyes E.;
RT	"Cloning and expression of a novel member of the low voltage-activated
RL	T-type calcium channel family";
J. Neurosci.	19:1912-1921(1999)."
CC	-1 FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC	ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC	IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC	CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC	CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1I
CC	GIVES RISE TO T-TYPE CALCIUM CURRENTS. T-TYPE CALCIUM CHANNELS
CC	BELONG TO THE "LOW-VOLTAGE ACTIVATED (LVA)" GROUP AND ARE STRONGLY
CC	BLOCKED BY NICKEL AND MIBEGADDIL. A PARTICULARITY OF THIS TYPE OF
CC	CHANNELS IS AN OPENING AT QUITE NEGATIVE POTENTIALS, AND A
CC	VOLTAGE-DEPENDENT INACTIVATION. T-TYPE CHANNELS SERVE PACEMAKING
CC	FUNCTIONS IN BOTH CENTRAL NEURONS AND CARDIAC NODAL CELLS AND
CC	SUPPORT CALCIUM SIGNALING IN SECRETORY CELLS AND VASCULAR SMOOTH
CC	MUSCLE. THEY MAY ALSO BE INVOLVED IN THE MODULATION OF FIRING
CC	PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING
CC	AS WELL AS IN CELL GROWTH PROCESSES. GATES IN VOLTAGE RANGES
CC	SIMILAR TO, BUT HIGHER THAN ALPHA 1G OR ALPHA 1H.
CC	-1 SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1 TISSUE SPECIFICITY: BRAIN.
CC	-1 DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC	HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC	POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC	PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC	SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC	-1 PWM: IN RESPONSE TO RAISING OF INTRACELLULAR CALCIUM, THE T-TYPE
CC	CHANNELS ARE ACTIVATED BY CAM-KINASE II (BY SIMILARITY).
CC	-1 SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC	FAMILY.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; AF086827; AADI7796.1; "
DR	InterPro: IPR002077; Ca_channel.
DR	InterPro: IPR002111; Cat_channel.Tryp.
DR	InterPro: IPR000636; Cation_chan.non_lig.
DR	InterPro: IPR001682; Channel_pore_Ca_Na.
DR	Pfam: PF00520; Ion_Trans; 4.
DM	PRINTS: PR00167; CACHANNEL.
DW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM	Calcium channel; Glycoprotein; Repeat; Multigene family;
RW	Calcium-binding; Phosphorylation.
FT	REPEAT 64 823
FT	REPEAT 584 823
FT	REPEAT 1116 1393
FT	REPEAT 1431 1692
FT	DOMAIN 1 76
FT	TRANSSEM 77 97
FT	TRANSSEM 98 115
FT	TRANSSEM 116 137
FT	DOMAIN 138 146
FT	TRANSSEM 147 166
FT	TRANSSEM 167 171
FT	TRANSSEM 172 189
FT	DOMAIN 190 209
FT	TRANSSEM 210 230
FT	DOMAIN 231 371
FT	TRANSSEM 372 396
FT	DOMAIN 397 598

FT	TRANSNMEM	599	619	S1 OF REPEAT II (POTENTIAL).
FT	DOMAIN	620	632	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	633	654	S2 OF REPEAT II (POTENTIAL).
FT	DOMAIN	655	660	CYTOPLASMIC (POTENTIAL).
FT	TRANSNMEM	661	679	S3 OF REPEAT II (POTENTIAL).
FT	DOMAIN	680	687	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	688	711	S4 OF REPEAT II (POTENTIAL).
FT	DOMAIN	712	722	CYTOPLASMIC (POTENTIAL).
FT	TRANSNMEM	723	743	S5 OF REPEAT II (POTENTIAL).
FT	DOMAIN	744	795	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	796	820	S6 OF REPEAT II (POTENTIAL).
FT	DOMAIN	821	1125	CYTOPLASMIC (POTENTIAL).
FT	TRANSNMEM	1126	1148	S1 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1149	1166	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	1167	1187	S2 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1188	1197	CYTOPLASMIC (POTENTIAL).
FT	TRANSNMEM	1198	1217	S3 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1218	1231	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	1232	1253	S4 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1254	1263	CYTOPLASMIC (POTENTIAL).
FT	TRANSNMEM	1264	1287	S5 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1288	1364	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	1365	1390	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1391	1445	CYTOPLASMIC (POTENTIAL).
FT	TRANSNMEM	1446	1466	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1467	1480	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	1481	1502	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1503	1509	CYTOPLASMIC (POTENTIAL).
FT	TRANSNMEM	1510	1528	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1529	1542	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	1543	1566	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1567	1580	CYTOPLASMIC (POTENTIAL).
FT	TRANSNMEM	1581	1601	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1602	1664	EXTRACELLULAR (POTENTIAL).
FT	TRANSNMEM	1665	1692	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1693	1835	CYTOPLASMIC (POTENTIAL).
FT	SITE	355	355	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	779	779	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1339	1339	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1637	1637	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	CARBOHYD	171	171	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	309	309	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1301	1301	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1304	1304	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	1835 AA;	205207 MW;	850807468BE82C0BE CRC64;
Query Match				
Best Local Similarity		3.0%;	Score 7;	DB 1;
Matches		7;	Conservative	0;
			Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	146 PGTPAPA	152	-	-
Db	467 PGTPAPA	473	-	-
RESULT 29				
MGA_HUMAN				
ID	MGA_HUMAN	STANDARD:	PRT:	1856 AA.
AC	043451;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Maltase-glucoamylase, intestinal [Includes: Maltase (EC 3.2.1.20) (Alpha-glucosidase), glucoamylase (EC 3.2.1.3) (Glucon 1,4-alpha-glucosidase)].			
DE	MGM OR MGA OR MGAML.			
OS	Homo sapiens (Human).			



CC -1- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.  
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CC -----  
DR EMBL: AE000795; AAB84518.1; -  
DR InterPro: IPR001209; Ribosomal\_S14.  
DR Pfam: PF00253; Ribosomal\_S14; 1.  
DR PROSITE: PS00527; RIBOSOMAL\_S14; 1.  
KW Ribosomal protein; Complete proteome.  
SQ SEQUENCE 50 AA; 5850 MW; A5B5972652DF2171 CRC64;  
  
Query Match 2.6%; Score 6; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 100 RKCSRC 105  
DB 13 RKCSRC 18  
  
RESULT 31  
TATA\_RICPR  
ID TATA\_RICPR STANDARD; PRT; 54 AA.  
AC Q9ACJ1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Sec-Independent protein translocase protein tata/e homolog.  
GN TATA OR RP749.  
OS Rickettsia prowazekii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiidae; Rickettsia.  
OX NCBI\_TaxID=782;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MADRID E;  
RX MEDLINE=99039499; PubMed=9823893;  
RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,  
RA Sicheit-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,  
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
RT "The genome sequence of Rickettsia prowazekii and the origin of  
RT mitochondria";  
RL Nature 396:133-140(1998).  
CC -1- FUNCTION: REQUIRED FOR CORRECT LOCALIZATION OF PRECURSOR PROTEINS  
CC BEARING SIGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF  
CC S/T-R-X-F-L-K. THIS SEC-INDEPENDENT PATHWAY IS TERMED TAT FOR  
CC TWIN-ARGININE TRANSLLOCATION SYSTEM. THIS SYSTEM MAINLY TRANSPORTS  
CC PROTEINS WITH BOUND COFACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: MEMBRANE BOUND (PROBABLE).  
CC -1- SIMILARITY: BELONGS TO THE TATA/E FAMILY.  
CC -----  
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CC -----  
DR EMBL: AJ235273; CAAL5177.1; -  
DR InterPro: IPR003369; MTA\_Hc106.  
DR Pfam: PF02416; MTA\_Hc106; 1.  
KW Transport; Protein transport; Translocation; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 1 21 POTENTIAL.

SQ SEQUENCE 54 AA; 5884 MW; 607EAE2A977FA3C7 CRC64;  
  
Query Match 2.6%; Score 6; DB 1; Length 54;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 225 LIVLIL 230  
DB 9 LIVLIL 14  
  
RESULT 32  
Y416\_ARCFU  
ID Y416\_ARCFU STANDARD; PRT; 62 AA.  
AC Q29831;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein AF0416 precursor.  
GN AF0416.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;  
OC Archaeoglobus.  
OX NCBI\_TaxID=2234;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriakides N.C.,  
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
RA Overbeek S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
RA Corton M.D., Spriggs T., Arlanch P., Kaine B.P., Sykes S.M.,  
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
RT reducing archaeon Archaeoglobus fulgidus";  
RL Nature 390:364-370(1997).  
CC -----  
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CC -----  
DR EMBL: AE001075; AAB90816.1; -  
DR TIGR: AF0416; -  
KW Hypothetical protein; Signal; Complete proteome.  
FT CHAIN 1 22 POTENTIAL.  
FT SIGNAL 23 62 HYPOTHETICAL PROTEIN AF0416.  
SQ SEQUENCE 62 AA; 6819 MW; 52BAC837861A8C6 CRC64;  
  
Query Match 2.6%; Score 6; DB 1; Length 62;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 129 ANATVE 134  
DB 27 ANATVE 32  
  
RESULT 33  
IAPP\_FELCA  
ID IAPP\_FELCA STANDARD; PRT; 89 AA.  
AC P12967;

```

DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, last sequence update)
DT 01-NOV-1995 (Rel. 32, last annotation update)
DE Islet amyloid polypeptide precursor (Amylin).
GN IAPP.
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
ON NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89345542; PubMed=2668946;
RA Nishi M., Chan S.O., Nagamatsu S., Bell G.I., Steiner D.F.;
RT "Conservation of the sequence of islet amyloid polypeptide in five
RL mammals is consistent with its putative role as an islet hormone.";
RN Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).
RP SEQUENCE OF 34-50.
RX MEDLINE=87231921; PubMed=3035556;
RA Westermarck P., Wernstedt C., Willander E., Hayden D.W., O'Brien T.D.,
RA Johnson K.H.;
RT "Amyloid fibrils in human insulinoma and islets of Langerhans of the
RT diabetic cat are derived from a neuropeptide-like protein also
RT present in normal islet cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3881-3885(1987).
CC -1- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE
CC UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING
CC ADIPOCYTE GLUCOSE METABOLISM.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC -----
DR EMBL; M25388; AAA30813.1; -
DR PIR; A33542; A33542.
DR PIR; B26619; B26619.
DR InterPro; IPR001693; Calc_CGRP_IAPP.
DR InterPro; IPR000443; Islet_Amyloid.
DR Pfam; PF00214; Calc_CGRP_1.
DR PRINTS; PR00818; ISLETAMYLOID.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Hormone; Cleavage on pair of basic residues; Amidation; Amyloid;
KW Signal.
FT SIGNAL. 1 22
FT PEPTIDE 34 70 POTENTIAL.
FT DISULFID 35 40 ISLET AMYLOID POLYPEPTIDE.
FT MOD RES 70 70 BY SIMILARITY.
FT SEQUENCE 89 AA; 9831 MW; 0834D783DBAD72A8 CRC64;
SQ

```

Query Match 2.6%; Score 6; DB 1; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 VLIYVL 229  
 Db 9 VLIYVL 14

RESULT 34  
 RL25\_BUCAL STANDARD; PRT; 95 AA.  
 AC P57238;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE 50S ribosomal protein L25.

```

GN REPLY OR BU138.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiote bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
ON NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RL Buchnera sp. ABS.";
RN Nature 407:81-86(2000).
CC -1- SIMILARITY: BELONGS TO THE L25P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; AP001118; BAB12856.1; -
DR InterPro; IPR001021; Ribosomal_L25p.
DR Pfam; PF01386; Ribosomal_L25p; 1.
DR PRODOM; PD012503; Ribosomal_L25p; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 95 AA; 11336 MW; C234CE06D0F7A84C CRC64;

```

Query Match 2.6%; Score 6; DB 1; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 QRHSFK 23  
 Db 78 QRHSFK 83

RESULT 35  
 RLAL\_ALTRAL STANDARD; PRT; 110 AA.  
 ID RLAL\_ALTRAL  
 AC P49148;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, last sequence update)  
 DT 01-NOV-1997 (Rel. 35, last annotation update)  
 DE 60S acidic ribosomal protein P1 (Allergen Alt a 12) (Alt a XII).  
 GN ALTA12.  
 OS Alternaria alternata.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.  
 ON NCBI\_TaxID=5599;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=08-0203-BERLIN;  
 RX MEDLINE=95206305; PubMed=7898496;  
 RA Achatz G., Oberkofler H., Lechenauer E., Simon B., Unger A.,  
 RA Kandler D., Ebner C., Prillinger H., Kraft D., Breitenbach M.;  
 RT "Molecular cloning of major and minor allergens of Alternaria  
 RT alternata and Cladosporium herbarum.";  
 RL Mol. Immunol. 32:213-227(1995).  
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF  
 CC PROTEIN SYNTHESIS.  
 CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL  
 CC SUBUNIT.  
 CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----
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CC -----

DR EMBL: X84216; CAA58989.1; -

DR InterPro: IPR001813; 60s\_ribosomal.

DR Pfam: PF00428; 60s\_ribosomal.2.

KW Ribosomal protein; Phosphorylation; Allergen.

SQ SEQUENCE 110 AA; 11736 MW; F06A23B67C3259F CRC64;

Query Match 2.6%; Score 6; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEE 155  
| | | | |  
Db 86 APAEE 91

RESULT 36  
RLA2\_SCHPO STANDARD; PRT; 110 AA.  
AC P08094;  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 60S acidic ribosomal protein P2-alpha (A2) (L40C) (L12ET).  
GN RPP2A OR RPA2 OR SPBP87.06.  
OS Schizosaccharomyces pombe (Fission Yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88067727; PubMed=3684587;  
RA Beltrame M., Bianchi M.E.;  
RT "Sequence of the cDNA for one acidic ribosomal protein of Schizosaccharomyces pombe.";  
RL Nucleic Acids Res. 15:9089-9089(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90220620; PubMed=2325655;  
RA Beltrame M., Bianchi M.E.;  
RT "A gene family for acidic ribosomal proteins in Schizosaccharomyces pombe: two essential and two nonessential genes.";  
RL Mol. Cell. Biol. 10:2341-2348(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RA Beck A., Reinhardt R., Lyne M., Rajandream M.A., Barrell B.G.;  
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-40.  
RX MEDLINE=84038947; PubMed=6355773;  
RA Otake E., Higo K.-H., Itoh T.;  
RT "Yeast ribosomal proteins: VII. Cytoplasmic ribosomal proteins from Schizosaccharomyces pombe.";  
RL Mol. Genet. 191:519-524(1983).  
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF PROTEIN SYNTHESIS.  
CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL SUBUNIT.  
CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).  
CC -1- MISCELLANEOUS: YEASTS CONTAIN 4 INDIVIDUAL SMALL RIBOSOMAL A PROTEINS (RPA) WHICH CAN BE CLASSIFIED INTO TWO COUPLES OF SIMILAR BUT NOT IDENTICAL SEQUENCES. EACH COUPLE IS DISTINCTLY RELATED TO ONE OF THE TWO A PROTEINS PRESENT IN MULTICELLULAR ORGANISMS.  
CC -1- MISCELLANEOUS: RPA3 AND RPA4 ARE ESSENTIAL FOR CELL SURVIVAL, WHEREAS RPA1 AND RPA2 ARE NOT.  
CC -1- SIMILARITY: ALL FOUR RPA SHOW 35% IDENTITY. RPA4 IS HIGHLY RELATED TO RPA2.  
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.

CC -----

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CC -----

DR EMBL: Y00466; CAA68528.1; -

DR EMBL: M3138; AA3535.1; -

DR EMBL: AL032684; CAN21791.1; -

DR PIR: B34715; R6BY22.

DR InterPro: IPR001813; 60s\_ribosomal.

DR Pfam: PF00428; 60s\_ribosomal.1.

KW Ribosomal protein; Phosphorylation; Multigene family.

SQ SEQUENCE 110 AA; 11158 MW; 2B45A4E51606FE CRC64;

Query Match 2.6%; Score 6; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEE 155  
| | | | |  
Db 83 APAEE 88

RESULT 37  
RL12\_AERPE STANDARD; PRT; 111 AA.  
AC Q919W9;  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 50S ribosomal protein L12p.  
GN RPL12P OR APE2170.  
OS Aeropyrum pernix.  
OC Archaea; Crenarchaeota; Desulfurococcaceae; Desulfurococcaceae;  
OC Aeropyrum.  
OX NCBI\_TaxID=56636;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K1;  
RX MEDLINE=99310339; PubMed=10382966;  
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatkawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankei A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Ogunchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
RT "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1.";  
RL DNA Res. 6:83-101(1999)  
CC -1- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.  
CC -----

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CC -----

DR EMBL: AP00063; BAA81181.1; -

DR InterPro: IPR001813; 60s\_ribosomal.

DR Pfam: PF00428; 60s\_ribosomal.1.

KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 111 AA; 11794 MW; 2330740B03C6412A CRC64;



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Query Match      2.6%; Score 6; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEE 155
    |||||
Db 77 APAEE 82

RESULT 38
RLA2_BRAFL STANDARD; PRT; 116 AA.
ID RLA2_BRAFL STANDARD; PRT; 116 AA.
AC 001725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE 60S acidic ribosomal protein p2.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=77339;
RN [1]
RP SEQUENCE FROM N.A.
RA Tweedie S., Charlton J., Clark V., Bird A.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
CC PROTEIN SYNTHESIS.
CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS. AT THE LARGE RIBOSOMAL
CC SUBUNIT.
CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: Z63263; CAB05855.1; -
DR InterPro: IPR001813; 60S_rribosomal.
DR Pfam: PF00428; 60S_rribosomal; 1.
KW Ribosomal protein; Phosphorylation.
SQ SEQUENCE 116 AA; 11557 MW; 39C1654F10DC00C CRC64;

Query Match      2.6%; Score 6; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEE 155
    |||||
Db 88 APAEE 93

RESULT 39
HY1B_HUMAN STANDARD; PRT; 117 AA.
ID HY1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region H63 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; Pubmed=6298778;
RA Rechavi G., Kam D., Glazer L., Zakut R., Givol D.;

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RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -----
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CC -----
DR EMBL: J00240; AAA52988.1; -
DR PIR: A02024; HVH0HG.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IgV; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H63.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match      2.6%; Score 6; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 TMTTDT 81
    |||||
Db 88 TMTTDT 93

RESULT 40
MUTT_BUCAI STANDARD; PRT; 124 AA.
ID MUTT_BUCAI STANDARD; PRT; 124 AA.
AC P57298;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mutator mult protein (7,8-dihydro-8-oxoguanine-triphosphatase)
DE (8-oxo-dcnpase) (EC 3.6.1.-) (dcnp pyrophosphohydrolase).
GN MUTT OR BU202.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TOKYO 1998;
RX MEDLINE=20445173; Pubmed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: INVOLVED IN THE GO SYSTEM RESPONSIBLE FOR REMOVING AN
CC OXIDATIVELY DAMAGED FORM OF GUANINE (7,8-DIHYDRO-8-OXOGUANINE)
CC FROM DNA AND THE NUCLEOTIDE POOL. 8-OXO-DGTP IS INSERTED OPPOSITE
CC DA AND DC RESIDUES OF TEMPLATE DNA WITH ALMOST EQUAL EFFICIENCY
CC THUS LEADING TO A.T TO G.C TRANSVERSIONS. MUTT SPECIFICALLY
CC DEGRADES 8-OXO-DGTP TO THE MONOPHOSPHATE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 8-OXO-DGMP + H(2)O = 8-OXO-DGMP +
CC PYROPHOSPHATE.
CC -1- COPFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
CC
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DR EMBL: AP001118; BAB12919.1; -  
DR InterPro: IPR000086; NUDIX\_hydrolase.  
DR Pfam: PF00293; NUDIX.1.  
DR PRINTS: PR00502; NUDIXFAMILY.  
DR PROSITE: PS00893; NUDIX.1.  
KW Mutator protein; DNA replication; DNA repair; Hydrolase; Magnesium;  
KW Complete proteome.  
FT DOMAIN 26 47 NUDIX BOX.  
SQ SEQUENCE 124 AA; 15061 MW; E112D460C70801F CRC64;

Query Match  
Best Local Similarity 100.0%; Score 6; DB 1; Length 124;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 220 VGIIVL 225  
|||||  
DB 46 VGIIVL 51

RESULT 41  
Y192\_RICPR STANDARD; PRT; 128 AA.  
AC O9ZDX2;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein RPI92.  
GN RPI92.  
OS Rickettsia prowazekii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxId=782;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MADRID E;  
RX MEDLINE=99039499; PubMed=9823893;  
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,  
RA Sichevitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naestlund A.K.,  
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
RT "The genome sequence of Rickettsia prowazekii and the origin of  
RT mitochondria."  
RL Nature 396:133-140(1998).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -----  
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DR EMBL: AJ235270; CAA14658.1; -  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 30 50 POTENTIAL.  
FT TRANSMEM 65 85 POTENTIAL.  
FT TRANSMEM 93 113 POTENTIAL.  
SQ SEQUENCE 128 AA; 13943 MW; 6C12DCD7EE348223 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 6; DB 1; Length 128;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 220 VGIIVL 225  
|||||  
DB 77 VGIIVL 82

RESULT 42  
TYRT\_STRGA STANDARD; PRT; 134 AA.  
ID TYRT\_STRGA  
AC P55047;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Tyrosinase co-factor (URF402).  
GN MELC1.  
OS Streptomyces glaucescens.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxId=1907;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13032 / ETH 22794 / GLA.0;  
RX MEDLINE=88040431; PubMed=3118334;  
RA Huber M., Huettler R., Lerch K.;  
RT "The promoter of the Streptomyces glaucescens mel operon."  
RL Nucleic Acids Res. 15:8106-8106(1987).  
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO DELIVER COPPER TO  
CC TYROSINASE.  
CC -----  
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DR EMBL: Y00457; CAA68512.1; -  
KW Melanin biosynthesis; Copper.  
SQ SEQUENCE 134 AA; 13593 MW; 1E874145A7D1B9AE CRC64;

Query Match  
Best Local Similarity 100.0%; Score 6; DB 1; Length 134;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 206 PGTPTS 211  
|||||  
DB 48 PGTPTS 53

RESULT 43  
PSAD\_ODOST STANDARD; PRT; 139 AA.  
ID PSAD\_ODOST  
AC P49481;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Photosystem I reaction center subunit II (Photosystem I 16 kDa  
DE polypeptide) (Pst-D).  
GN PSAD.  
OS Odontella sinensis.  
OC Chloroplast.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Biddulphiophycidae; Eupodiscates; Eupodiscaceae; Odontella.  
OX NCBI\_TaxId=2839;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kowalik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;  
RT "The chloroplast genome of a chlorophyll a+c-containing alga,  
RT Odontella sinensis."  
RL Plant Mol. Biol. Rep. 13:336-342(1995).  
CC -1- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-  
CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.  
CC -1- SIMILARITY: BELONGS TO THE PSAD FAMILY.  
CC -----  
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CC -----
DR EMBL: Z67753; CAA91679.1; -
DR Mendel: 13229; ODO81; Psad.1.
DR InterPro: IPR003685; Psad.
DR Pfam: PF02531; Psad.1.
KM Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
SQ SEQUENCE 139 AA; 15515 MW; 25F63D31CDDCAE8C CRC64;

Query Match 2.6%; Score 6; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 PSGEVQ 111
|||||
DB 88 PSGEVQ 93

RESULT 44
PSAD_SKECO STANDARD; PRT; 139 AA.
AC 096800;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Photosystem I reaction center subunit II (Photosystem I 16 kDa
DE polypeptide) (PSI-D).
GN PSAD.
OS Skeletonema costatum.
OC Chloroplast.
OC Eukaryota; Stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Thalassiosirophyceae; Thalassiosirales; Skeletonemataceae;
OC Skeletonema.
OX NCBI_Taxid=2843;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-323;
RA Tada N., Otsuka S., Oyaizu H., Matsumoto S.;
RT "Plasid DNA sequences of Skeletonema costatum NIES 323."
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-
CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.
CC -1- SIMILARITY: BELONGS TO THE PSAD FAMILY.
CC -----
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CC -----
DR EMBL: AJ132263; CAA10621.1; -
DR InterPro: IPR003685; Psad.
DR Pfam: PF02531; Psad.1.
KM Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
SQ SEQUENCE 139 AA; 15504 MW; AFD7319C87EBC265 CRC64;

Query Match 2.6%; Score 6; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 PSGEVQ 111
|||||
DB 88 PSGEVQ 93

RESULT 45

```

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PSAD_SYNY3 STANDARD; PRT; 140 AA.
AC P19569;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem I reaction center subunit II (Photosystem I 16 kDa
DE polypeptide) (PSI-D).
GN PSAD OR S1R0737.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_Taxid=1148;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=69034300; Pubmed=3141423.
RA Reilly P., Holmes J.D., Pan Y.-C.E., Nelson N.;
RT "Molecular cloning and sequencing of the psad gene encoding subunit
RT II of photosystem I from the cyanobacterium, Synechocystis sp. PCC
RT 6803."
RL J. Biol. Chem. 263:17658-17662(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; Pubmed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugitara M., Sasamoto S., Kimura T.,
RA Osunouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okamura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-
CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.
CC -1- SUBUNIT: PS I FROM SYNECHOCYSTIS SP. CONTAINS SEVEN DIFFERENT
CC POLYPEPTIDES. THE POLYPEPTIDE CORRESPONDING TO SUBUNIT II FROM
CC HIGHER PLANTS IS MISSING.
CC -1- SIMILARITY: BELONGS TO THE PSAD FAMILY.
CC -----
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CC -----
DR EMBL: J04195; AAA8625.1; -
DR EMBL: D90899; BAA16688.1; -
DR PIR: A32124; A32124.
DR InterPro: IPR003685; Psad.
DR Pfam: PF02531; Psad.1.
KM Photosynthesis; Photosystem I; Complete proteome.
FT INTMET 0
FT SEQUENCE 140 AA; 15513 MW; 263C35D5B47B9F8E CRC64;

Query Match 2.6%; Score 6; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 PSGEVQ 111
|||||
DB 89 PSGEVQ 94

RESULT 46
PSAD_GUITH STANDARD; PRT; 141 AA.
AC 078502;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE Photosystem I reaction center subunit II (Photosystem I 16 kDa polypeptide) (PSI-D).

GN PSAD.

OS Guillardia theta (Cryptomonas phl).

CG Chloroplast.

OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

ON NCBI\_Taxid=55529;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99128221; PubMed=9929392;

RA Douglas S.E., Penny S.L.;

RT "The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its common ancestry with red algae."

RL J. Mol. Evol. 48:236-244(1999).

CC -1- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.

CC -1- SIMILARITY: BELONGS TO THE PSAD FAMILY.

CC -----

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CC -----

DR EMBL: AF041468; AAC35693.1; -

DR InterPro: IPR003685; Psad.

DR Pfam: PF02531; Psad: 1

KM Photosynthesis I; Chloroplast; Thylakoid; Membrane.

SQ SEQUENCE 141 AA; 15687 MW; 5ADE5DB37DBC89E CRC64;

Query Match 2.6%; Score 6; DB 1; Length 141;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 PSEVO 111

DB 91 PSEVO 96

RESULT 47

EXBD\_NEIGO STANDARD; PRT; 144 AA.

AC 006434;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Biopolymer transport exbd protein.

GN EXBD.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_Taxid=485;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FA19;

RX MEDLINE=97285757; PubMed=9140974;

RA Biswas G.D., Anderson J.E., Sparling P.F.;

RT "Cloning and functional characterization of Neisseria gonorrhoeae tonb, exbd and exbd genes."

RL tonb, exbd and exbd genes."

CC -1- FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).

CC -1- SUBUNIT: THE ACCESSORY PROTEINS EXBD AND EXBD SEEM TO FORM A COMPLEX WITH TONB (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (Probable).

CC -1- SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.

CC -----

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CC -----

DR EMBL: U79563; AAC45288.1; -

DR InterPro: IPR003400; Exbd.

DR Pfam: PF02472; Exbd: 1.

KW Transport; Protein transport; Transmembrane; Inner membrane.

FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 19 39 POTENTIAL.

FT DOMAIN 40 144 PERIPLASMIC (POTENTIAL).

SQ SEQUENCE 144 AA; 15514 MW; 4819D6B5138E9339 CRC64;

Query Match 2.6%; Score 6; DB 1; Length 144;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 227 VLLIVF 232

DB 28 VLLIVF 33

RESULT 48

EXBD\_NEIMA STANDARD; PRT; 144 AA.

AC P95376;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Biopolymer transport exbd protein.

GN EXBD OR NMA1983 OR NMA1728.

OS Neisseria meningitidis (serogroup A).

OS Neisseria meningitidis (serogroup B).

OS Neisseria meningitidis (serogroup C).

OS Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_Taxid=65699, 491, 135720;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=8013.6 / SEROGROUP C;

RX MEDLINE=97158676; PubMed=9006036;

RA Stojiljkovic I., Strinivasan N.;

RT "Neisseria meningitidis tonb, exbd, and exbd genes: Ton-dependent utilization of protein-bound iron in Neisseriae."

RL J. Bacteriol. 179:805-812(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;

RX MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S., Jagers K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491."

RL Nature 404:502-506(2000).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=MC58 / SEROGROUP B;

RX MEDLINE=20175755; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwyn M.L., Debey R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B., Cotton M.D., Utecher T.R., Khoui H., Qin H., Yamathayan J., Gill J., Scarlato V., Maignani V., Piza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;

RT "Complete genome sequence of Neisseria meningitidis serogroup B strain

RT MC58.":  
RL Science 287:1809-1815(2000).  
CC -1- FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT  
CC TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).  
CC -1- SUBUNIT: THE ACCESSORY PROTEIN EXB AND EXD SEEM TO FORM A  
CC COMPLEX WITH TONB (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane  
CC (Probable).  
CC -1- SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.  
CC -----  
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CC -----  
CC EMBL: U77738; AAC44836.1; -  
DR EMBL: AL162757; CAB85203.1; -  
DR EMBL: AE002523; AAF42073.1; -  
DR TIGR: NMB1728; -  
DR InterPro: IPR003400; Exbd.  
DR Pfam: PF02472; Exbd; 1.  
KW Transport; Protein transport; Transmembrane; Inner membrane;  
KW Complete proteome.  
FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 19 39 POTENTIAL.  
FT DOMAIN 40 144 PERIPLASMIC (POTENTIAL).  
SQ SEQUENCE 144 AA: 15514 MW: 96DCD7A142DAC370 CRC64;

Query Match  
Best Local Similarity 2.6%; Score 6; DB 1; Length 144;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 IVLIVF 232  
DB 28 IVLIVF 33

RESULT 49  
SMG\_BUCAI STANDARD; PRT; 157 AA.  
AC P57562;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Smg protein homolog.  
GN SMG OR B0495.  
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
OS symbiotic bacterium).  
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
OX NCBI\_TaxID=118099;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Tokyo 1998;  
RX MEDLINE=20445173; PubMed=10993077;  
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.:  
RT "Genome sequence of the endocellular bacterial symbiont of aphids  
RT Buchnera sp. APS."  
RL Nature 407:81-86(2000).  
CC -1- SIMILARITY: TO E.COLI SMG.  
CC -----  
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CC -----  
CC EMBL: AF001119; BAB13188.1; -

KW Complete proteome.  
SQ SEQUENCE 157 AA: 18662 MW: 9958D9CACA47CFEE0 CRC64;

Query Match  
Best Local Similarity 2.6%; Score 6; DB 1; Length 157;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 IVLIVL 228  
DB 126 IVLIVL 131

RESULT 50  
WH16\_STRCO STANDARD; PRT; 157 AA.  
ID WH16\_STRCO  
AC P23157;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 16.7 kDa protein in white locus (White ORF II).  
GN SC6G9.14.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RX MEDLINE=91171868; PubMed=2077356;  
RA Davis N.K., Chater K.F., Bruton C.J.:  
RT "Spore colour in Streptomyces coelicolor A3(2) involves the  
RT developmentally regulated synthesis of a compound biosynthetically  
RT related to polyketide antibiotics."  
RL Mol. Microbiol. 4:1679-1691(1990).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Seeger K.J., Harris D., James K.D., Parkhill J., Barrell B.G.,  
RA Rajandream M.A.:  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SCHB/CURC FAMILY.  
CC -----  
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CC -----  
CC EMBL: X55942; CA39407.1; -  
DR EMBL: AL079356; CAB45605.1; -  
DR PIR: S11973; S11973.  
SQ SEQUENCE 157 AA: 16669 MW: 2E650E3BED9F0CBD CRC64;

Query Match  
Best Local Similarity 2.6%; Score 6; DB 1; Length 157;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAAE 154  
DB 149 PAPAAE 154

Search completed: August 13, 2002, 08:41:32  
Job time: 211 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:38:22 ; Search time 26.68 Seconds  
(without alignments)  
1510.788 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_27\_259  
Perfect score: 233  
Sequence: 1 TTARQEEVPGQTAPQ00RH.....YLCTGIVLIIVLIVFV 233

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 17294929 residues

Word size : 5

Total number of hits satisfying chosen parameters: 14653

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

1: SPREMBL\_19:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phase:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertibrate:\*  
15: sp\_unclassified:\*  
16: sp\_rvirus:\*  
17: sp\_bacteriap:\*  
sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.4	109	5	Q9WZB6
2	8	3.4	217	4	Q9HA66
3	8	3.4	464	16	Q9Z7U4
4	8	3.4	468	4	Q96E62
5	8	3.4	494	16	Q9ZDD2
6	8	3.4	685	16	Q9JWP0
7	8	3.4	801	5	Q23635
8	7	3.0	100	5	Q9V5T2
9	7	3.0	106	17	Q9HL72
10	7	3.0	144	2	O69204
11	7	3.0	151	15	O56349
12	7	3.0	155	10	Q39133
13	7	3.0	158	10	Q9FNT2
14	7	3.0	165	5	Q19762
15	7	3.0	184	17	Q97WNS
16	7	3.0	219	16	Q9RW97

17	7	3.0	231	4	Q96EX2	Q96EX2 homo sapien
18	7	3.0	241	10	Q9FT78	Q9FT78 arabidopsis
19	7	3.0	249	16	Q98EG1	Q98EG1 rhizobium l
20	7	3.0	255	10	Q9S8T8	Q9S8T8 hordeum vul
21	7	3.0	255	10	Q9SP44	Q9SP44 hordeum vul
22	7	3.0	255	10	Q43488	Q43488 hordeum vul
23	7	3.0	256	5	Q9VW71	Q9VW71 drosophila
24	7	3.0	256	16	Q9PD13	Q9PD13 xyella fas
25	7	3.0	256	16	Q9PC71	Q9PC71 xyella fas
26	7	3.0	256	16	Q9P9V6	Q9P9V6 xyella fas
27	7	3.0	259	10	P93608	P93608 triticum ae
28	7	3.0	262	10	O81288	O81288 arabidopsis
29	7	3.0	263	5	Q17806	Q17806 caenorhabd
30	7	3.0	266	2	Q9ZFB0	Q9ZFB0 rhodobacter
31	7	3.0	268	10	P93607	P93607 triticum ae
32	7	3.0	272	16	Q988Y8	Q988Y8 rhizobium l
33	7	3.0	295	2	Q32850	Q32850 mycobacteri
34	7	3.0	299	2	Q93D93	Q93D93 streptococc
35	7	3.0	313	2	O50268	O50268 agrobacteri
36	7	3.0	326	4	Q9BVC4	Q9BVC4 homo sapien
37	7	3.0	330	4	Q96SU5	Q96SU5 homo sapien
38	7	3.0	346	13	Q98TDT	Q98TDT paratichthy
39	7	3.0	365	16	Q9YF60	Q9YF60 neisseria m
40	7	3.0	365	16	Q9JY44	Q9JY44 neisseria m
41	7	3.0	366	10	O80413	O80413 zea mays (m
42	7	3.0	380	8	Q79658	Q79658 pueraria ma
43	7	3.0	390	2	Q9RK28	Q9RK28 streptomyce
44	7	3.0	397	17	O58434	O58434 pyrococcus
45	7	3.0	401	5	Q9BWM3	Q9BWM3 onchocerca
46	7	3.0	405	11	Q9CGR2	Q9CGR2 mus musculu
47	7	3.0	419	10	Q9FN24	Q9FN24 arabidopsis
48	7	3.0	450	5	O17854	O17854 caenorhabd
49	7	3.0	452	4	Q9H7M8	Q9H7M8 homo sapien
50	7	3.0	458	10	Q9AY47	Q9AY47 oryza sativ
51	7	3.0	465	16	Q98CE4	Q98CE4 rhizobium l
52	7	3.0	471	10	Q9ATX0	Q9ATX0 zea mays (m
53	7	3.0	485	2	Q93DB1	Q93DB1 streptococc
54	7	3.0	494	16	Q97N19	Q97N19 streptococc
55	7	3.0	495	10	Q93VSS	Q93VSS arabidopsis
56	7	3.0	497	4	Q9H6L5	Q9H6L5 homo sapien
57	7	3.0	526	2	Q9R3F9	Q9R3F9 streptomyce
58	7	3.0	526	12	Q9Q899	Q9Q899 spodoptera
59	7	3.0	532	12	Q9DYA7	Q9DYA7 avian pneum
60	7	3.0	532	12	Q9DYA5	Q9DYA5 avian pneum
61	7	3.0	532	12	Q9DYA4	Q9DYA4 avian pneum
62	7	3.0	532	12	Q9DYA3	Q9DYA3 avian pneum
63	7	3.0	532	12	Q9DYA2	Q9DYA2 avian pneum
64	7	3.0	532	12	Q9DYA1	Q9DYA1 avian pneum
65	7	3.0	532	12	Q9DYA0	Q9DYA0 avian pneum
66	7	3.0	532	12	Q91S36	Q91S36 avian pneum
67	7	3.0	534	12	Q9DYP9	Q9DYP9 avian pneum
68	7	3.0	537	12	Q9WR13	Q9WR13 avian pneum
69	7	3.0	537	12	Q9QD13	Q9QD13 avian pneum
70	7	3.0	537	12	Q9QD12	Q9QD12 avian pneum
71	7	3.0	537	12	Q9QD11	Q9QD11 avian pneum
72	7	3.0	540	10	Q9FNT2	Q9FNT2 arabidopsis
73	7	3.0	542	5	Q9GUY4	Q9GUY4 penaeus jap
74	7	3.0	548	16	O06404	O06404 mycobacteri
75	7	3.0	548	17	Q97UB8	Q97UB8 sulfolobus
76	7	3.0	551	4	Q9Y6T3	Q9Y6T3 homo sapien
77	7	3.0	556	2	Q9ZFS8	Q9ZFS8 streptomyce
78	7	3.0	556	2	Q9S2C0	Q9S2C0 streptomyce
79	7	3.0	572	5	O02605	O02605 paramyxi
80	7	3.0	572	5	O02606	O02606 paramyxi
81	7	3.0	575	11	O88339	O88339 rattus norv
82	7	3.0	576	4	Q9HA18	Q9HA18 homo sapien
83	7	3.0	589	16	Q9HVT0	Q9HVT0 pseudomonas
84	7	3.0	596	10	Q9FNT3	Q9FNT3 arabidopsis
85	7	3.0	599	2	Q9F8V2	Q9F8V2 streptomyce
86	7	3.0	612	2	Q9Z6I4	Q9Z6I4 streptomyce
87	7	3.0	640	8	Q9CEM6	Q9CEM6 aegiceras c
88	7	3.0	640	8	Q9GET9	Q9GET9 solanella
89	7	3.0	657	8	Q9GDB8	Q9GDB8 tricyrtis l

90	7	3.0	660	8	Q9GDV9	Q9gdv9 tricytllis a	163	6	2.6	80	12	Q9WN64	Q9wn64 hepatitis c
91	7	3.0	669	10	Q9M1G3	Q9m1g3 arabidopsis	164	6	2.6	80	12	Q9WN63	Q9wn63 hepatitis c
92	7	3.0	670	8	Q9BAQ4	Q9baq4 buxus citrlr	165	6	2.6	80	12	Q9WN62	Q9wn62 hepatitis c
93	7	3.0	677	5	Q9VBK7	Q9vbk7 drosophila	166	6	2.6	80	12	Q9WN61	Q9wn61 hepatitis c
94	7	3.0	694	8	Q32008	Q32008 clerodendru	167	6	2.6	80	12	Q9WN60	Q9wn60 hepatitis c
95	7	3.0	695	8	Q9MUR4	Q9mur4 solanum nit	168	6	2.6	80	12	Q9WN59	Q9wn59 hepatitis c
96	7	3.0	697	8	Q9TLC9	Q9tlc9 lampocapro	169	6	2.6	80	12	Q9WN58	Q9wn58 hepatitis c
97	7	3.0	702	6	Q9SJT0	Q9sjt0 macaca fasc	170	6	2.6	80	12	Q9WN57	Q9wn57 hepatitis c
98	7	3.0	717	4	Q9NXL0	Q9nxl0 homo sapien	171	6	2.6	80	12	Q9WN56	Q9wn56 hepatitis c
99	7	3.0	734	8	Q9RUT3	Q9rut3 guettarda u	172	6	2.6	80	12	Q9WN55	Q9wn55 hepatitis c
100	7	3.0	744	8	Q32737	Q32737 onoseris hy	173	6	2.6	80	12	Q9WN54	Q9wn54 hepatitis c
101	7	3.0	761	8	Q9TLL1	Q9tll1 streptomyc	174	6	2.6	80	12	Q9WN53	Q9wn53 hepatitis c
102	7	3.0	780	5	Q9SYK4	Q9syk4 clona savig	175	6	2.6	80	12	Q9WN52	Q9wn52 hepatitis c
103	7	3.0	837	5	P90666	P90666 anthocidarl	176	6	2.6	80	12	Q9WN50	Q9wn50 hepatitis c
104	7	3.0	838	5	Q27422	Q27422 caenorhabd1	177	6	2.6	80	12	Q9WN48	Q9wn48 hepatitis c
105	7	3.0	838	5	Q18761	Q18761 caenorhabd1	178	6	2.6	82	12	Q9X524	Q9x524 thlobacillu
106	7	3.0	970	16	Q9ZKJ8	Q9zkj8 rhizobium m	179	6	2.6	82	12	Q9G303	Q9g303 hepatitis c
107	7	3.0	1058	16	Q9TJ19	Q9tj19 clostridium	180	6	2.6	82	16	Q97NXL	Q97nxl streptococ
108	7	3.0	1110	13	Q91255	Q91255 petromyzon	181	6	2.6	83	5	Q23104	Q23104 caenorhabd1
109	7	3.0	1247	5	Q9VX80	Q9vx80 drosophila	182	6	2.6	84	2	Q9ZHY7	Q9zhy7 thlobacillu
110	7	3.0	1318	5	Q19733	Q19733 caenorhabd1	183	6	2.6	85	10	Q9FW74	Q9fw74 oryza sativ
111	7	3.0	1461	5	Q9GYB7	Q9gyb7 leishmania	184	6	2.6	86	5	Q21699	Q21699 caenorhabd1
112	7	3.0	1698	2	Q9LCO0	Q9lco0 staphylococ	185	6	2.6	87	5	Q20368	Q20368 caenorhabd1
113	7	3.0	1742	16	Q55583	Q55583 synechocyst	186	6	2.6	90	5	Q9XVX2	Q9xvx2 caenorhabd1
114	7	3.0	1834	11	Q9EQ59	Q9eq59 ratcus norv	187	6	2.6	90	12	Q99CY8	Q99cy8 bovine herp
115	7	3.0	2026	2	Q9DPJ4	Q9dpj4 neisseria m	188	6	2.6	93	4	Q9H5A9	Q9h5a9 homo sapien
116	7	3.0	2938	11	Q61769	Q61769 mus musculu	189	6	2.6	93	8	Q36903	Q36903 hansenua w
117	7	3.0	3739	2	Q9ZC14	Q9zcg14 streptomyc	190	6	2.6	94	10	Q9FEW0	Q9fwh0 oryza sativ
118	7	3.0	4685	2	Q93HJ2	Q93hj2 streptomyc	191	6	2.6	94	16	Q99VS9	Q99vs9 staphylococ
119	6	2.6	22	1	Q9V2S4	Q9v2s4 halobacteri	192	6	2.6	101	11	Q9D7U2	Q9d7u2 mus musculu
120	6	2.6	36	16	Q97S76	Q97s76 streptococ	193	6	2.6	104	16	Q92D67	Q92d67 listeria in
121	6	2.6	37	16	Q97OP3	Q97op3 streptococ	194	6	2.6	104	17	Q9GWS7	Q9gws7 sulfolobu
122	6	2.6	44	16	Q9KLB9	Q9klb9 vibrio chol	195	6	2.6	105	5	Q91706	Q91706 drosophila
123	6	2.6	45	12	Q68613	Q68613 hepatitis c	196	6	2.6	105	5	P92201	P92201 drosophila
124	6	2.6	45	12	Q68614	Q68614 hepatitis c	197	6	2.6	105	5	P92201	P92201 drosophila
125	6	2.6	45	12	Q68617	Q68617 hepatitis c	198	6	2.6	106	16	Q9A2W3	Q9a2w3 callobacter
126	6	2.6	45	12	Q68618	Q68618 hepatitis c	199	6	2.6	109	4	Q95724	Q95724 homo sapien
127	6	2.6	45	12	Q68619	Q68619 hepatitis c	200	6	2.6	109	5	Q61467	Q61467 caenorhabd1
128	6	2.6	45	12	Q68620	Q68620 hepatitis c	201	6	2.6	109	11	Q9Z155	Q9z155 mus dunni (
129	6	2.6	45	12	Q68625	Q68625 hepatitis c	202	6	2.6	109	11	Q9Z157	Q9z157 mus dunni (
130	6	2.6	53	16	Q92CG3	Q92cg3 rickettsia	203	6	2.6	109	11	Q9Z156	Q9z156 mus famulus
131	6	2.6	55	5	P90700	P90700 brugia mala	204	6	2.6	110	3	Q14317	Q14317 schizosacch
132	6	2.6	59	9	Q9ZXH2	Q9zxh2 enococcus	205	6	2.6	110	5	Q21156	Q21156 caenorhabd1
133	6	2.6	59	13	Q91859	Q91859 fuqu rubrip	206	6	2.6	111	3	Q9H6U9	Q9h6u9 aspergillus
134	6	2.6	59	16	Q9KCA1	Q9kca1 bacillus ha	207	6	2.6	112	5	Q9NA97	Q9na97 caenorhabd1
135	6	2.6	62	16	Q92GE4	Q92ge4 rickettsia	208	6	2.6	112	5	Q9NAM5	Q9nam5 arabidopsis
136	6	2.6	73	12	P90335	P90335 panicum mos	209	6	2.6	113	5	Q9N923	Q9n923 trypanosoma
137	6	2.6	74	12	Q91E76	Q91e76 chilo iride	210	6	2.6	113	10	Q9EFT9	Q9eft9 arabidopsis
138	6	2.6	75	16	Q99Z45	Q99z45 streptococ	211	6	2.6	114	12	Q91PM8	Q91pm8 hepatitis c
139	6	2.6	76	12	Q68496	Q68496 hepatitis c	212	6	2.6	114	12	Q91PM7	Q91pm7 hepatitis c
140	6	2.6	76	12	Q68497	Q68497 hepatitis c	213	6	2.6	114	12	Q91PM6	Q91pm6 hepatitis c
141	6	2.6	76	12	Q68498	Q68498 hepatitis c	214	6	2.6	114	12	Q91PM5	Q91pm5 hepatitis c
142	6	2.6	76	12	Q68499	Q68499 hepatitis c	215	6	2.6	114	12	Q91PM4	Q91pm4 hepatitis c
143	6	2.6	77	16	Q99VK3	Q99vk3 staphylococ	216	6	2.6	114	12	Q91PM3	Q91pm3 hepatitis c
144	6	2.6	80	12	Q9W8C0	Q9w8c0 hepatitis c	217	6	2.6	114	12	Q91PM1	Q91pm1 hepatitis c
145	6	2.6	80	12	Q9W447	Q9w447 hepatitis c	218	6	2.6	114	12	Q91PL9	Q91pl9 hepatitis c
146	6	2.6	80	12	Q9W415	Q9w415 hepatitis c	219	6	2.6	114	12	Q91PL8	Q91pl8 hepatitis c
147	6	2.6	80	12	Q9W9W8	Q9w9w8 hepatitis c	220	6	2.6	114	12	Q91PL7	Q91pl7 hepatitis c
148	6	2.6	80	12	Q9W9B4	Q9w9b4 hepatitis c	221	6	2.6	114	12	Q91PL4	Q91pl4 hepatitis c
149	6	2.6	80	12	Q9W903	Q9w903 hepatitis c	222	6	2.6	114	12	Q91PL3	Q91pl3 hepatitis c
150	6	2.6	80	12	Q9W852	Q9w852 hepatitis c	223	6	2.6	114	12	Q91PL2	Q91pl2 hepatitis c
151	6	2.6	80	12	Q9W9M3	Q9w9m3 hepatitis c	224	6	2.6	114	12	Q91PL1	Q91pl1 hepatitis c
152	6	2.6	80	12	Q9W9K3	Q9w9k3 hepatitis c	225	6	2.6	114	12	Q91PL0	Q91pl0 hepatitis c
153	6	2.6	80	12	Q9WNT6	Q9wn76 hepatitis c	226	6	2.6	114	12	Q91PK9	Q91pk9 hepatitis c
154	6	2.6	80	12	Q9WNT7	Q9wn77 hepatitis c	227	6	2.6	114	12	Q91PK8	Q91pk8 hepatitis c
155	6	2.6	80	12	Q9WNT5	Q9wn75 hepatitis c	228	6	2.6	114	12	Q91PK7	Q91pk7 hepatitis c
156	6	2.6	80	12	Q9WNT4	Q9wn74 hepatitis c	229	6	2.6	114	12	Q91PK6	Q91pk6 hepatitis c
157	6	2.6	80	12	Q9WNT3	Q9wn73 hepatitis c	230	6	2.6	114	12	Q91PK5	Q91pk5 hepatitis c
158	6	2.6	80	12	Q9WNT2	Q9wn72 hepatitis c	231	6	2.6	114	12	Q91PK4	Q91pk4 hepatitis c
159	6	2.6	80	12	Q9WNT0	Q9wn70 hepatitis c	232	6	2.6	114	12	Q91PK3	Q91pk3 hepatitis c
160	6	2.6	80	12	Q9WN69	Q9wn69 hepatitis c	233	6	2.6	114	12	Q91PK2	Q91pk2 hepatitis c
161	6	2.6	80	12	Q9WN68	Q9wn68 hepatitis c	234	6	2.6	114	12	Q91PK1	Q91pk1 hepatitis c
162	6	2.6	80	12	Q9WN67	Q9wn67 hepatitis c	235	6	2.6	114	12	Q91PK0	Q91pk0 hepatitis c



236	6	2.6	114	12	Q9IPJ9	Q9IPJ9 hepatitis c	309	6	2.6	149	5	Q9VAI6	Q9VAI6 drosophila
237	6	2.6	115	4	Q9BTD1	Q9BTD1 homo sapien	310	6	2.6	149	16	Q9K7Y0	Q9K7Y0 bacillus ha
238	6	2.6	115	13	Q90YW9	Q90YW9 ictalurus p	311	6	2.6	150	10	Q9SUN5	Q9SUN5 arabidopsis
239	6	2.6	118	17	Q9YET0	Q9YET0 aeryprum p	312	6	2.6	150	11	Q9CQW4	Q9CQW4 mus musculu
240	6	2.6	119	10	Q43548	Q43548 malus domes	313	6	2.6	151	5	Q93267	Q93267 osterlagia
241	6	2.6	119	16	Q92J28	Q92J28 rickettsia	314	6	2.6	151	15	Q56356	Q56356 human immun
242	6	2.6	120	17	Q9EXJ2	Q9EXJ2 klebsiella	315	6	2.6	152	11	Q9D0D8	Q9D0D8 mus musculu
243	6	2.6	120	17	Q97AD9	Q97AD9 thermoplasma	316	6	2.6	153	7	Q56805	Q56805 xanthomonas
244	6	2.6	121	12	Q72213	Q72213 hepatitis c	317	6	2.6	153	7	Q9XRJ4	Q9XRJ4 equus asinu
245	6	2.6	121	17	Q58660	Q58660 pyrococcus	318	6	2.6	154	10	Q9LUR6	Q9LUR6 arabidopsis
246	6	2.6	124	4	Q9UL92	Q9UL92 homo sapien	319	6	2.6	154	12	Q916J8	Q916J8 hepatitis c
247	6	2.6	125	4	Q9UL95	Q9UL95 homo sapien	320	6	2.6	154	12	Q916J7	Q916J7 hepatitis c
248	6	2.6	125	16	Q51048	Q51048 borrelia bu	321	6	2.6	154	12	Q916J6	Q916J6 hepatitis c
249	6	2.6	130	5	Q9VWK6	Q9VWK6 drosophila	322	6	2.6	154	12	Q916J5	Q916J5 hepatitis c
250	6	2.6	131	5	Q27236	Q27236 schistosoma	323	6	2.6	154	12	Q916J4	Q916J4 hepatitis c
251	6	2.6	132	12	P89035	P89035 pantum mos	324	6	2.6	154	12	Q916J3	Q916J3 hepatitis c
252	6	2.6	133	5	Q9V508	Q9V508 bacillus sp	325	6	2.6	154	12	Q916J2	Q916J2 hepatitis c
253	6	2.6	133	5	Q9V107	Q9V107 drosophila	326	6	2.6	154	12	Q916J1	Q916J1 hepatitis c
254	6	2.6	133	16	Q92JL7	Q92JL7 rickettsia	327	6	2.6	154	12	Q916J0	Q916J0 hepatitis c
255	6	2.6	133	17	Q9YGO3	Q9YGO3 aeryprum p	328	6	2.6	154	12	Q916I9	Q916I9 hepatitis c
256	6	2.6	135	5	Q17016	Q17016 anopheles g	329	6	2.6	154	12	Q916I8	Q916I8 hepatitis c
257	6	2.6	135	16	Q68188	Q68188 hepatitis c	330	6	2.6	154	12	Q916I7	Q916I7 hepatitis c
258	6	2.6	135	16	Q9KUF7	Q9KUF7 vibrio chol	331	6	2.6	154	12	Q916I6	Q916I6 hepatitis c
259	6	2.6	136	2	Q93D35	Q93D35 uncultured	332	6	2.6	154	12	Q916I5	Q916I5 hepatitis c
260	6	2.6	136	11	Q9CRJ5	Q9CRJ5 mus musculu	333	6	2.6	154	12	Q916I4	Q916I4 hepatitis c
261	6	2.6	136	16	Q92EM0	Q92EM0 campylobact	334	6	2.6	154	12	Q916I3	Q916I3 hepatitis c
262	6	2.6	136	16	Q92EM0	Q92EM0 listeria in	335	6	2.6	155	10	Q916I2	Q916I2 hepatitis c
263	6	2.6	137	12	Q911I1	Q911I1 hepatitis c	336	6	2.6	155	16	Q9K044	Q9K044 arabidopsis
264	6	2.6	137	12	Q911I0	Q911I0 hepatitis c	337	6	2.6	155	16	Q92DP0	Q92DP0 vibrio chol
265	6	2.6	137	12	Q911I9	Q911I9 hepatitis c	338	6	2.6	156	11	Q9JDF0	Q9JDF0 listeria in
266	6	2.6	137	12	Q911H9	Q911H9 hepatitis c	339	6	2.6	157	7	Q9XRJ0	Q9XRJ0 mus musculu
267	6	2.6	137	12	Q911H8	Q911H8 hepatitis c	340	6	2.6	158	2	Q9AH55	Q9AH55 diccerorhinu
268	6	2.6	137	12	Q911H7	Q911H7 hepatitis c	341	6	2.6	158	16	Q9JY91	Q9JY91 neisseria m
269	6	2.6	137	12	Q911H6	Q911H6 hepatitis c	342	6	2.6	159	4	Q960S0	Q960S0 homo sapien
270	6	2.6	137	12	Q911H5	Q911H5 hepatitis c	343	6	2.6	160	6	Q9N1I6	Q9N1I6 gorilla gor
271	6	2.6	137	12	Q911H4	Q911H4 hepatitis c	344	6	2.6	160	17	Q9LIM4	Q9LIM4 streptomyces
272	6	2.6	137	12	Q911H3	Q911H3 hepatitis c	345	6	2.6	161	10	Q972G4	Q972G4 sulfolobus
273	6	2.6	137	12	Q911H2	Q911H2 hepatitis c	346	6	2.6	161	10	Q941Q0	Q941Q0 marchantia
274	6	2.6	137	12	Q911H1	Q911H1 hepatitis c	347	6	2.6	161	17	Q9UYPO	Q9UYPO pyrococcus
275	6	2.6	137	12	Q911G9	Q911G9 hepatitis c	348	6	2.6	165	2	Q9R9X9	Q9R9X9 pseudomonas
276	6	2.6	137	12	Q911G8	Q911G8 hepatitis c	349	6	2.6	166	17	Q97U85	Q97U85 sulfobus
277	6	2.6	137	12	Q911G7	Q911G7 hepatitis c	350	6	2.6	167	16	Q9CD40	Q9CD40 mycobacteri
278	6	2.6	137	12	Q911G6	Q911G6 hepatitis c	351	6	2.6	168	2	Q04079	Q04079 xanthomonas
279	6	2.6	137	12	Q911G5	Q911G5 hepatitis c	352	6	2.6	168	10	Q9EFK1	Q9EFK1 arabidopsis
280	6	2.6	137	12	Q911G4	Q911G4 hepatitis c	353	6	2.6	168	10	Q9SH25	Q9SH25 arabidopsis
281	6	2.6	137	12	Q911G3	Q911G3 hepatitis c	354	6	2.6	169	10	Q9SXV0	Q9SXV0 cryza sativ
282	6	2.6	137	12	Q911G2	Q911G2 hepatitis c	355	6	2.6	169	12	Q917P8	Q917P8 hepatitis c
283	6	2.6	137	12	Q911G1	Q911G1 hepatitis c	356	6	2.6	170	10	Q98778	Q98778 avena sativ
284	6	2.6	137	12	Q911G0	Q911G0 hepatitis c	357	6	2.6	170	17	Q9HLM5	Q9HLM5 thermoplasma
285	6	2.6	137	12	Q911F9	Q911F9 hepatitis c	358	6	2.6	172	16	Q9RUS6	Q9RUS6 delinococcus
286	6	2.6	137	12	Q911F8	Q911F8 hepatitis c	359	6	2.6	173	16	Q92AB0	Q92AB0 listeria in
287	6	2.6	137	12	Q911F6	Q911F6 hepatitis c	360	6	2.6	174	2	Q9ZFE9	Q9ZFE9 klebsiella
288	6	2.6	137	12	Q911F5	Q911F5 hepatitis c	361	6	2.6	175	5	Q9VBD9	Q9VBD9 drosophila
289	6	2.6	137	12	Q911F4	Q911F4 hepatitis c	362	6	2.6	176	5	Q17629	Q17629 caenorhabdi
290	6	2.6	137	12	Q911F3	Q911F3 hepatitis c	363	6	2.6	177	17	Q59038	Q59038 methanococ
291	6	2.6	137	12	Q911F2	Q911F2 hepatitis c	364	6	2.6	178	3	Q9UR55	Q9UR55 kluyveromyc
292	6	2.6	137	12	Q911F1	Q911F1 hepatitis c	365	6	2.6	179	10	Q9AWN0	Q9AWN0 cryza sativ
293	6	2.6	137	12	Q911F0	Q911F0 hepatitis c	366	6	2.6	180	3	Q99008	Q99008 tolypocladi
294	6	2.6	137	12	Q911E9	Q911E9 hepatitis c	367	6	2.6	183	2	Q9K287	Q9K287 streptomyces
295	6	2.6	137	12	Q911E8	Q911E8 hepatitis c	368	6	2.6	185	16	Q25457	Q25457 helicobacte
296	6	2.6	137	12	Q911E7	Q911E7 hepatitis c	369	6	2.6	186	12	Q91Y22	Q91Y22 hepatitis c
297	6	2.6	137	12	Q911E6	Q911E6 hepatitis c	370	6	2.6	186	12	Q91Y21	Q91Y21 hepatitis c
298	6	2.6	137	12	Q911E5	Q911E5 hepatitis c	371	6	2.6	186	12	Q91Y20	Q91Y20 hepatitis c
299	6	2.6	137	12	Q911E4	Q911E4 hepatitis c	372	6	2.6	186	12	Q91Y19	Q91Y19 hepatitis c
300	6	2.6	139	2	Q9AKS1	Q9AKS1 pseudomonas	373	6	2.6	186	12	Q91Y18	Q91Y18 hepatitis c
301	6	2.6	139	2	Q53856	Q53856 spiroplasma	374	6	2.6	186	12	Q91Y17	Q91Y17 hepatitis c
302	6	2.6	139	6	Q96TL4	Q96TL4 oplostoma	375	6	2.6	186	12	Q91Y16	Q91Y16 hepatitis c
303	6	2.6	139	6	Q95K12	Q95K12 macaca fasc	376	6	2.6	186	12	Q91Y15	Q91Y15 hepatitis c
304	6	2.6	139	16	Q9UR37	Q9UR37 neisseria m	377	6	2.6	186	12	Q91Y14	Q91Y14 hepatitis c
305	6	2.6	141	16	Q91531	Q91531 pseudomonas	378	6	2.6	186	12	Q91Y13	Q91Y13 hepatitis c
306	6	2.6	144	10	Q9SMD6	Q9SMD6 lamnaria d	379	6	2.6	186	12	Q91Y12	Q91Y12 hepatitis c
307	6	2.6	144	16	Q51117	Q51117 borrelia bu	380	6	2.6	186	12	Q91Y11	Q91Y11 hepatitis c
308	6	2.6	148	8	Q09353	Q09353 lycopodium	381	6	2.6	186	12	Q91Y10	Q91Y10 hepatitis c

382	6	2.6	186	12	Q91YX9	Q91YX9 hepatitis c	455	6	2.6	212	10	Q9FTK1	Q9FTK1 oryza sativ
383	6	2.6	186	12	Q91YX8	Q91YX8 hepatitis c	456	6	2.6	213	13	Q9YH82	Q9YH82 gallus gall
384	6	2.6	186	12	Q91YX7	Q91YX7 hepatitis c	457	6	2.6	213	13	Q9PFR9	Q9PFR9 gallus gall
385	6	2.6	186	12	Q91YX6	Q91YX6 hepatitis c	458	6	2.6	214	16	Q92710	Q92710 listeria in
386	6	2.6	186	12	Q91YX5	Q91YX5 hepatitis c	459	6	2.6	215	2	Q9XA90	Q9XA90 streptomyce
387	6	2.6	186	12	Q91Y12	Q91Y12 hepatitis c	460	6	2.6	215	5	Q9Y5S1	Q9Y5S1 leishmania
388	6	2.6	186	12	Q91Y11	Q91Y11 hepatitis c	461	6	2.6	218	5	Q9V6P3	Q9V6P3 dirosophila
389	6	2.6	186	12	Q91Y10	Q91Y10 hepatitis c	462	6	2.6	218	16	Q9K790	Q9K790 bacillus ha
390	6	2.6	186	12	Q91YK9	Q91YK9 hepatitis c	463	6	2.6	218	17	Q9HNX8	Q9HNX8 halobacteri
391	6	2.6	186	12	Q91YK8	Q91YK8 hepatitis c	464	6	2.6	219	5	Q9VAF1	Q9VAF1 dirosophila
392	6	2.6	186	12	Q91YK6	Q91YK6 hepatitis c	465	6	2.6	220	4	Q96S01	Q96S01 homo sapien
393	6	2.6	186	12	Q91YK5	Q91YK5 hepatitis c	466	6	2.6	220	8	Q9T4W8	Q9T4W8 cyanophora
394	6	2.6	186	12	Q91YK4	Q91YK4 hepatitis c	467	6	2.6	221	15	Q91019	Q91019 human immun
395	6	2.6	186	12	Q91YK3	Q91YK3 hepatitis c	468	6	2.6	222	4	Q9H532	Q9H532 homo sapien
396	6	2.6	186	12	Q91YK2	Q91YK2 hepatitis c	469	6	2.6	222	10	Q93VG5	Q93VG5 streptococ
397	6	2.6	186	12	Q91YK1	Q91YK1 hepatitis c	470	6	2.6	223	12	Q10691	Q10691 cymbidium m
398	6	2.6	186	12	Q91YK0	Q91YK0 hepatitis c	471	6	2.6	223	16	Q9A0K2	Q9A0K2 streptococ
399	6	2.6	186	12	Q91YJ9	Q91YJ9 hepatitis c	472	6	2.6	224	3	Q03322	Q03322 helicobacte
400	6	2.6	186	12	Q91YJ8	Q91YJ8 hepatitis c	473	6	2.6	224	16	Q25350	Q25350 streptomyce
401	6	2.6	186	12	Q91YJ7	Q91YJ7 hepatitis c	474	6	2.6	226	2	Q86726	Q86726 streptomyce
402	6	2.6	186	12	Q91YJ6	Q91YJ6 hepatitis c	475	6	2.6	226	10	Q9LNB7	Q9LNB7 arabidopsis
403	6	2.6	186	12	Q91YJ5	Q91YJ5 hepatitis c	476	6	2.6	226	15	Q87114	Q87114 chimpanzee
404	6	2.6	186	12	Q91YJ4	Q91YJ4 hepatitis c	477	6	2.6	227	16	Q9CD41	Q9CD41 mycobacteri
405	6	2.6	186	12	Q91YJ3	Q91YJ3 hepatitis c	478	6	2.6	228	12	Q92454	Q92454 bombyx mori
406	6	2.6	186	12	Q91YJ1	Q91YJ1 hepatitis c	479	6	2.6	229	16	Q9CK96	Q9CK96 pasteurella
407	6	2.6	186	12	Q91YJ0	Q91YJ0 hepatitis c	480	6	2.6	230	5	Q61518	Q61518 caenorhabdi
408	6	2.6	186	12	Q91YI9	Q91YI9 hepatitis c	481	6	2.6	230	10	Q9F1S1	Q9F1S1 arabidopsis
409	6	2.6	186	12	Q91YI8	Q91YI8 hepatitis c	482	6	2.6	230	10	Q9ATN6	Q9ATN6 zea mays
410	6	2.6	186	12	Q91YI7	Q91YI7 hepatitis c	483	6	2.6	231	2	P77975	P77975 shewanella
411	6	2.6	186	12	Q91YI6	Q91YI6 hepatitis c	484	6	2.6	231	7	Q08613	Q08613 cyphotilapi
412	6	2.6	186	12	Q91YI5	Q91YI5 hepatitis c	485	6	2.6	232	5	Q9VYGA	Q9VYGA dirosophila
413	6	2.6	186	12	Q91YI4	Q91YI4 hepatitis c	486	6	2.6	232	10	Q49910	Q49910 nicotiana t
414	6	2.6	187	2	Q52564	Q52564 pseudomonas	487	6	2.6	232	12	Q9M3U3	Q9M3U3 nicotiana t
415	6	2.6	188	4	Q96T59	Q96T59 homo sapien	488	6	2.6	236	12	Q85028	Q85028 pseudobacteri
416	6	2.6	188	5	Q96T59	Q96T59 homo sapien	489	6	2.6	236	17	Q9AHV1	Q9AHV1 halobacteri
417	6	2.6	189	2	Q9L0W6	Q9L0W6 chaetastus	490	6	2.6	236	23	Q9XBI0	Q9XBI0 bacillus ce
418	6	2.6	190	2	Q9ALK4	Q9ALK4 escherichia	491	6	2.6	239	5	Q9NB10	Q9NB10 manduca sex
419	6	2.6	190	15	Q9DVI6	Q9DVI6 human immun	492	6	2.6	239	10	Q23889	Q23889 oryza sativ
420	6	2.6	192	12	Q81A14	Q81A14 hepatitis c	493	6	2.6	241	5	Q9GPI3	Q9GPI3 dirosophila
421	6	2.6	192	12	Q81A32	Q81A32 hepatitis c	494	6	2.6	241	5	Q95UN3	Q95UN3 dirosophila
422	6	2.6	192	12	Q81A35	Q81A35 hepatitis c	495	6	2.6	241	5	Q95NK2	Q95NK2 dirosophila
423	6	2.6	192	12	Q81397	Q81397 hepatitis c	496	6	2.6	241	5	Q95NM6	Q95NM6 dirosophila
424	6	2.6	194	4	Q9UG17	Q9UG17 homo sapien	497	6	2.6	247	5	Q9XVS9	Q9XVS9 caenorhabdi
425	6	2.6	194	12	Q68581	Q68581 hepatitis c	498	6	2.6	247	16	Q9ZK30	Q9ZK30 helicobacte
426	6	2.6	194	16	Q97D08	Q97D08 clostridium	499	6	2.6	248	2	P71465	P71465 lacticobacill
427	6	2.6	195	2	Q9R5Y6	Q9R5Y6 azotobacter	500	6	2.6	248	16	Q9ZC09	Q9ZC09 listeria in
428	6	2.6	195	5	Q16759	Q16759 caenorhabdi	501	6	2.6	249	3	Q74385	Q74385 schistosach
429	6	2.6	196	5	Q26864	Q26864 trypanosoma	502	6	2.6	250	4	Q9NVS3	Q9NVS3 homo sapien
430	6	2.6	196	16	P95270	P95270 mycobacteri	503	6	2.6	250	4	Q96G66	Q96G66 homo sapien
431	6	2.6	197	9	Q38147	Q38147 bacteriopha	504	6	2.6	250	11	Q9CR18	Q9CR18 mus musculu
432	6	2.6	197	12	Q83114	Q83114 mastadenovi	505	6	2.6	251	2	Q9S2R7	Q9S2R7 streptomyce
433	6	2.6	198	12	Q69020	Q69020 human herpe	506	6	2.6	251	16	Q92YR4	Q92YR4 rhizobium m
434	6	2.6	198	16	Q9KFE3	Q9KFE3 bacillus ha	507	6	2.6	253	16	Q98B77	Q98B77 rhizobium l
435	6	2.6	199	16	Q9Z809	Q9Z809 rhizobium m	508	6	2.6	254	2	Q9K3Y6	Q9K3Y6 streptomyce
436	6	2.6	200	16	Q9K570	Q9K570 mycobacteri	509	6	2.6	254	10	Q43422	Q43422 cucumis sat
437	6	2.6	201	2	Q9K523	Q9K523 mycobacteri	510	6	2.6	254	10	Q9S8K2	Q9S8K2 cucumis sat
438	6	2.6	201	5	Q9VUS1	Q9VUS1 rhinosceros	511	6	2.6	254	16	Q9A4Y5	Q9A4Y5 caulobacter
439	6	2.6	203	7	Q9XRNO	Q9XRNO rhinosceros	512	6	2.6	256	8	Q940R4	Q940R4 pleurotus o
440	6	2.6	204	5	Q19022	Q19022 caenorhabdi	513	6	2.6	257	4	Q9PIV9	Q9PIV9 homo sapien
441	6	2.6	204	11	Q922V3	Q922V3 mus musculu	514	6	2.6	257	10	Q04233	Q04233 victoria faba
442	6	2.6	204	16	Q92T45	Q92T45 rhizobium m	515	6	2.6	258	5	Q9N4P4	Q9N4P4 caenorhabdi
443	6	2.6	205	5	Q45937	Q45937 caenorhabdi	516	6	2.6	260	10	Q9S0B4	Q9S0B4 oryza sativ
444	6	2.6	207	5	Q76756	Q76756 apis mellif	517	6	2.6	260	10	Q9AS67	Q9AS67 oryza sativ
445	6	2.6	207	15	Q91028	Q91028 human immun	518	6	2.6	263	2	Q05370	Q05370 actinobacil
446	6	2.6	208	13	Q9OYR6	Q9OYR6 ictalurus p	519	6	2.6	265	17	Q97AN5	Q97AN5 thermoplasma
447	6	2.6	208	15	Q91026	Q91026 human immun	520	6	2.6	267	6	Q02764	Q02764 oryctolagus
448	6	2.6	208	16	Q9ABR4	Q9ABR4 caulobacter	521	6	2.6	268	10	P93654	P93654 arabidopsis
449	6	2.6	209	3	Q93915	Q93915 schizopnyll	522	6	2.6	268	16	Q92B38	Q92B38 listeria in
450	6	2.6	209	13	Q9PSN8	Q9PSN8 trimeresuru	523	6	2.6	269	2	Q9R9E2	Q9R9E2 bacillus su
451	6	2.6	209	15	Q9O6Y5	Q9O6Y5 human immun	524	6	2.6	269	5	Q9XV58	Q9XV58 caenorhabdi
452	6	2.6	209	15	Q91043	Q91043 human immun	525	6	2.6	270	11	Q99K19	Q99K19 mus musculu
453	6	2.6	211	13	Q9PWP2	Q9PWP2 gallus gall	526	6	2.6	270	16	Q9A3H3	Q9A3H3 caulobacter
454	6	2.6	212	5	Q9VYI4	Q9VYI4 dirosophila	527	6	2.6	270	16	Q98BP8	Q98BP8 mycoplasma

528	6	2.6	272	2	Q93Q65	Q93Q65 klebsiella	601	6	2.6	325	10	Q9SWA2	Q9swa2 acetabulari
529	6	2.6	272	5	O17311	O17311 drosophila	602	6	2.6	326	5	Q9VLE9	Q9vle9 drosophila
530	6	2.6	272	5	O17312	O17312 drosophila	603	6	2.6	326	16	P73753	P73753 synechocyst
531	6	2.6	272	5	Q9VUJ1	Q9vuj1 drosophila	604	6	2.6	327	2	Q9RPD1	Q9rpd1 rhodobacter
532	6	2.6	273	2	Q9FCH8	Q9fch8 streptomyce	605	6	2.6	327	2	O54790	O54790 rhodobacter
533	6	2.6	273	17	Q57735	Q57735 pyrococcus	606	6	2.6	327	11	Q9CYU4	Q9cyu4 mus musculu
534	6	2.6	274	5	O16860	O16860 drosophila	607	6	2.6	328	5	Q9V5B6	Q9v5b6 drosophila
535	6	2.6	274	5	Q9VAD9	Q9vad9 drosophila	608	6	2.6	328	17	Q9VCB9	Q9vcb9 thermoplasma
536	6	2.6	274	5	Q964T5	Q964t5 porcellio s	609	6	2.6	329	12	O09798	O09798 human herpe
537	6	2.6	274	5	Q95RR6	Q95rr6 drosophila	610	6	2.6	329	16	Q9PC8	Q9pc8 ureaplasma
538	6	2.6	274	9	O64041	O64041 bacteriopho	611	6	2.6	329	16	Q9CKZ3	Q9ckz3 pasteurella
539	6	2.6	274	12	Q91B76	Q91b76 adoxophyes	612	6	2.6	330	2	Q9RK26	Q9rk26 streptomyce
540	6	2.6	274	16	O31981	O31981 bacillus su	613	6	2.6	330	16	Q92XE3	Q92xe3 rhizobium m
541	6	2.6	275	16	O34437	O34437 bacillus su	614	6	2.6	330	17	Q97AR5	Q97ars thermoplasma
542	6	2.6	275	16	Q97FS8	Q97fs8 clostridium	615	6	2.6	331	3	Q9UWZ0	Q9uwz0 candida alb
543	6	2.6	277	4	Q961D9	Q961d9 homo sapien	616	6	2.6	332	2	O68170	O68170 lactococcus
544	6	2.6	280	17	Q9V2J1	Q9v2j1 pyrococcus	617	6	2.6	332	12	Q9PVL8	Q9pvl8 xestia c-nl
545	6	2.6	281	4	Q9BZ90	Q9bzz0 homo sapien	618	6	2.6	333	4	Q9BVH1	Q9bvh1 homo sapien
546	6	2.6	281	10	Q9XE15	Q9xe15 oryza sativ	619	6	2.6	334	4	Q96ES7	Q96es7 homo sapien
547	6	2.6	281	12	P89133	P89133 simian hemo	620	6	2.6	335	16	Q99VY7	Q99vy7 staphylococ
548	6	2.6	281	17	Q9HPJ3	Q9hpj3 halobacteri	621	6	2.6	335	16	Q93ZFO	Q93zfo staphylococ
549	6	2.6	283	10	Q9SJB6	Q9sjb6 arabidopsis	622	6	2.6	337	5	Q9GV75	Q9gv75 trypanosoma
550	6	2.6	284	3	O42914	O42914 schizosacch	623	6	2.6	337	16	Q92VY7	Q92vy7 rhizobium m
551	6	2.6	284	16	Q9WYW7	Q9wyw7 thermotoga	624	6	2.6	339	16	Q91OZ1	Q91oz1 pseudomonas
552	6	2.6	284	16	Q98GL4	Q98gl4 rhizobium l	625	6	2.6	340	11	Q9DBT3	Q9dbt3 mus musculu
553	6	2.6	286	5	Q9VBE0	Q9vbe0 drosophila	626	6	2.6	340	13	Q9YHY2	Q9yhy2 lampetra fl
554	6	2.6	286	16	Q9CKX6	Q9ckx6 pasteurella	627	6	2.6	341	5	O19550	O19550 caenorhabdi
555	6	2.6	289	4	Q96N10	Q96n10 homo sapien	628	6	2.6	342	2	O88130	O88130 neisseria
556	6	2.6	294	2	Q9XAM3	Q9xam3 lactobacill	629	6	2.6	342	2	O86332	O86332 neisseria e
557	6	2.6	294	5	Q9V62	Q9v62 drosophila	630	6	2.6	342	2	Q9R3R1	Q9r3r1 neisseria l
558	6	2.6	294	10	Q9L653	Q9l653 oryza sativ	631	6	2.6	342	2	Q9R3R0	Q9r3r0 neisseria c
559	6	2.6	294	16	O07242	O07242 mycobacteri	632	6	2.6	342	2	Q9R3A4	Q9r3a4 neisseria p
560	6	2.6	296	12	O69118	O69118 human herpe	633	6	2.6	342	2	Q9R3A3	Q9r3a3 neisseria m
561	6	2.6	296	16	O87127	O87127 pseudomonas	634	6	2.6	342	2	Q9R3R3	Q9r3r3 neisseria m
562	6	2.6	297	9	Q38373	Q38373 lactococcus	635	6	2.6	342	2	O86406	O86406 neisseria p
563	6	2.6	297	16	Q9CEW6	Q9cew6 lactococcus	636	6	2.6	342	2	O86379	O86379 neisseria c
564	6	2.6	298	2	Q91O67	Q91o67 streptomyce	637	6	2.6	342	2	O86413	O86413 neisseria s
565	6	2.6	299	4	Q9Y4N1	Q9y4n1 homo sapien	638	6	2.6	342	2	O86386	O86386 neisseria f
566	6	2.6	299	16	Q98GB2	Q98gb2 rhizobium l	639	6	2.6	342	2	O86416	O86416 neisseria s
567	6	2.6	300	16	Q929B2	Q929b2 listeria in	640	6	2.6	342	2	O86400	O86400 neisseria m
568	6	2.6	301	16	Q947Y9	Q947y9 caulobacter	641	6	2.6	342	2	O86407	O86407 neisseria p
569	6	2.6	302	10	Q9ATN1	Q9atn1 zea mays (m	642	6	2.6	342	2	O86336	O86336 neisseria p
570	6	2.6	303	2	Q9Z9P7	Q9z9p7 bacillus ha	643	6	2.6	342	2	Q9R807	Q9r807 neisseria m
571	6	2.6	304	6	Q9N120	Q9n120 oryctolagus	644	6	2.6	342	2	Q9R808	Q9r808 neisseria p
572	6	2.6	305	5	Q9N5W0	Q9n5w0 caenorhabdi	645	6	2.6	342	2	O86409	O86409 neisseria p
573	6	2.6	308	4	Q9UFU3	Q9ufu3 homo sapien	646	6	2.6	342	2	O86401	O86401 neisseria p
574	6	2.6	309	11	Q9EQA6	Q9eqa6 mus musculu	647	6	2.6	342	2	O86387	O86387 neisseria f
575	6	2.6	309	11	Q9EQA4	Q9eqa4 mus musculu	648	6	2.6	342	2	O86377	O86377 neisseria p
576	6	2.6	310	2	Q9ZAL1	Q9zal1 escherichia	649	6	2.6	342	2	O86410	O86410 neisseria a
577	6	2.6	310	16	Q910X5	Q910x5 pseudomonas	650	6	2.6	342	2	Q9R806	Q9r806 neisseria p
578	6	2.6	311	17	O26780	O26780 methanocet	651	6	2.6	342	2	O86390	O86390 neisseria p
579	6	2.6	312	16	Q9P1X5	Q9p1x5 campylobact	652	6	2.6	343	3	Q9P866	Q9p866 candida alb
580	6	2.6	312	17	Q97UJ3	Q97uj3 sulfolobus	653	6	2.6	343	3	Q9P7S8	Q9p7s8 schizosacch
581	6	2.6	313	2	O05094	O05094 bacillus su	654	6	2.6	343	10	Q91VW5	Q91vw5 arabidopsis
582	6	2.6	313	16	P94529	P94529 mus musculu	655	6	2.6	344	2	O82858	O82858 acetobacter
583	6	2.6	314	11	Q9EQA5	Q9eqa5 mus musculu	656	6	2.6	344	10	O91LY4	O91ly4 brassica na
584	6	2.6	315	4	Q9UHD9	Q9uhj9 homo sapien	657	6	2.6	345	5	Q9U3J8	Q9u3j8 caenorhabdi
585	6	2.6	315	4	Q9UF01	Q9uf01 homo sapien	658	6	2.6	345	5	O95VP7	O95vp7 leishmania
586	6	2.6	315	10	Q9SWA1	Q9swa1 acetabulari	659	6	2.6	345	16	Q98RH7	Q98rh7 mycoplasma
587	6	2.6	315	10	Q9SWA0	Q9swa0 acetabulari	660	6	2.6	347	2	O59797	O59797 neisseria g
588	6	2.6	315	11	O62943	O62943 rattus norv	661	6	2.6	347	16	Q9RKM2	Q9rkm2 delnoccocus
589	6	2.6	315	12	Q98UL3	Q98ul3 hepatitis c	662	6	2.6	348	2	Q9ZBJ3	Q9zbj3 streptomyce
590	6	2.6	315	12	Q98UL4	Q98ul4 hepatitis c	663	6	2.6	348	10	Q9ATR9	Q9atr9 pennisetum
591	6	2.6	315	12	O9WMZ7	O9wmz7 nanovirus-1	664	6	2.6	349	2	Q9EYV1	Q9eyv1 clostridium
592	6	2.6	317	5	O18947	O18947 caenorhabdi	665	6	2.6	349	16	Q97K00	Q97k00 clostridium
593	6	2.6	317	10	Q94HA7	Q94ha7 oryza sativ	666	6	2.6	350	16	Q9PPI2	Q9ppi2 xylella fas
594	6	2.6	317	13	Q919B8	Q919b8 gallus gall	667	6	2.6	351	17	Q971V4	Q971v4 sulfolobus
595	6	2.6	318	16	Q92XE4	Q92xe4 rhizobium m	668	6	2.6	352	4	Q9BYE7	Q9bye7 homo sapien
596	6	2.6	318	16	Q92FN4	Q92fn4 listeria in	669	6	2.6	352	16	Q9A0B4	Q9a0b4 streptococc
597	6	2.6	320	16	Q9P8G4	Q9p8g4 candida alb	670	6	2.6	353	7	Q9VPD8	Q9vpd8 drosophila
598	6	2.6	320	16	Q92SG2	Q92sg2 rhizobium m	671	6	2.6	353	7	Q9TNZ2	Q9tnz2 sus scrofa
599	6	2.6	322	2	O32511	O32511 delnoccocus	672	6	2.6	353	16	Q9RSX8	Q9rsx8 delnoccocus
600	6	2.6	325	10	O80682	O80682 arabidopsis	673	6	2.6	353	17	Q9UXV8	Q9uxv8 pyrococcus

674	6	2.6	354	4	09H254	09H254 homo sapien	747	6	2.6	400	16	0988C1	0988C1 rhizobium 1
675	6	2.6	354	10	094LH4	094LH4 oryza sativ	748	6	2.6	401	16	007563	007563 bacillus su
676	6	2.6	355	2	093IP2	093IP2 burkholderi	749	6	2.6	402	5	09VDQ4	09VDQ4 drosophila
677	6	2.6	355	10	081748	081748 arabdidsps	750	6	2.6	403	2	007675	007675 haemophilus
678	6	2.6	356	2	09L340	09L340 sphingomona	751	6	2.6	406	12	011374	011374 molluscum c
679	6	2.6	357	16	091256	091256 pseudomonas	752	6	2.6	407	10	09SXD7	09SXD7 arabdidsps
680	6	2.6	357	16	09CHR2	09chr2 lactococcus	753	6	2.6	409	10	09SBM1	09sbm1 volvox cart
681	6	2.6	359	16	09CHR9	09chr9 lactococcus	754	6	2.6	410	11	09JRD2	09jrd2 rattus norv
682	6	2.6	361	6	019075	019075 sus scrofa	755	6	2.6	410	11	09JRD1	09jrd1 rattus norv
683	6	2.6	361	7	019242	019242 sus scrofa	756	6	2.6	410	11	09JRD2	09jrd2 mus musculu
684	6	2.6	361	7	019244	019244 sus scrofa	757	6	2.6	411	13	09J206	09j206 carassius a
685	6	2.6	361	7	031066	031066 sus scrofa	758	6	2.6	411	16	09PA21	09pa21 xylella me
686	6	2.6	362	16	092K12	092K12 rhizobium m	759	6	2.6	413	2	0937R4	0937r4 bruceella fa
687	6	2.6	363	7	030870	030870 papio hamad	760	6	2.6	413	5	09VM09	09vm09 drosophila
688	6	2.6	363	7	09BCZ0	09bcz0 papio cynoc	761	6	2.6	414	2	032383	032383 streptomyce
689	6	2.6	363	7	031067	031067 sus scrofa	762	6	2.6	414	10	09ART0	09art0 oryza sativ
690	6	2.6	364	6	09TSW2	09tsw2 sus scrofa	763	6	2.6	414	16	053279	053279 mycobacteri
691	6	2.6	364	6	091243	091243 sus scrofa	764	6	2.6	414	16	092RKO	092rko rhizobium m
692	6	2.6	364	7	019245	019245 sus scrofa	765	6	2.6	415	11	09WTQ3	09wtq3 rattus norv
693	6	2.6	364	7	031068	031068 sus scrofa	766	6	2.6	415	11	09EPW2	09epw2 mus musculu
694	6	2.6	364	10	P93070	P93070 betula verr	767	6	2.6	417	5	015828	015828 leishmania
695	6	2.6	364	16	092RJR9	092rj9 rhizobium m	768	6	2.6	417	16	092RGO	092rgo rhizobium m
696	6	2.6	365	2	09XDJ9	09xdj9 bacteroides	769	6	2.6	418	16	098DY8	098dy8 rhizobium l
697	6	2.6	365	5	09U220	09u220 caenorhabdi	770	6	2.6	419	16	055115	055115 synchocyst
698	6	2.6	366	2	09KZ00	09kz00 streptomyc	771	6	2.6	419	16	09PJ00	09pj00 chlamydia m
699	6	2.6	366	4	096PM9	096pm9 homo sapien	772	6	2.6	419	16	09K013	09k013 neisseria m
700	6	2.6	366	7	031069	031069 sus scrofa	773	6	2.6	419	16	09JVI6	09jvi6 neisseria m
701	6	2.6	367	17	096X16	096x16 sulfolobus	774	6	2.6	419	16	09HMY1	09hmv1 pseudomonas
702	6	2.6	368	2	086984	086984 thermomono	775	6	2.6	420	2	P97011	P97011 streptomyce
703	6	2.6	369	2	052807	052807 amycolatops	776	6	2.6	420	2	09ZAG7	09zag7 actinobacil
704	6	2.6	369	10	065663	065663 arabdidsps	777	6	2.6	420	4	09H255	09h255 homo sapien
705	6	2.6	370	16	09RTU4	09rtu4 delnoccus	778	6	2.6	420	4	096QB5	096qb5 homo sapien
706	6	2.6	371	5	046052	046052 drosophila	779	6	2.6	420	16	09CUR2	09c1s2 pasteurella
707	6	2.6	371	10	09C914	09c914 arabdidsps	780	6	2.6	421	2	09X7X2	09x7x2 streptomyce
708	6	2.6	372	3	012121	012121 saccharomyc	781	6	2.6	421	5	09BIC9	09bic9 trichinella
709	6	2.6	372	10	09C913	09c913 arabdidsps	782	6	2.6	421	16	092RKO	092rko rhizobium m
710	6	2.6	372	16	09KRG6	09krg6 bacillus ha	783	6	2.6	422	5	045786	045786 caenorhabdi
711	6	2.6	374	13	09W6F8	09w6f8 xenopus lae	784	6	2.6	423	2	09ZH30	09zh30 listeria mo
712	6	2.6	375	16	09RW21	09rw21 delnoccus	785	6	2.6	423	2	093Q15	093q15 listeria mo
713	6	2.6	376	5	09W566	09w566 drosophila	786	6	2.6	423	16	09K6E8	09k6e8 bacillus ha
714	6	2.6	378	11	P89002	P89002 praomys nat	787	6	2.6	423	16	0927U2	0927u2 listeria in
715	6	2.6	378	17	097U03	097u03 sulfolobus	788	6	2.6	424	10	094DK9	094dk9 oryza sativ
716	6	2.6	379	2	087181	087181 streptococc	789	6	2.6	425	2	09F7M3	09f7m3 uncultured
717	6	2.6	379	2	09AQJ1	09aqj1 streptococc	790	6	2.6	425	3	09C0Q7	09c0q7 neurospora
718	6	2.6	380	5	093878	093878 caenorhabdi	791	6	2.6	425	10	09LDO2	09ldo2 nicotiana t
719	6	2.6	381	3	043031	043031 schizosacch	792	6	2.6	426	3	096M33	096m33 podospora a
720	6	2.6	381	10	09CAC3	09cac3 arabdidsps	793	6	2.6	427	2	099PX1	099px1 vibrio algi
721	6	2.6	382	5	022541	022541 caenorhabdi	794	6	2.6	427	2	P95326	P95326 myxococcus
722	6	2.6	383	2	09Z3A8	09z3a8 burkholderi	795	6	2.6	427	5	09VG80	09vg80 drosophila
723	6	2.6	383	5	09VD25	09vd25 drosophila	796	6	2.6	428	2	032417	032417 mycoplasma
724	6	2.6	384	4	096GN1	096gn1 homo sapien	797	6	2.6	428	2	09R3N6	09r3n6 mycoplasma
725	6	2.6	384	5	09V612	09v612 drosophila	798	6	2.6	428	2	09RCX7	09rcx7 mycoplasma
726	6	2.6	384	16	0986H2	0986h2 rhizobium 1	799	6	2.6	428	2	09RCX5	09rcx5 mycoplasma
727	6	2.6	385	11	091YH1	091yhl cricetulus	800	6	2.6	428	2	09RCX3	09rcx3 mycoplasma
728	6	2.6	385	5	0966D5	0966d5 caenorhabdi	801	6	2.6	429	2	09RGX6	09rgx6 mycoplasma
729	6	2.6	386	10	09FNV1	09fnv1 dactylis gl	802	6	2.6	429	2	09RGX4	09rgx4 mycoplasma
730	6	2.6	388	4	096H72	096h72 mus sapien	803	6	2.6	429	4	096B82	096b82 homo sapien
731	6	2.6	391	11	09D9N3	09d9n3 mus musculu	804	6	2.6	430	12	039780	039780 equine hepp
732	6	2.6	391	16	098A00	098a00 rhizobium 1	805	6	2.6	431	16	09KSH6	09ksh6 vibrio chol
733	6	2.6	391	17	09HOK2	09hok2 halobacteri	806	6	2.6	432	5	09M216	09m216 drosophila
734	6	2.6	392	6	09BDQ4	09bdq4 canis famli	807	6	2.6	433	2	09X8V6	09x8v6 streptomyce
735	6	2.6	392	10	09M9C3	09m9c3 arabdidsps	808	6	2.6	433	3	074763	074763 schizosacch
736	6	2.6	392	17	09U2Z8	09u2z8 pyrococcus	809	6	2.6	437	10	09LD33	09ld33 cryptosacch
737	6	2.6	393	2	09EMC4	09emc4 streptomyce	810	6	2.6	439	2	053589	053589 staphilococ
738	6	2.6	394	5	09N4W1	09n4w1 caenorhabdi	811	6	2.6	439	4	09H2V8	09h2v8 homo sapien
739	6	2.6	396	5	09XXC7	09xxc7 caenorhabdi	812	6	2.6	440	16	092UL9	092ul9 rickettsia
740	6	2.6	397	5	09GR07	09grg7 leishmania	813	6	2.6	442	16	005507	005507 bacillus su
741	6	2.6	397	11	070348	070348 mus musculu	814	6	2.6	444	5	09U9C7	09u9c7 caenorhabdi
742	6	2.6	397	11	099K08	099k08 mus musculu	815	6	2.6	445	16	034545	034545 bacillus su
743	6	2.6	399	5	043935	043935 trichomonas	816	6	2.6	448	5	094304	094304 caenorhabdi
744	6	2.6	399	6	09TSM1	09tsw1 sus scrofa	817	6	2.6	448	16	0960U7	0960u7 drosophila
745	6	2.6	400	2	0938T4	0938t4 streptococc	818	6	2.6	448	16	031428	031428 bacillus su
746	6	2.6	400	16	09A0M2	09a0m2 streptococc	819	6	2.6	449	11	09CYK8	09cyk8 mus musculu

820	6	2.6	450	16	083238	08338	treponema p	893	6	2.6	510	5	024425	024425 drosophila
821	6	2.6	451	11	035254	035254	rattus norv	894	6	2.6	510	10	042875	042875 lycopersico
822	6	2.6	452	1	091176	09116	streptomyces	895	6	2.6	516	1	09c4m3	09c4m3 halobacteri
823	6	2.6	452	3	09HEB4	09HEB4	neurospora	896	6	2.6	516	16	0970P4	0970P4 streptococ
824	6	2.6	452	10	094BV5	094BV5	arabidopsis	897	6	2.6	516	17	097AE0	097AE0 thermoplas
825	6	2.6	453	2	093S03	093S03	pseudomonas	898	6	2.6	518	10	095VG8	095VG8 arabidopsis
826	6	2.6	453	16	093S01	093S01	psuedomonas	899	6	2.6	523	3	094CQ1	094CQ1 oryza sativ
827	6	2.6	453	16	09K8Q5	09K8Q5	bacillus ha	900	6	2.6	525	10	09VUC9	09VUC9 drosophila
828	6	2.6	454	4	09BRL1	09BRL1	homo sapien	901	6	2.6	526	3	060097	060097 schizosacch
829	6	2.6	454	16	092HL2	092HL2	ricketsia	902	6	2.6	526	5	09Y110	09Y110 trichomonas
830	6	2.6	459	5	095R06	095R06	drosophila	903	6	2.6	526	11	054887	054887 mus musculu
831	6	2.6	460	17	09HKK1	09HKK1	thermoplas	904	6	2.6	526	12	085027	085027 pseudocorale
832	6	2.6	464	16	084498	084498	chlamydia t	905	6	2.6	526	16	09RUB1	09RUB1 delnoco
833	6	2.6	466	2	09AQ17	09AQ17	streptococ	906	6	2.6	528	5	0960B6	0960B6 drosophila
834	6	2.6	466	2	09AFH1	09AFH1	streptococ	907	6	2.6	529	12	085213	085213 pity virus
835	6	2.6	466	2	093T13	093T13	streptococ	908	6	2.6	531	17	09HKH9	09HKH9 thermoplas
836	6	2.6	466	15	09DSK6	09DSK6	human immu	909	6	2.6	532	5	095R30	095R30 drosophila
837	6	2.6	467	12	P89433	P89433	hepates simp	910	6	2.6	534	2	09RPV9	09RPV9 bacillus me
838	6	2.6	468	4	09N2L2	09N2L2	homo sapien	911	6	2.6	534	5	018515	018515 hydra atten
839	6	2.6	468	17	028528	028528	archaeoglob	912	6	2.6	535	2	052716	052716 klebsiella
840	6	2.6	469	10	09FV71	09FV71	arabidopsis	913	6	2.6	535	2	076919	076919 drosophila
841	6	2.6	469	10	09FNV1	09FNV1	arabidopsis	914	6	2.6	536	12	09WRT5	09WRT5 macaca m
842	6	2.6	470	10	09SUL6	09SUL6	arabidopsis	915	6	2.6	536	12	09J2L9	09J2L9 macaca m
843	6	2.6	471	8	095B76	095B76	cycas taiwa	916	6	2.6	537	5	09V8K8	09V8K8 drosophila
844	6	2.6	471	8	095B75	095B75	cycas taiwa	917	6	2.6	539	16	09RWQ4	09RWQ4 delnoco
845	6	2.6	472	10	09FTH7	09FTH7	oryza sativ	918	6	2.6	540	5	09NA46	09NA46 caenorhabd
846	6	2.6	473	10	049868	049868	hordeum vul	919	6	2.6	540	6	095K25	095K25 macaca fasc
847	6	2.6	473	11	099K48	099K48	mus musculu	920	6	2.6	541	10	048583	048583 arabidopsis
848	6	2.6	473	11	063887	063887	mus sp. non	921	6	2.6	542	16	098B11	098B11 mycoplasma
849	6	2.6	474	5	061472	061472	aplysia cal	922	6	2.6	543	16	098102	098102 rhizobium l
850	6	2.6	474	16	09RR21	09RR21	delnoco	923	6	2.6	543	16	092XV7	092XV7 rhizobium m
851	6	2.6	476	11	09RCU34	09RCU34	mus musculu	924	6	2.6	545	5	09VM14	09VM14 drosophila
852	6	2.6	476	15	09A990	09A990	caulobacter	925	6	2.6	545	6	09MYV0	09MYV0 bos tauru
853	6	2.6	477	15	09QF42	09QF42	human immu	926	6	2.6	546	16	09CE14	09CE14 lactococcus
854	6	2.6	478	5	09UKF4	09UKF4	caenorhabd	927	6	2.6	547	2	059117	059117 arthrobacte
855	6	2.6	480	15	09QF41	09QF41	human immu	928	6	2.6	547	4	096MS8	096MS8 homo sapien
856	6	2.6	480	5	09BHF5	09BHF5	leishmania	929	6	2.6	551	16	09H0D4	09H0D4 pseudomon
857	6	2.6	480	16	09RYX7	09RYX7	delnoco	930	6	2.6	552	4	096NM5	096NM5 homo sapien
858	6	2.6	481	16	09A211	09A211	caulobacter	931	6	2.6	556	2	09L8K4	09L8K4 mycobacteri
859	6	2.6	484	2	09KH18	09KH18	lactobacill	932	6	2.6	556	10	09FM25	09FM25 arabidopsis
860	6	2.6	484	5	0965H9	0965H9	caenorhabd	933	6	2.6	557	10	09LXV3	09LXV3 arabidopsis
861	6	2.6	484	16	083499	083499	treponema p	934	6	2.6	559	2	030349	030349 burkholderi
862	6	2.6	487	10	09SYL8	09SYL8	arabidopsis	935	6	2.6	559	11	063135	063135 rattus norv
863	6	2.6	491	16	09CFE8	09CFE8	lactococcus	936	6	2.6	559	16	092R30	092R30 rhizobium m
864	6	2.6	491	16	0984W7	0984W7	rhizobium l	937	6	2.6	561	2	09X9P8	09X9P8 streptomyces
865	6	2.6	492	16	09KSG1	09KSG1	vibrio chol	938	6	2.6	561	10	09T014	09T014 arabidopsis
866	6	2.6	494	11	09ER20	09ER20	mus musculu	939	6	2.6	563	2	069070	069070 streptomyces
867	6	2.6	494	11	091X69	091X69	mus musculu	940	6	2.6	567	5	096156	096156 plasmodium
868	6	2.6	494	16	09RWF6	09RWF6	delnoco	941	6	2.6	567	16	09A4P0	09A4P0 caulobacter
869	6	2.6	495	2	09VJ38	09VJ38	pseudomonas	942	6	2.6	568	4	096P21	096P21 homo sapien
870	6	2.6	496	5	09V9J2	09V9J2	drosophila	943	6	2.6	570	10	09SNE7	09SNE7 oryza sativ
871	6	2.6	497	11	063612	063612	rattus norv	944	6	2.6	573	16	09KTD7	09KTD7 vibrio chol
872	6	2.6	497	16	09PEX2	09PEX2	xylella fas	945	6	2.6	573	16	09CTP6	09CTP6 lactococcus
873	6	2.6	498	16	097JG4	097JG4	clostridium	946	6	2.6	575	2	09APR6	09APR6 uncultured
874	6	2.6	499	5	094996	094996	tetrahymena	947	6	2.6	575	3	09RJQ2	09RJQ2 streptomyces
875	6	2.6	500	2	09RAU2	09RAU2	lactococcus	948	6	2.6	575	2	09Y7A8	09Y7A8 neurospora
876	6	2.6	500	2	093MY8	093MY8	lactococcus	949	6	2.6	575	16	098EP8	098EP8 drosophila
877	6	2.6	500	16	09CEP8	09CEP8	lactococcus	950	6	2.6	578	10	09LTF6	09LTF6 rhizobium l
878	6	2.6	502	5	018672	018672	caenorhabd	951	6	2.6	578	10	09XGNO	09XGNO arabidopsis
879	6	2.6	502	12	088621	088621	beet necrot	952	6	2.6	579	2	09REN3	09REN3 zymomonas m
880	6	2.6	503	12	086591	086591	equine he	953	6	2.6	580	5	09GUB3	09GUB3 dictyostel
881	6	2.6	503	5	09VUL4	09VUL4	drosophila	954	6	2.6	583	3	09P768	09P768 schizosacch
882	6	2.6	503	12	039779	039779	equine he	955	6	2.6	583	5	09BNA5	09BNA5 plasmodium
883	6	2.6	504	12	089481	089481	hantaan vir	956	6	2.6	583	5	09BHB3	09BHB3 plasmodium
884	6	2.6	504	16	09KBB9	09KBB9	procambur	957	6	2.6	585	3	P78978	P78978 yarrowia li
885	6	2.6	505	5	090913	090913	vibrio chol	958	6	2.6	585	10	048713	048713 arabidopsis
886	6	2.6	505	16	09KLU9	09KLU9	drosophila	959	6	2.6	586	4	09LMT7	09LMT7 oryza sativ
887	6	2.6	506	5	09V789	09V789	caenorhabd	960	6	2.6	586	10	09UHT3	09UHT3 homo sapien
888	6	2.6	507	5	045182	045182	caenorhabd	961	6	2.6	588	5	09VKV9	09VKV9 drosophila
889	6	2.6	508	5	021897	021897	bacteroides	962	6	2.6	588	9	09BOD1	09BOD1 staphylococ
890	6	2.6	509	2	09RCK3	09RCK3	mus musculu	963	6	2.6	592	5	09XV50	09XV50 caenorhabd
891	6	2.6	509	11	09D0Q2	09D0Q2	candida alb	964	6	2.6	592	8	0957Q7	0957Q7 dogania sub
892	6	2.6	510	3	093992	093992	candida alb	965	6	2.6	593	15	09D5K7	09D5K7 human immu

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966 6 2.6 594 4 09C0A9 09C0A9 homo sapien
967 6 2.6 594 5 096041 096041 bombyx mori
968 6 2.6 595 8 09M199 09M199 typhionecte
969 6 2.6 596 10 09A463 09A463 oryza sativ
970 6 2.6 598 3 09P6X0 09P6X0 neurospora
971 6 2.6 599 3 024629 024629 drosophila
972 6 2.6 601 8 09XPH6 09XPH6 chelonla my
973 6 2.6 603 16 09XPE4 09XPE4 xylella fas
974 6 2.6 603 16 09A8D8 09A8D8 rhizobium l
975 6 2.6 605 8 09XPE4 09XPE4 eumeces egr
976 6 2.6 605 11 09D2H6 09D2H6 mus musculu
977 6 2.6 606 5 09NCQ2 09NCQ2 drosophila
978 6 2.6 608 2 045998 045998 caulobacter
979 6 2.6 608 16 09ABG0 09ABG0 caulobacter
980 6 2.6 610 5 096659 096659 hirudo medi
981 6 2.6 611 4 096H2 096H2 homo sapien
982 6 2.6 612 8 094SW4 094SW4 exocoetus v
983 6 2.6 613 5 09VLA2 09VLA2 drosophila
984 6 2.6 613 15 09DSJ2 09DSJ2 human immun
985 6 2.6 614 11 088561 088561 mus musculu
986 6 2.6 615 4 09P120 09P120 homo sapien
987 6 2.6 616 16 09PCM5 09PCM5 xylella fas
988 6 2.6 619 4 094917 094917 homo sapien
989 6 2.6 619 5 09VA04 09VA04 drosophila
990 6 2.6 622 16 092PP2 092PP2 rhizobium m
991 6 2.6 632 3 09Y7A5 09Y7A5 coprinus cl
992 6 2.6 632 3 09Y7A6 09Y7A6 coprinus cl
993 6 2.6 635 5 09VUK7 09VUK7 drosophila
994 6 2.6 635 12 069087 069087 human herpe
995 6 2.6 638 2 092389 092389 streptomyce
996 6 2.6 638 11 09D5P1 09D5P1 mus musculu
997 6 2.6 642 12 098310 098310 molluscum c
998 6 2.6 643 4 09NWL6 09NWL6 homo sapien
999 6 2.6 652 2 09F5N2 09F5N2 rhizobium m
1000 6 2.6 652 5 09VCK9 09VCK9 drosophila

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## ALIGNMENTS

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RESULT 1
ID 09W2B6 PRELIMINARY: PRT: 109 AA.
AC 09W2B6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CG13494 PROTEIN.
CN CG13494.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunlov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostreli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003455; AAF46776.1; -.
DR HSSP; P01180; IMPO.
DR Flybase; FBgn0034671; CG13494.
SQ SEQUENCE 109 AA; 10413 MW; 84E0A6C087990895 CRC64;

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Query Match 3.48; Score 8; DB 5; Length 109;
Best Local Similarly 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 220 VGIIVLY 227
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Db 27 VGIIVLY 34

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RESULT 2
ID 09HA66 PRELIMINARY: PRT: 217 AA.
AC 09HA66;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ12165 FTS, CLONE MAMMA1000612, MODERATELY SIMILAR TO HOMO
DE SAPIENS G. PROTEIN BETA SUBUNIT MRNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Issogal T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA Niimiya K., Iwayanagi T.;
RT "MEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AK022227; BAB13990.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 4.
DR PRINTS; PR00320; GPROTEINBRP.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00578; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS50082; WD_REPEATS_2; 2.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.

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SQ SEQUENCE 217 AA; 23817 MW; 31600C65FBE99DA3 CRC64;

Query Match 3.4%; Score 8; DB 4; Length 217;

Best Local Similarity 100.0%; Pred. No. 3.8; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 TMNTSPT 148  
Db 19 TMNTSPT 26

RESULT 3  
092704 PRELIMINARY; PRT; 464 AA.  
AC 092704;  
DT 01-MAY-1999 (TREMblrel. 10, Created)  
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE TRANSCRIPTION TERMINATION FACTOR.  
GN RHO OR CPN0610 OR CP0137.  
OS Chlamydia pneumoniae (Chlamydia phila pneumoniae).  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83558;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CML029;  
RX MEDLINE=99206606; PubMed=10192388;  
RA Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=AR39;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Baas S.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
RA Galim M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,  
RA Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis Mofn and Chlamydia pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).  
RL [3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=J138;  
RX MEDLINE=20330349; PubMed=10871362;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CML029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).  
RL Nucleic Acids Res. 28:2311-2314(2000).  
CC -1- SIMILARITY: TO ATPASE ALPHA/BETA CHAINS FAMILY.  
DR EMBL: AE001645; AAD18749.1; -;  
DR EMBL: AE002175; AAF38020.1; -;  
DR EMBL: AP002547; BAA98817.1; -;  
DR HSSP: P03002; 1A8V.  
DR PRCI-2DPAGE; Q92704; -;  
DR TIGR: CP0137; -;  
DR InterPro: IPR000194; ATPase\_alpha\_beta.  
DR InterPro: IPR002059; Cold\_shock.  
DR Pfam: PF00006; ATP-synt\_ab; 1.  
DR SMART: SM00357; CSP; 1.  
KW Complete proteome; Hydrogen ion transport; Hydrolyase.  
SQ SEQUENCE 464 AA; 51818 MW; D00F6001AB6BC18 CRC64;

Query Match 3.4%; Score 8; DB 16; Length 464;  
Best Local Similarity 100.0%; Pred. No. 7.4; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 223 IVLIVLLI 230

Db 248 IVLIVLLI 255

RESULT 4  
096E62 PRELIMINARY; PRT; 468 AA.  
AC 096E62;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE SIMILAR TO TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 10A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY, AND ADENOCARCINOMA;  
RA Strausberg R.;  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC012866; AAH12866.1; -;  
KW Receptor.  
SQ SEQUENCE 468 AA; 50061 MW; 7E9661859A550CD4 CRC64;

Query Match 3.4%; Score 8; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 7.5; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 EMCRCR 104  
Db 202 EMCRCR 209

RESULT 5  
092DD2 PRELIMINARY; PRT; 494 AA.  
AC 092DD2;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE LIN0882 PROTEIN.  
GN LIN0882.  
OS Listeria innocua.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1642;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIP 11262 / SEROVAR 6A;  
RX PubMed=11679669;  
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,  
RA Charbit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,  
RA Domann E., Dominguez-Bernal G., Duchaud E., Duranti L., Dussurget O.,  
RA Entian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,  
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,  
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,  
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,  
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,  
RA Vazquez-Holand J.-A., Voss H., Wehlund J., Cossart P.;  
RT "Comparative genomics of Listeria species."; Science 294:849-852(2001).  
RL EMBL: AL596166; CAC96114.1; -;  
DR Listlist; LIN00882; -;  
KW Complete proteome.  
SQ SEQUENCE 494 AA; 56324 MW; 90CFE64DE83B0A00 CRC64;

Query Match 3.4%; Score 8; DB 16; Length 494;

Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIVL 228  
|||||  
Db 231 GIIVLIVL 238

## RESULT 6

O9JWP0 PRELIMINARY; PRT; 685 AA.  
AC O9JWP0;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10).  
GN MEG OR NMA0275.  
OS Neisseria meningitidis (serogroup A).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=65699;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;  
RX MEDLINE=20222556; PubMed=10761919;  
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,  
RA Jørgels K., Leather S., Moule S., Mungall K., Quail M.A.,  
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
RA Whitehead S., Spratt B.G., Barrall B.G.;  
RT "Complete DNA sequence of a serogroup A strain of Neisseria  
RT meningitidis Z2491."  
RL Nature 404:502-506(2000).  
DR EMBL; AL162752; CAB83583.1; -.  
DR HSSP; P00959; 1MEA.  
DR InterPro: IPR001412; tRNA-synt\_1.  
DR InterPro: IPR002304; tRNA-synt\_met.  
DR InterPro: IPR002547; tRNA\_bind.  
DR Pfam; PF01588; tRNA\_bind; 1.  
DR PRINTS; PRO1041; TRNASYNTHET.  
DR POSITIVE; PS00178; AA\_TRNA\_LIGASE\_I; 1.  
KW Aminoacyl-tRNA synthetase; Ligase; Complete proteome.  
SQ SEQUENCE 685 AA; 76984 MW; 07FDA5915ED3BEF3 CRC64;

Query Match 3.4%; Score 8; DB 16; Length 685;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAE 155  
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Db 561 TPAPAE 568

## RESULT 7

O23635 PRELIMINARY; PRT; 801 AA.  
AC O23635;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE ZK84.1 PROTEIN.  
GN ZK84.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodermidae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Alnough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laiter N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans."  
RL Nature 368:32-38(1994).

RM [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Kirsten J.;  
RT "The sequence of C. elegans cosmid ZK84."  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U23181; AAC48204.1; -.  
SQ SEQUENCE 801 AA; 77123 MW; 070D8F085A71EF28 CRC64;

Query Match 3.4%; Score 8; DB 5; Length 801;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEET 156  
|||||  
Db 267 PAPAEET 274

## RESULT 8

O9V5T2 PRELIMINARY; PRT; 100 AA.  
AC O9V5T2;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
DE CG13231 PROTEIN.  
GN CG13231.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.

RC MEDLINE=20196006; PubMed=10731132;  
RX STRAIN-BERKELEY;  
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang O., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Adil J.F., Agbayani A., An H.-J., Andrews-Plannoch C., Baldwin D.,  
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,



RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Schaefer F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M.D., Skupski M.P., Smith T.,  
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT The genome sequence of *Drosophila melanogaster*.  
RL Science 287:2185-2195(2000).  
DR EMBL: AEO03827; AAF58716.1; -;  
DR FlyBase: FBgn0033580; CG13231.  
SQ SEQUENCE 100 AA; 10738 MW; A273705DC9F72137 CRC64;

Query Match 3.0%; Score 7; DB 5; Length 100;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 PAPAEE 155  
Db 19 PAPAEE 25

RESULT 9  
ID Q9HL72 PRELIMINARY; PRT; 106 AA.  
AC Q9HL72;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE PROBABLE 50S RIBOSOMAL PROTEIN L12.  
GN TA0358.  
OS Thermoplasma acidophilum.  
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;  
OC Thermoplasma.  
OX NCBI\_TaxID=2303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 1728;  
RX MEDLINE=20479972; PubMed=11029001;  
RA Repp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
RA Mewes H.-W., Flisman D., Stocker S., Lupas A.N., Baumeister W.;  
RT "The genome sequence of the thermacidophilic scavenger *Thermoplasma*  
RT *acidophilum*."  
RL Nature 407:508-513(2000).  
DR EMBL: AL445064; CAC11502.1; -;  
DR InterPro: IPR001813; 60s\_ribosomal.  
DR Pfam: PF00428; 60s\_ribosomal; 1.  
KW Ribosomal protein; Complete proteome.  
SQ SEQUENCE 106 AA; 11677 MW; DFB2EC1137DF478C CRC64;

Query Match 3.0%; Score 7; DB 17; Length 106;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 PAPAEE 155  
Db 66 PAPAEE 72

RESULT 10  
ID 069204 PRELIMINARY; PRT; 144 AA.  
AC 069204;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 15.4 KDA PROTEIN.

OS Actinosynnema pretiosum (subsp. auranticum).  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Pseudonocardineae; Actinosynnemataceae;  
OC Actinosynnema.  
OX NCBI\_TaxID=42198;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC31565;  
RX MEDLINE=98174059; PubMed=9512878;  
RA August P.R., Tang L., Yoon Y.J., Ning S., Mueller R., Yu T.W.,  
RA Taylor M., Hoffmann D., Kim C.G., Zhang X., Hutchinson C.R.,  
RA Floss H.G.;  
RT "Biosynthesis of the ansamycin antibiotic rifamycin: deductions from  
RT the molecular analysis of the rif biosynthetic gene cluster of  
RT *Amycolatopsis mediterranei* S699.";  
RL Chem. Biol. 5:69-79(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC31565;  
RX MEDLINE=98165773; PubMed=9497318;  
RA Kim C.G., Yu T.W., Fryhle C.B., Handa S., Floss H.G.;  
RT "3-Amino-5-hydroxybenzoic acid synthase, the terminal enzyme in the  
RT formation of the precursor of mc7N units in rifamycin and related  
RT antibiotics.";  
RL J. Biol. Chem. 273:6030-6040(1998).  
DR EMBL: U33059; AAC13999.1; -;  
DR InterPro: IPR003594; HATPase\_c.  
DR Pfam: PF02518; HATPase\_c; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 144 AA; 15360 MW; 3CF9D1669D3B4D6C CRC64;

Query Match 3.0%; Score 7; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 PGPAPA 152  
Db 15 PGPAPA 21

RESULT 11  
ID 056349 PRELIMINARY; PRT; 151 AA.  
AC 056349;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 2.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11709;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=POL;  
RA Heredia A.;  
RT "Phylogenetic analysis of circulating HIV-2 strains in Portugal.";  
RL AIDS Res. Hum. Retroviruses 0:0-0(1998).  
DR EMBL: AF039490; AAB99979.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR Pfam: PF00517; GP41; 1.  
KW Transmembrane.

FT NON\_TER 1 1  
RT NON\_TER 151 151  
SQ SEQUENCE 151 AA; 18112 MW; 8B42239D646B974B CRC64;

## Query Match

Best Local Similarity 3.0%; Score 7; DB 15; Length 151;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 IVGIIVL 225  
|||||||  
Db 129 IVGIIVL 135

## RESULT 12

O39133  
ID O39133 PRELIMINARY; PRT; 155 AA.  
AC O39133;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE MAJOR LATEX PROTEIN TYPE3 (MAJOR LATEX-LIKE PROTEIN).  
GN MLP3.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_Taxid=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COL 0;  
RA Grellier F., Cooke R., Laudie M., Raynal M., Delseny M.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COL-0;  
RA Muller S., Klime S., Hauser M.T.;  
RT "Molecular and phylogenetic analysis of a gene family in Arabidopsis  
thaliana with similarities to major latex, pathogenesis-related and  
ripening-induced proteins.";  
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: X91961; CAA63027.1; -;  
DR EMBL: AJ306138; CAC83602.1; -;  
SQ SEQUENCE 155 AA; 17879 MW; 61DC38712D035CFE CRC64;

## Query Match

Best Local Similarity 3.0%; Score 7; DB 10; Length 155;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 91 RNEENSPE 97  
|||||||  
Db 123 RNEENSPE 129

## RESULT 13

O9FNT2  
ID O9FNT2 PRELIMINARY; PRT; 158 AA.  
AC O9FNT2;  
DT 01-MAR-2001 (TREMblrel. 16, Created)  
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE RS2 PROTEIN.  
GN RS2.  
OS Beta vulgaris (Sugar beet).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.  
OX NCBI\_Taxid=3555;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, REGINA; TISSUE-STORAGE ORGAN;  
RA Fowler M.R., Gartland J., Norton W., Slater A., Elliott M.C.,

RA Scott N.W.;  
RT "Rs2: a sugar beet gene related to the latex-allergen family.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ278989; CAC18641.1; -;  
SQ SEQUENCE 158 AA; 16099 MW; 12DFB67F1AF439A0 CRC64;

Query Match  
Best Local Similarity 3.0%; Score 7; DB 10; Length 158;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEET 156  
|||||||  
Db 42 APAEET 48

## RESULT 14

O19762  
ID O19762 PRELIMINARY; PRT; 165 AA.  
AC O19762;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE F23H12.3 PROTEIN.  
GN F23H12.3.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_Taxid=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kershaw J.K.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C. elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL: Z74472; CAA98941.1; -;  
SQ SEQUENCE 165 AA; 18513 MW; 1E2C7A2653179E12 CRC64;

Query Match  
Best Local Similarity 3.0%; Score 7; DB 5; Length 165;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIV 227  
|||||||  
Db 89 GIIVLIV 95

## RESULT 15

O97WNS  
ID O97WNS PRELIMINARY; PRT; 184 AA.  
AC O97WNS;  
DT 01-OCT-2001 (TREMblrel. 18, Created)  
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)  
DE HYPOTHETICAL PROTEIN SS02176.  
GN SS02176.  
OS Sulfolobus solfataricus.  
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.  
OX NCBI\_Taxid=2287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726;  
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
Rayner M.J., Chan-Welner C.C.-Y., Clausen I.G., Curtis B.A.,  
De Moors A., Trauso G., Fletcher C., Gordon P.M.K.,  
Heikamp de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
 RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.,  
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
 DR EMBL: AE006823; AAK42351.1; -  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 184 AA; 21050 MW; 555DF2EED2172D7 CRC64;

Query Match 3.0%; Score 7; DB 17; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LVLIV 231  
 |||||  
 DB 164 LVLIV 170

RESULT 16  
 Q9RM97 PRELIMINARY; PRT; 219 AA.  
 AC Q9RM97;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE HYPOTHETICAL 22.6 KDA PROTEIN.  
 GN DR0772.  
 OS Deinococcus radiodurans.  
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.  
 OX NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RI;  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eissen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium Deinococcus  
 RT radiodurans RI.";  
 RL Science 286:1571-1577(1999).  
 DR EMBL: AE001932; AAF10355.1; -  
 DR TIGR: DR0772; -  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 219 AA; 22631 MW; 72AD261C8B37AB2F CRC64;

Query Match 3.0%; Score 7; DB 16; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 GTPAPAA 153  
 |||||  
 DB 205 GTPAPAA 211

RESULT 17  
 Q96EX2 PRELIMINARY; PRT; 231 AA.  
 AC Q96EX2;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE SIMILAR TO HYPOTHETICAL PROTEIN FLJ14627.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=MUSCLE, AND RHABDOMYOSARCOMA;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011878; AAH1878.1; -  
 SO SEQUENCE 231 AA; 25722 MW; B4D36B0360D3C57C CRC64;

Query Match 3.0%; Score 7; DB 4; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 GTPAPAA 152  
 |||||  
 DB 56 GTPAPAA 62

RESULT 18  
 Q9FT78 PRELIMINARY; PRT; 241 AA.  
 AC Q9FT78;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE P23 CO-CHAPERONE.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bower S.;  
 RT "A plant p23: the missing link suggesting glucocorticoid receptors  
 RT exist in plants.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ297951; CAC16575.1; -  
 SO SEQUENCE 241 AA; 25455 MW; 90989FE950DC3D CRC64;

Query Match 3.0%; Score 7; DB 10; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAABET 156  
 |||||  
 DB 228 APAABET 234

RESULT 19  
 Q98EG1 PRELIMINARY; PRT; 249 AA.  
 AC Q98EG1;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE M14259 PROTEIN.  
 GN M14259.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).  
 DR EMBL: AP003003; BAB50958.1; -  
 KM Complete Proteome.  
 SQ SEQUENCE 249 AA; 27855 MW; D780EDB3298A2A40 CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 16; Length 249;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 149 PAPAEE 155  
 |||||  
 Db 176 PAPAEE 182

RESULT 20  
 Q9SB18 PRELIMINARY; PRT; 255 AA.  
 AC Q9SB18;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE DEHYDRIN 8.  
 GN DHN8.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. DICKTOO;  
 RA Choi D.-W., Zhu B., Close T.J.;  
 RT "The barley (Hordeum vulgare L.) dehydrin multigene family: sequences,  
 RT chromosome assignments, and expression characteristics of 11 dhn genes  
 RT of cv. Dicktoo";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF043093; AAD02259.1; -  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2.  
 DR PROSITE: PS00823; DEHYDRIN\_2; 2.  
 SQ SEQUENCE 255 AA; 27726 MW; 08D7FAFF7F811AAF CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 10; Length 255;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 149 PAPAEE 155  
 |||||  
 Db 206 PAPAEE 212

RESULT 21  
 Q9SP4 PRELIMINARY; PRT; 255 AA.  
 AC Q9SP4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE DEHYDRIN.  
 GN DHN8.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. MOREX;  
 RA Choi D.-W., Close T.J.;  
 RT "Morex barley (Hordeum vulgare L. cv. Morex) dehydrin multigene  
 RT family";

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF181458; AAF01696.1; -  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2.  
 DR PROSITE: PS00823; DEHYDRIN\_2; 2.  
 SQ SEQUENCE 255 AA; 27670 MW; 5289E18CB420BF3B CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 10; Length 255;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 149 PAPAEE 155  
 |||||  
 Db 206 PAPAEE 212

RESULT 22  
 Q43488 PRELIMINARY; PRT; 255 AA.  
 AC Q43488;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PAF93. PROTEIN.  
 GN PAF93.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. GEORGIE; TISSUE=GREEN LEAF;  
 RA Grossi M., Gullì M., Stanca A.M., Cattivelli L.;  
 RT "Characterization of two barley genes that respond rapidly to  
 RT dehydration stress";  
 RL Plant Sci. 105:71-80(1995).  
 DR EMBL: X84056; CA58875.1; -  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2.  
 DR PROSITE: PS00823; DEHYDRIN\_2; 2.  
 SQ SEQUENCE 255 AA; 27666 MW; 49C4618BC95A77FD CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 10; Length 255;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 149 PAPAEE 155  
 |||||  
 Db 206 PAPAEE 212

RESULT 23  
 Q9VV71 PRELIMINARY; PRT; 256 AA.  
 AC Q9VV71;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CG4229. PROTEIN (LD44179P).  
 GN CG4229.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Chame M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart M.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kenison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svltkas R., Tector C., Turner R., Venter L., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein D.A., Welschbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Y, CN BW SP;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Change M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nunco J., Pacleb J., Paregas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celnik S.,  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE003527; AAF49451.1; -;  
 DR EMBL: AT061476; AAL29024.1; -;  
 DR FLYbase: FBgn0036639; CG4229.  
 DR InterPro: IPR004011; GYR.  
 DR InterPro: IPR004019; YLP.  
 DR Pfam: PF02756; GYR: 3.  
 DR Pfam: PF02757; YLP: 5.  
 SQ SEQUENCE 256 AA; 27418 MW; 10712DB970A13F5D CRC64;

Query Match 3.0%; Score 7; DB 5; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 AAPAEE 156  
 DB 165 AAPAEE 171

RESULT 24  
 Q9PD13 PRELIMINARY; PRT; 256 AA.  
 AC Q9PD13;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL PROTEIN XF1591.

GN XF1591.  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OC Xylella.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvarenga R., Alves L.M.C., Arya J.E., Bala G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Barro M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Paciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Fetto J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hohenisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madelira A.M.B.N., Madelira H.M.F., Matsukuma A.Y.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,  
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
 RA da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,  
 RA Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Zeldanis J., Zetubel J.C.,  
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";  
 RL Nature 406:151-159(2000).  
 DR EMBL: AE003987; AAF84400.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 256 AA; 27888 MW; E38B51EFD82010 CRC64;

Query Match 3.0%; Score 7; DB 16; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAAE 155  
 DB 65 PAPAAE 71

RESULT 25  
 Q9PCT1 PRELIMINARY; PRT; 256 AA.  
 AC Q9PCT1;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL PROTEIN XF1697.  
 GN XF1697.  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OC Xylella.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvarenga R., Alves L.M.C., Arya J.E., Bala G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hohelsel J.D., Junqueira M.L., Kempers E.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,  
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Truflfi D., Tsai S.M., Tsuchioka M.H.,  
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;  
 RA "The genome sequence of the plant pathogen *Xylella fastidiosa*.";  
 RL Nature 406:151-159(2000).  
 DR EMBL: AE003994; AAF84506.1; -;  
 KM Hypothetical protein, Complete proteome.  
 SQ SEQUENCE 256 AA; 27871 MW; 283DDA924DD82015 CRC64;

Query Match 3.0%; Score 7; DB 16; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
 Db 65 PAPAEE 71

RESULT 26  
 Q9P9V6 PRELIMINARY; PRT; 256 AA.  
 AC Q9P9V6;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE HYPOHETICAL PROTEIN XF2765.  
 GN XF2765.  
 OS *Xylella fastidiosa*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OC *Xylella*.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvaenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hohelsel J.D., Junqueira M.L., Kempers E.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Truflfi D., Tsai S.M., Tsuchioka M.H.,  
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;  
 RA "The genome sequence of the plant pathogen *Xylella fastidiosa*.";  
 RL Nature 406:151-159(2000).  
 DR EMBL: AE004082; AAF85550.1; -;  
 KM Hypothetical protein, Complete proteome.  
 SQ SEQUENCE 256 AA; 27887 MW; 366AB505E74097 CRC64;

Query Match 3.0%; Score 7; DB 16; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
 Db 65 PAPAEE 71

RESULT 27  
 P93608 PRELIMINARY; PRT; 259 AA.  
 ID P93608;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE COLD ACCLIMATION PROTEIN WCOR410C.  
 GN WCOR410C.  
 OS *Triticum aestivum* (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC *Triticeae*; *Triticum*.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NORSTAR; TISSUE=SHOOT;  
 RA Danyluk J., Sarhan F.;  
 RT "Identification of a gene encoding an acidic dehydrin in wheat.";  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U73211; AAB18202.1; -;  
 DR InterPro: IPR00167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2.  
 DR PROSITE: PS00823; DEHYDRIN 2; 2.  
 SQ SEQUENCE 259 AA; 27945 MW; 9B9A45D96AA05961 CRC64;

Query Match 3.0%; Score 7; DB 10; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
 Db 210 PAPAEE 216

RESULT 28  
 O81288 PRELIMINARY; PRT; 262 AA.  
 ID O81288;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE T14P8.5 OR AT4G02450.  
 GN T14P8.5 OR AT4G02450.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA WASHU;  
 RT "The A. thaliana Genome Sequencing Project."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Kallicki J., Elliott G., Cloud J.;  
 RT "The sequence of A. thaliana T14P8."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Waterston R.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF069298; AAC19287.1; -;  
 DR EMBL: AL61494; CAB80738.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 262 AA; 27944 MW; 67BBF89EEF6625D6 CRC64;

Query Match 3.0%; Score 7; DB 10; Length 262;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 PAPAEE 156  
 Db 249 APAEE 255

RESULT 29  
 Q17806 PRELIMINARY; PRT; 263 AA.  
 AC Q17806;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 GN C08A9.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardiner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thelery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Spirot J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;  
 RA Latreille P.;  
 RT "The sequence of C. elegans cosmid C08A9";  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U42844; AAB53817.1; -;  
 SQ SEQUENCE 263 AA; 30460 MW; EDF6EA44080AD135 CRC64;

Query Match 3.0%; Score 7; DB 5; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 VLIVLLI 230  
 Db 116 VLIVLLI 122

RESULT 30  
 Q9ZFB0 PRELIMINARY; PRT; 266 AA.  
 ID Q9ZFB0  
 AC Q9ZFB0;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 GN Y1B0.  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;  
 OC Rhodospirillum;  
 OX NCBI\_TaxID=1063;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-2.4.1;  
 RX MEDLINE=94442363; PubMed=10511537;  
 RA Mackenzie C., Simmons A.E., Kaplan S.;  
 RT "Multiple Chromosomes in Bacteria: The Yin and Yang of trp Gene  
 Localization in Rhodospirillum rubrum 2.4.1.";  
 RL Genetics 153:525-538(1999).  
 DR EMBL: AF108766; AAD09126.1; -;  
 SQ SEQUENCE 266 AA; 27988 MW; D45992B6BE77215D CRC64;

Query Match 3.0%; Score 7; DB 2; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAEE 155  
 Db 37 PAPAEE 43

RESULT 31  
 P93607 PRELIMINARY; PRT; 268 AA.  
 ID P93607  
 AC P93607;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 GN WCO410B.  
 OS Triticum aestivum (wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticaceae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. NORSTAR; TISSUE=SHOOT;

RA Danyluk J., Sarhan F.;  
 RT "Identification of a gene encoding an acidic dehydrin in wheat."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U73210; AAB18201.1; -;  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2;  
 DR PROSITE: PS00823; DEHYDRIN\_2; 1.  
 SQ SEQUENCE 268 AA; 28837 MW; BA8AFE7C17D1D631 CRC64;

Query Match 3.0%; Score 7; DB 10; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAAEE 155  
 |||||  
 Db 219 PAPAAEE 225

RESULT 32  
 Q988Y8 PRELIMINARY; PRT; 272 AA.  
 AC Q988Y8:  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DE ARC TRANSPORTER, POLYAMINE TRANSPORT PROTEIN, PERMEASE  
 DE PROTEIN.  
 GN MLR6537.  
 OS Rhizobium loti (Mesorhizobium loti)  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RA MEDLINE=21082930; PubMed=11214966;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno M.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti."  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL: AP003009; BAB52809.1; -;  
 DR InterPro: IPR000515; BPD\_transp.  
 DR Pfam: PF00528; BPD\_transp; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 272 AA; 29561 MW; 7B023F194CEA5DE8 CRC64;

Query Match 3.0%; Score 7; DB 16; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLLIVF 232  
 |||||  
 Db 24 IVLLIVF 30

RESULT 33  
 ID 032850 PRELIMINARY; PRT; 295 AA.  
 AC 032850:  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DE HYPOHETICAL 29.4 KDA PROTEIN (FRAGMENT).  
 GN MBE4863A.  
 OS Mycobacterium bovis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCG\_FRENCH;  
 RA Kim J.K., Choe Y.K.;  
 RT "Mycobacterium bovis BCG clone E4863."  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF009829; AAB63811.1; -;  
 DR InterPro: IPR002965; P-rich\_extensn.  
 DR PRINTS: PR01217; PRICHEXTENS.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 295 AA; 29421 MW; 04E69DF13B9A7EEC CRC64;

Query Match 3.0%; Score 7; DB 2; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QQTVAPO 16  
 |||||  
 Db 264 QQTVAPO 270

RESULT 34  
 Q93D93 PRELIMINARY; PRT; 299 AA.  
 ID Q93D93  
 AC Q93D93:  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE PROTEINASE HTPX-LIKE PROTEIN.  
 DE HTPX.  
 GN Streptococcus mutans.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1309;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT11;  
 RA Tao L., Tanzer J.M.;  
 RT "Novel sucrose-dependent adhesion cofactors (sdc) in Streptococcus  
 RT mutans."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF397166; AAL04088.1; -;  
 SQ SEQUENCE 299 AA; 32725 MW; 6409CB04766D9F8B CRC64;

Query Match 3.0%; Score 7; DB 2; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLLIVF 232  
 |||||  
 Db 14 IVLLIVF 20

RESULT 35  
 ID 050268 PRELIMINARY; PRT; 313 AA.  
 AC 050268:  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DE KOAB.  
 GN KOAB.  
 OS Agrobacterium tumefaciens.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=358;  
 RN [1]  
 RP SEQUENCE FROM N.A.



RX MEDLINE=99141607; PubMed=9987134;  
 RA Lyi S.M., Jafri S., Winans S.C.;  
 RT "Mannoplic acid and agropindic acid catabolism region of the octopine-  
 RT type Ti plasmid pT15955";  
 RL Mol. Microbiol. 31:339-347(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Winans S.C., Zhu J., Oger P.M., Schrammeyer B., Hooykaas P.J.,  
 RA Farand S.K.;  
 RT "Octopine-type Ti plasmid sequence";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF242881; AAB8473.1; -;  
 DR InterPro: IPR000515; BPD\_transp.  
 DR Pfam: PF00528; BPD\_transp.1.  
 KM Plasmid.  
 SQ SEQUENCE 313 AA; 34078 MW; 28B6D54AE94BE6C2 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLLIVF 232  
 DB 149 IVLLIVF 155

RESULT 36  
 Q9BVC4 PRELIMINARY; PRT; 326 AA.  
 AC Q9BVC4;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE SIMILAR TO G BETA-LIKE PROTEIN (HYPOTHEICAL 35.9 KDA PROTEIN).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA, CHORIOCARCINOMA;  
 RA Strausberg R.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=UTERUS, LEIOMYOSARCOMA;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL: BC01313; AA01313.1; -;  
 DR EMBL: BC017119; AA017119.1; -;  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 6.  
 DR PRINTS: PR00320; GPROTEINBRPT.  
 DR SMART: SM00320; WD40; 6.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
 DR PROSITE: PS00682; WD\_REPEATS\_2; 3.  
 DR PROSITE: PS02924; WD\_REPEATS\_REGION; 1.  
 KW Repeat; WD repeat; Hypothetical protein.  
 SQ SEQUENCE 326 AA; 35876 MW; 43A600DAEF2B6543 CRC64;

Query Match 3.0%; Score 7; DB 4; Length 326;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 MNTSPGT 148  
 DB 1 MNTSPGT 7

RESULT 37

Q96S05  
 ID Q96S05 PRELIMINARY; PRT; 330 AA.  
 AC Q96S05;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CDNA FLJ14627 FIS, CLONE NT2RP2000289.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,  
 RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,  
 RA Nakamura Y., Nagahara K., Masuno Y., Sasaki N.;  
 RT "NEDO human cDNA sequencing project";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK027533; BAB55182.1; -;  
 SQ SEQUENCE 330 AA; 36563 MW; 831A04E0693C131 CRC64;

Query Match 3.0%; Score 7; DB 4; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 PGTAPPA 152  
 DB 56 PGTAPPA 62

RESULT 38  
 Q98TD7 PRELIMINARY; PRT; 346 AA.  
 AC Q98TD7;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CCAAT/ENHANCER BINDING PROTEIN BETA.  
 GN JRC/EBPB.  
 OS Paralleichthys olivaceus (Flounder).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Pleuronectoidae; Paralleichthyidae; Paralleichthys.  
 OC NCBI\_TaxID=8255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tucker C.S., Hirono I., Aoki T.;  
 RT "Molecular cloning of CCAAT/enhancer binding proteins in Japanese  
 RT flounder Paralleichthys olivaceus, a first report of C/EBP in fish.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB049813; BAB40971.1; -;  
 DR InterPro: IPR001871; bZIP.  
 DR SMART: SM00338; BRLZ; 1.  
 SQ SEQUENCE 346 AA; 39086 MW; 2772CF80D59BEC05 CRC64;

Query Match 3.0%; Score 7; DB 13; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 PGTAPPA 152  
 DB 241 PGTAPPA 247

RESULT 39  
 Q9JY60 PRELIMINARY; PRT; 365 AA.  
 ID Q9JY60  
 AC Q9JY60;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

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DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CYTOCHROME C OXIDASE, SUBUNIT IIL.
GN NMB1723.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
ON NCB1_TaxID=491;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.U.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathesan J.,
RA Gill J., Scalapato V., Maignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002522; AAF42068.1; -.
DR TIGR; NMB1723; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; Cyt.CI.
DR InterPro; IPR002329; Cyt.CI.C.
DR Pfam; PF00034; cytochrome_c; 2.
DR PRINTS; PR00605; CYTOCHROME.CI.C.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 365 AA; 40039 MW; AF344435A51EB4A2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 365;
Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 TPAPAE 154
|111111|
Db 321 TPAPAE 327

RESULT 40
Q9J744 PRELIMINARY; PRT; 365 AA.
ID Q9J744
AC Q9J744
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PUTATIVE CYTOCHROME C.
GN NMA1977.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
ON NCB1_TaxID=65699;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Whitbread M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whithead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162757; CAB85197.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; Cyt.CI.
DR InterPro; IPR002329; Cyt.CI.C.
DR Pfam; PF00034; cytochrome_c; 2.

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DR PRINTS; PR00605; CYTOCHROME.CI.C.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 365 AA; 40011 MW; AF223552A51EB4A2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 365;
Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 TPAPAE 154
|111111|
Db 321 TPAPAE 327

RESULT 41
ID 080413 PRELIMINARY; PRT; 366 AA.
AC 080413
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MITOCHONDRIAL PHOSPHATE TRANSPORTER.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
ON NCB1_TaxID=4577;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-H84; TISSUE=ROOT;
RX MEDLINE=99364542; PubMed=10437831;
RA Takabatake R., Hata S., Taniguchi M., Kouchi H., Sugiyama T., Izui K.;
RT "Isolation and characterization of cDNAs encoding mitochondrial
RT phosphate transporters in soybean, maize, rice, and Arabidopsis.";
RL Plant Mol. Biol. 40:479-486(1999).
DR EMBL; AB016064; BAA31583.1; -.
DR InterPro; IPR001993; Mitoch-carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
SQ SEQUENCE 366 AA; 38658 MW; 7A372332D8D416CE CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 10; Length 366;
Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 TPAPAE 154
|111111|
Db 353 TPAPAE 359

RESULT 42
O79658 PRELIMINARY; PRT; 360 AA.
ID O79658
AC O79658
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CYTOCHROME B.
GN CYTB.
OS Pucrasia macrolopha (Koklass pheasant).
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Pucrasia.
ON NCB1_TaxID=9061;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=99184957; PubMed=10082609;
RX Kimball R.T., Braun E.L., Zwartjes P.W., Crowe T.M., Ligon J.D.;
RT "A molecular phylogeny of the pheasants and partridges suggests that
RT these lineages are not monophyletic.";

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RL Mol. Phylogenet. Evol. 11:38-54(1999).  
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B565) WHICH ARE NOT COVALENTLY  
CC BOUND TO THE PROTEIN (BY SIMILARITY).  
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
DR EMBL: AF028800; AAC62190.1; -  
DR InterPro: IPR000179; Cyt\_b\_b6.  
DR Pfam: PF00033; cytochrome\_b\_n; 1.  
DR PROSITE: PS00192; CYTOCHROME\_B\_HEME; 1.  
DR PROSITE: PS00193; CYTOCHROME\_B\_OO; UNKNOWN.1.  
DR Electron transport; Heme; Mitochondrion; Respiratory chain;  
KW Transmembrane.  
SQ SEQUENCE 380 AA; EF9224EAL1C491C3 CRC64;

Query Match 3.0%; Score 7; DB 8; Length 380;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLIYVLI 230  
|111111|  
DB 299 VLIYVLI 305

RESULT 43  
O9RK28 ID O9RK28 PRELIMINARY; PRT; 390 AA.  
AC O9RK28;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE HYPOTHETICAL 42.3 KDA PROTEIN.  
GN SCF15.09.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Oliver K., Harris D.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL: AL132856; CAB60469.1; -  
KM Hypothetical protein.  
SQ SEQUENCE 390 AA; 42349 MW; A21C43451BE4B92 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 146 PGTPAPA 152  
|111111|

DB 227 PGTPAPA 233

RESULT 44  
O58434 ID O58434 PRELIMINARY; PRT; 397 AA.  
AC O58434;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HYPOTHETICAL 43.6 KDA PROTEIN PH0703.  
GN PH0703.  
OS Pyrococcus horikoshii.  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-OT3;  
RX MEDLINE=98344137; PubMed=9679194;  
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Koshida N., Oguchi A.,  
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
RA Masuchi Y., Shizuya H., Kikuchi H.;  
RT "Complete sequence and gene organization of the genome of a hyper-  
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
RL DNA Res. 5:55-76(1998).  
DR EMBL: AF000003; BAA29794.1; -  
DR InterPro: IPR00265; MgtE.  
DR Pfam: PF01769; MgtE; 2.  
DR Hypothetical protein; Complete proteome.  
SQ SEQUENCE 397 AA; 43585 MW; FD4B7456F42FBBA6 CRC64;

Query Match 3.0%; Score 7; DB 17; Length 397;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 227 VLIYFV 233  
|111111|  
DB 133 VLIYFV 139

RESULT 45  
O9BJM3 ID O9BJM3 PRELIMINARY; PRT; 401 AA.  
AC O9BJM3;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CATHERSIN L-LIKE CYSTEINE PROTEINASE.  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Guilliano D.B., Blaxter M.L., Williams S.A., Lustigman S.;  
RT "Characterization of a Novel Developmentally Regulated Family of  
RT Cysteine Proteinases from Filarial Nematodes.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF331036; AAK16514.1; -  
DR HSPD: O17473; 1BMU.  
DR MEROPS: C01.055; -  
DR InterPro: IPR000668; Peptidase\_C1.  
DR InterPro: IPR000169; Thiolprol\_act\_site.  
DR Pfam: PF00112; Peptidase\_C1; 1.  
DR PRINTS: PR00705; PAPA1N.  
DR PROSITE: PS00139; THIOL\_PROTEASE\_CYS; 1.  
DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; 1.  
KM Hydrolase; Thiol protease.  
SQ SEQUENCE 401 AA; 45511 MW; 58E10CE3913A3F66 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 5; Length 401;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IYLLIVF 232  
 |||||  
 Db 5 IYLLIVF 11

RESULT 46  
 Q9CRR2 PRELIMINARY; PRT; 405 AA.  
 AC Q9CRR2;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE ADRENERGIC RECEPTOR, BETA 1 (FRAGMENT).  
 GN ADRL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shlnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Araiawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Katsukawa T., Saito R.,  
 Kadoya K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,  
 R. Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 Schriml L. M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,  
 Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilming L.,  
 Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL: AK018378; BAB31185.1; -.  
 DR MGD: MGI:87937; Adrb1.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHOOPS.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT NON TER 1 1  
 SQ SEQUENCE 405 AA; 44741 MW; 4F0F3FBB956FEF24 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 11; Length 405;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 IYLLIV 231  
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 Db 6 IYLLIV 12

RESULT 47  
 Q9FN24

ID Q9FN24 PRELIMINARY; PRT; 419 AA.  
 AC Q9FN24;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE SIMILARITY TO CHP-RICH ZINC FINGER PROTEIN.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=98162728; PubMed=9501997;  
 RA Nakamura Y., Sato S., Kaneko T., Kötani H., Asamizu E., Miyajima N.,  
 Tabata S.,  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.  
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen  
 RT physically assigned P1 clones."  
 RL DNA Res. 4:401-414(1997).  
 DR EMBL: AB007644; BAB10733.1; -  
 DR InterPro: IPR002219; DAG\_PE-bind.  
 DR InterPro: IPR002215; Serpin.  
 DR SMART: SM00109; C1; 4.  
 DR PROSITE: PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE: PS00284; SERPIN; UNKNOWN.1.  
 SQ SEQUENCE 419 AA; 48481 MW; B38FLA57A45645C5 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 10; Length 419;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KCSRCPs 107  
 |||||  
 Db 227 KCSRCPs 233

RESULT 48  
 ID 017854 PRELIMINARY; PRT; 450 AA.  
 AC 017854;  
 DT 01-JAN-1998 (TReMBLrel. 05, Created)  
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE F28G4.4 PROTEIN.  
 GN F28G4.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Rhabditidae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wall M.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL: Z93381; CAB07607.1; -.  
 SQ SEQUENCE 450 AA; 52757 MW; 498F8D9286FEF8F1 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 5; Length 450;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 VLYVLI 230  
 |||||

Db 11 VLIVL1 17

RESULT 49

ID Q9H7M8 PRELIMINARY; PRT; 452 AA.

AC Q9H7M8;

DT 01-MAR-2001 (TREMblrel. 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE FLJ00042 PROTEIN (FRAGMENT).

GN FLJ00042.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SPLEN;

RA Ohara O., Nagase T., Kikuno R., Okumura K.;

RT "The nucleotide sequence of a long cDNA clone isolated from human

RT spleen."

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK024450; BAB15740.1; -.

DR InterPro; IPR001806; Ras\_transf.

DR PRINTS; PRO0449; RASTRNSFRMG.

DR SMART; SM00010; small\_GTPase; 1.

KM CTP-binding.

FT NON\_TER

SQ SEQUENCE 452 AA; 48320 MW; FD10D84EA1652B7 CRC64;

Query Match

Best Local Similarity 3.0%; Score 7; DB 4; Length 452;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQOQRHS 21

Db 39 PQOQRHS 45

RESULT 50

Q9AY47

AC Q9AY47;

DT 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE PUTATIVE NUCLEIC ACID BINDING PROTEIN.

GN OSJNBA0027P10.5.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI\_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Hsiao J.,

RA Zisman V., Pal G., Bowman C.L., Fujii C.Y., Vanaken S.E., Craven B.,

RA Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L.,

RA Fraser C.M.;

RT "Oryza sativa chromosome 10 BAC OSJNBA0027P10 genomic sequence."

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC084763; AAC60186.1; -.

DR InterPro; IPR004087; KH.

DR Pfam; PF00013; KH-domain; 3.

DR SMART; SM00322; KH; 3.

DR PROSITE; PSS0084; KH\_TYPE\_1; 3.

SQ SEQUENCE 458 AA; 48410 MW; 671AAACD8E75446D CRC64;

Query Match 3.0%; Score 7; DB 10; Length 458;

Best Local Similarity 100.0%; Pred. No. 80;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAEE 155

Db 20 PAPAEE 26

Search completed: August 13, 2002, 08:42:13  
Job time: 231 sec

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